

NOV 24 2000
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SEQUENCE LISTING

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<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
 INVOLVED IN GENETIC STABILITY, GENE EXPRESSION,
 AND PROTEIN SECRETION AND FOLDING

<130> BGI-127CP

<140> 09/602,839

<141> 2000-06-23

<150> 60/141031

<151> 1999-06-25

<150> 60/143752

<151> 1999-07-14

<150> 60/151671

<151> 1999-08-08

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<223> RXA01278

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ctt aag gat cta aac aag gtc cgc aac atc ggc atc atg gcg cac atc 163
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gat gct ggt aag acc acg acc acc gaa cgc atc ctc ttc tac acc ggc 211
 Asp Ala Gly Lys Thr Thr Thr Thr Glu Arg Ile Leu Phe Tyr Thr Gly
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atc aac cgt aag gtc ggt gag acc cac gac ggt ggc gca acc acc gac 259
 Ile Asn Arg Lys Val Gly Glu Thr His Asp Gly Gly Ala Thr Thr Asp

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Phe Gly Lys Leu Thr Phe Val Arg Leu Tyr Ser Gly Lys Val Glu Pro	
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Lys Leu Phe Gln Met His Ala Asn Lys Glu Asn Pro Val Glu Val Ala	
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His Ala Gly Asn Ile Tyr Ala Phe Ile Gly Leu Lys Asp Thr Thr Thr	
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 Ala Gly Ser Gln Ala Phe Lys Glu Ala Val Ala Lys Ala Lys Pro Val
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 ctg tct cag atg ttc ggt tac gtc ggt gac ctt cgc tct aag acc cag 2131
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 ggt cgt gca aac tac tcc atg gtc ttc gat tcc tac gct gag gtc cca 2179
 Gly Arg Ala Asn Tyr Ser Met Val Phe Asp Ser Tyr Ala Glu Val Pro
 680 685 690

 gcc aac gtt gca gca gat gtt att gct gag cgc aac ggc acc gct tcc 2227
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Pro	Leu	Val	Met	Gln	Leu	Pro	Ile	Gly	Ala	Glu	Asp	Asn	Phe	Asp	Gly		
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Pro	Ile	Gly	Thr	Glu	Ala	Thr	Val	Glu	Glu	Ile	Pro	Ala	Glu	Leu	Ala		
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 Glu Pro Lys Thr Lys Ser Asp Gln Glu Lys Leu Gly Val Ala Ile Gln
 420 425 430
 Lys Leu Ala Glu Glu Asp Pro Thr Phe Thr Val His Leu Asp Asp Glu
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 Ser Gly Gln Thr Val Ile Gly Gly Met Gly Glu Leu His Leu Asp Val
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 Asp Pro Gln Val Ala Tyr Arg Glu Thr Ile Arg Lys Pro Val Glu Ser
 485 490 495
 Leu Ser Tyr Thr His Lys Lys Gln Thr Gly Gly Ser Gly Gln Phe Ala
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 Lys Val Ile Ile Thr Ile Glu Pro Tyr Ala Pro Glu Ala Asp Glu Leu
 515 520 525
 Glu Glu Gly Glu Ser Ala Ile Tyr Lys Phe Glu Asn Ala Val Thr Gly
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 Gly Arg Val Pro Arg Glu Tyr Ile Pro Ser Val Asp Ala Gly Ile Gln
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 Asp Ala Met Gln Tyr Gly Phe Leu Ala Gly Tyr Pro Leu Val Asn Val
 565 570 575
 Lys Ala Thr Leu Glu Asp Gly Ala Tyr His Asp Val Asp Ser Ser Glu
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 Met Ala Phe Lys Leu Ala Gly Ser Gln Ala Phe Lys Glu Ala Val Ala
 595 600 605
 Lys Ala Lys Pro Val Leu Leu Glu Pro Ile Met Ser Val Glu Ile Thr
 610 615 620
 Thr Pro Glu Glu Tyr Met Gly Glu Val Ile Gly Asp Val Asn Ser Arg
 625 630 635 640
 Arg Gly Gln Ile Ala Ser Met Asp Asp Arg Ala Gly Ala Lys Leu Val
 645 650 655
 Lys Ala Lys Val Pro Leu Ser Gln Met Phe Gly Tyr Val Gly Asp Leu
 660 665 670
 Arg Ser Lys Thr Gln Gly Arg Ala Asn Tyr Ser Met Val Phe Asp Ser
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695

700

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Val Glu Ile Leu Arg Val Lys Gly Ala Lys Asp Val Gly Lys Arg Ala
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gag cgt aac gct acc gaa ggt ctc gtt gca gtt tct ggc aac acc atg 307
Glu Arg Asn Ala Thr Glu Gly Leu Val Ala Val Ser Gly Asn Thr Met
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Val Glu Val Asn Ser Glu Thr Asp Phe Val Ala Lys Asn Ser Asp Phe
70 75 80 85

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Lys Glu Phe Ala Ala Lys Val Ala Asp Ala Ala Ala Ala Lys Ala
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Asn Ser Gln Glu Glu Leu Ala Ala Val Asp Val Asp Gly Gln Thr Ala
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gac gca gct ctg cag gag ttc tcc gca aag atc ggc gag aag ctt gag 499
Asp Ala Ala Leu Gln Glu Phe Ser Ala Lys Ile Gly Glu Lys Leu Glu
120 125 130

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Leu Arg Arg Ala Val Thr Leu Glu Gly Asp Lys Thr Ala Val Tyr Leu
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Ala Arg Gln Ala Ala Met Gln Ile Ala Ala Leu Lys Ala Ser Tyr Leu 180 185 190		
Thr Arg Glu Asp Val Pro Ala Glu Ile Ile Glu Lys Glu Arg Ser Ile 195 200 205		
Ala Glu Gln Ile Thr Arg Glu Glu Gly Lys Pro Glu Gln Ala Ile Pro 210 215 220		
Lys Ile Val Glu Gly Arg Leu Asn Gly Phe Tyr Lys Glu Asn Val Leu 225 230 235 240		
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 Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr Arg Val Thr Leu Val Pro
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Arg Gln Glu Ile Thr Asp Met Leu Arg Thr Asp Arg Gln Ser Thr Asp	
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Pro Thr Val Gln Ile Ala Ala Ser Ser Leu Met Gln Cys Thr Thr Asp	
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Glu Met Asp Pro Leu Ala Gly Thr Asp Asp Pro Arg Leu Pro Leu Val	
215 220 225	
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230 235 240 245	
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Leu Leu Asn Gly Glu Thr Asp Glu Glu Asn Gly Ala Arg Leu Thr Gly	
250 255 260	
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Asn Glu Ile Asp Thr Asn Arg Pro Ile Thr Gly Gly Phe Asn Ala Gln	
265 270 275	
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280 285 290	

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Leu Pro Leu Ser Phe Ala Gly Glu Asn Gly Glu Arg Gly Gly Thr Thr	
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375 380 385	
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Tyr Tyr Arg Val Phe Gly Phe Val Ser Leu Phe Thr Leu Phe Ala Ala	
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Tyr Ser Leu Asp Leu Ala Gly Ile Ala Gly Leu Ile Ile Gly Ile Gly	
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acc acc gcc gac tcc ttc gtg gtg ttc tat gag cgc atc aag gat gag	1507
Thr Thr Ala Asp Ser Phe Val Val Phe Tyr Glu Arg Ile Lys Asp Glu	
455 460 465	
atc cgt gaa gga aga tcc ttt aga tct gca gta cct cgt gca tgg gaa	1555
Ile Arg Glu Gly Arg Ser Phe Arg Ser Ala Val Pro Arg Ala Trp Glu	
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Ser Ala Lys Arg Thr Ile Val Thr Gly Asn Met Val Thr Leu Leu Gly	
490 495 500	
gct atc gtg att tac ttg ctc gcg gtc ggc gaa gtc aag ggc ttt gcc	1651
Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu Val Lys Gly Phe Ala	
505 510 515	
ttc acc ctg ggt ctg acc acc gta ttc gat ctc gtt gtc acc ttc ctg	1699
Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu Val Val Thr Phe Leu	
520 525 530	
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Ile	Thr	Ala	Pro	Leu	Val	Ile	Leu	Ala	Ser	Arg	Asn	Pro	Phe	Phe	Ala		
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Lys	Ser	Ser	Val	Asn	Gly	Met	Gly	Arg	Val	Met	Lys	Leu	Val	Glu	Glu		
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cgc	cgc	gcc	aac	ggc	gaa	ttg	gat	gag	cct	gag	tac	ctg	aaa	aag	atc	1843	
Arg	Arg	Ala	Asn	Gly	Glu	Leu	Asp	Glu	Pro	Glu	Tyr	Leu	Lys	Lys	Ile		
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cat	gcc	aag	aat	gcg	gca	gct	gat	aag	gct	tcc	act	gac	aat	tct	tcc	1891	
His	Ala	Lys	Asn	Ala	Ala	Ala	Asp	Lys	Ala	Ser	Thr	Asp	Asn	Ser	Ser		
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act	gac	aat	tct	gaa	gca	cct	ggc	acc	gat	acg	aac	caa	gag	gag	gag	1939	
Thr	Asp	Asn	Ser	Glu	Ala	Pro	Gly	Thr	Asp	Thr	Asn	Gln	Glu	Glu	Glu		
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Lys																	

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Val	Thr	Leu	Val	Pro	Gln	Gly	Gln	Asp	Pro	Thr	Gln	Asp	Gln	Leu	Asn		
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Gln	Ala	Arg	Thr	Ile	Leu	Glu	Asn	Arg	Val	Asn	Gly	Met	Gly	Val	Ser		
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Gly	Ala	Ser	Val	Val	Ala	Asp	Gly	Asn	Thr	Leu	Val	Ile	Thr	Val	Pro		
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Gly	Glu	Asn	Thr	Ala	Gln	Ala	Gln	Ser	Leu	Gly	Gln	Thr	Ser	Gln	Leu		
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Ile	Thr	Glu	Glu	Gln	Ala	Asn	Ala	Ser	Leu	Glu	Glu	Met	Asn	Thr	Ala		
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Val	Ala	Ser	Thr	Thr	Ala	Val	Glu	Gly	Glu	Glu	Ala	Thr	Glu	Pro	Glu		
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Pro	Val	Thr	Val	Ser	Ala	Thr	Pro	Met	Asp	Glu	Pro	Ala	Asn	Ser	Ile		

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Glu	Ala	Thr	Gln	Arg	Arg	Gln	Glu	Ile	Thr	Asp	Met	Leu	Arg	Thr	Asp				
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Arg	Gln	Ser	Thr	Asp	Pro	Thr	Val	Gln	Ile	Ala	Ala	Ser	Ser	Leu	Met				
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Gln	Cys	Thr	Thr	Asp	Glu	Met	Asp	Pro	Leu	Ala	Gly	Thr	Asp	Asp	Pro				
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Arg	Leu	Pro	Leu	Val	Ala	Cys	Asp	Pro	Ala	Val	Gly	Gly	Val	Tyr	Val				
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Leu	Asp	Pro	Ala	Pro	Leu	Leu	Asn	Gly	Glu	Thr	Asp	Glu	Glu	Asn	Gly				
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Ala	Arg	Leu	Thr	Gly	Asn	Glu	Ile	Asp	Thr	Asn	Arg	Pro	Ile	Thr	Gly				
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Gly	Phe	Asn	Ala	Gln	Ser	Gly	Gln	Met	Glu	Ile	Ser	Phe	Ala	Phe	Lys				
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Gln	Tyr	Leu	Gln	Gln	Gln	Ile	Ala	Ile	Thr	Leu	Asp	Ser	Gln	Val	Ile				
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Thr	Leu	Phe	Ala	Ala	Gly	Val	Leu	Val	Tyr	Gly	Leu	Leu	Val	Leu	Leu				
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Gly	Arg	Trp	Ile	Gly	Tyr	Ser	Leu	Asp	Leu	Ala	Gly	Ile	Ala	Gly	Leu				
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Arg	Ile	Lys	Asp	Glu	Ile	Arg	Glu	Gly	Arg	Ser	Phe	Arg	Ser	Ala	Val				
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Pro	Arg	Ala	Trp	Glu	Ser	Ala	Lys	Arg	Thr	Ile	Val	Thr	Gly	Asn	Met				
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Val Thr Leu Leu Gly Ala Ile Val Ile Tyr Leu Leu Ala Val Gly Glu
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Val Lys Gly Phe Ala Phe Thr Leu Gly Leu Thr Thr Val Phe Asp Leu
515 520 525

Val Val Thr Phe Leu Ile Thr Ala Pro Leu Val Ile Leu Ala Ser Arg
530 535 540

Asn Pro Phe Phe Ala Lys Ser Ser Val Asn Gly Met Gly Arg Val Met
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Lys Leu Val Glu Glu Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu
565 570 575

Tyr Leu Lys Lys Ile His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser
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Phe Val Leu Ile Val Val Gly Val Tyr Ala Leu Val Leu Leu Thr Gly
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gat cgt tct gcc aca cca aaa ttg ggt att gat ctg caa ggc gga acc 144
Asp Arg Ser Ala Thr Pro Lys Leu Gly Ile Asp Leu Gln Gly Gly Thr
35 40 45

cga gtg acc ctc gtg ccg cag ggg cag gat cca act cag gac cag ctg 192
Arg Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu
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aat cag gca cgc acc att ctg gaa aac cgt gtg aac ggc atg ggc gtt 240
Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val
65 70 75 80

tca ggt gca agc gtg gtc gct gac ggt aac acg ctg gtg atc act gtt 288
Ser Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val
85 90 95

ccc ggg gaa aat acc gca cag gcg caa tcc cta gga cag acc tcc cag 336
 Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln
 100 105 110

ctg ctg ttc cgt ccc gtt ggt cag gca gga atg ccc gat atg acc acg 384
 Leu Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr
 115 120 125

ttg atg cca gag ctg gaa gag atg gcc aac agg tgg gtt gaa tac ggc 432
 Leu Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly
 130 135 140

gtc atc acc gaa gag cag gca aat gcc tcc ttg gag gaa atg aac acc 480
 Val Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr
 145 150 155 160

gct gtt gca tcg acc act gcg gtg gaa ggc gaa gaa gca act gag cca 528
 Ala Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro
 165 170 175

gaa ccc gtc acc gtg tcg gcg acc cct atg gat gag cca gcc aac tcc 576
 Glu Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser
 180 185 190

att gag gca aca cag cga cgc cag gaa atc acg gac atg ctg cgc acc 624
 Ile Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr
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 35 40 45

Arg Val Thr Leu Val Pro Gln Gly Gln Asp Pro Thr Gln Asp Gln Leu
 50 55 60

Asn Gln Ala Arg Thr Ile Leu Glu Asn Arg Val Asn Gly Met Gly Val
 65 70 75 80

Ser Gly Ala Ser Val Val Ala Asp Gly Asn Thr Leu Val Ile Thr Val
 85 90 95

Pro Gly Glu Asn Thr Ala Gln Ala Gln Ser Leu Gly Gln Thr Ser Gln
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Leu Leu Phe Arg Pro Val Gly Gln Ala Gly Met Pro Asp Met Thr Thr

115	120	125
Leu Met Pro Glu Leu Glu Glu Met Ala Asn Arg Trp Val Glu Tyr Gly		
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Val Ile Thr Glu Glu Gln Ala Asn Ala Ser Leu Glu Glu Met Asn Thr		
145	150	155
Ala Val Ala Ser Thr Thr Ala Val Glu Gly Glu Glu Ala Thr Glu Pro		
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Glu Pro Val Thr Val Ser Ala Thr Pro Met Asp Glu Pro Ala Asn Ser		
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Ile Glu Ala Thr Gln Arg Arg Gln Glu Ile Thr Asp Met Leu Arg Thr		
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Asp Arg Gln Ser Thr Asp Pro Thr Val		
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aag tca tcg gtc aac ggc atg gga cga gtg atg aag ctc gtt gaa gaa	96
Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu	
20 25 30	
cgc cgc gcc aac ggt gaa ttg gat gag cct gag tac ctg aaa aag atc	144
Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile	
35 40 45	
cat gcc aag aat gcg gca gct gat aag gct tcc act gac aat tct tcc	192
His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser	
50 55 60	
act gac aat tct gaa gca cct ggc acc gat acg aac caa gag gag gag	240
Thr Asp Asn Ser Glu Ala Pro Gly Thr Asp Thr Asn Gln Glu Glu Glu	
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Lys	

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Lys Ser Ser Val Asn Gly Met Gly Arg Val Met Lys Leu Val Glu Glu
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Arg Arg Ala Asn Gly Glu Leu Asp Glu Pro Glu Tyr Leu Lys Lys Ile
 35 40 45

His Ala Lys Asn Ala Ala Ala Asp Lys Ala Ser Thr Asp Asn Ser Ser
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Lys

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 Met Thr Asp Ser Gln
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act gaa tca ctg tca act cag agc gta aaa cca gcc aaa aaa cgc agt 163
 Thr Glu Ser Leu Ser Thr Gln Ser Val Lys Pro Ala Lys Lys Arg Ser
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tgg ttc aac agc ctc tac acc ggt gac ggc ggc att gac ttc atc gcc 211
 Trp Phe Asn Ser Leu Tyr Thr Gly Asp Gly Gly Ile Asp Phe Ile Ala
 25 30 35

aaa acc aaa ctg tgg tac tgg atc acc ggc att ttg ctg gtt atc tcg 259
 Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile Leu Leu Val Ile Ser
 40 45 50

atc ctg ttc atc gcc atc cgt ggc ttc tcc ctg agc atc gat ttc cag 307
 Ile Leu Phe Ile Ala Ile Arg Gly Phe Ser Leu Ser Ile Asp Phe Gln
 55 60 65

ggc ggt acc aag atg agc atg cca gca tcg gat tac tcc acc gaa cag 355
 Gly Gly Thr Lys Met Ser Met Pro Ala Ser Asp Tyr Ser Thr Glu Gln
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gtg gag gaa acc ttt act gaa gcc acc ggc att act ccg gaa atc gtg 403
 Val Glu Glu Thr Phe Thr Glu Ala Thr Gly Ile Thr Pro Glu Ile Val
 90 95 100

cag atc gtc ggt tcc ggc gac gcc cgc acc ctg gag atc tac tcc gag	451
Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu Glu Ile Tyr Ser Glu	
105 110 115	
cga ctc agc gat gag gat gta gaa aaa gcc cgc ctg gcg atc tac gag	499
Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg Leu Ala Ile Tyr Glu	
120 125 130	
gaa tac caa ccc cta aac tct gag ggc cag cca agc cca gat gcc atc	547
Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro Ser Pro Asp Ala Ile	
135 140 145	
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Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser Thr Ile Thr Gln Arg	
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Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile Ala Ala Ile Tyr Ile	
170 175 180	
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Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala Ala Met Ala Ala Leu	
185 190 195	
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Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr Ala Val Ile Gly Leu	
200 205 210	
gaa gta tcc cca gca acc gtc atc ggt ctg ctc acc gtg ctg acc ttc	787
Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu Thr Val Leu Thr Phe	
215 220 225	
tcc atc tac gac acc gtc gtg gtc ttt gac aag gtc aga gaa aac acc	835
Ser Ile Tyr Asp Thr Val Val Val Phe Asp Lys Val Arg Glu Asn Thr	
230 235 240 245	
gaa ggc ttc gaa ggc agc cgc aga cga acc tac gcc gaa caa gcc aac	883
Glu Gly Phe Glu Gly Ser Arg Arg Arg Thr Tyr Ala Glu Gln Ala Asn	
250 255 260	
ctg gcg gtc aac cag acc ttc atg cgt tcg atc tcc acg aca atc atc	931
Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile Ser Thr Thr Ile Ile	
265 270 275	
tct gca ctt ccg atc atc gct ttg atg gtt gtc gcc gtc tgg atg atg	979
Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val Ala Val Trp Met Met	
280 285 290	
ggt gtt ggc acc ctc aaa gac ctc gca ctg atc cag ctg atc ggc gtc	1027
Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile Gln Leu Ile Gly Val	
295 300 305	
atc gaa ggc acc ttc tcc tcc gtc ttc ctg gca acc cca ctg ctg gtc	1075
Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala Thr Pro Leu Leu Val	
310 315 320 325	
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Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala His Thr Ala Ser Val	
330 335 340	

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Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile Asp Ala Thr Pro His
345 350 355

acc aac gcc gac gcc ttc gcg cac ggc acc gaa agc gac act gac ggt 1219
Thr Asn Ala Asp Ala Phe Ala His Gly Thr Glu Ser Asp Thr Asp Gly
360 365 370

gtg acc ccc gaa gca cct gca aaa cgt aca gta agc aaa ccc att gtg 1267
Val Thr Pro Glu Ala Pro Ala Lys Arg Thr Val Ser Lys Pro Ile Val
375 380 385

gat gat cac cga tca agc gga acc tgg cga cca ggc aga agc 1309
Asp Asp His Arg Ser Ser Gly Thr Trp Arg Pro Gly Arg Ser
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Ile Asp Phe Ile Ala Lys Thr Lys Leu Trp Tyr Trp Ile Thr Gly Ile
35 40 45

Leu Leu Val Ile Ser Ile Leu Phe Ile Ala Ile Arg Gly Phe Ser Leu
50 55 60

Ser Ile Asp Phe Gln Gly Gly Thr Lys Met Ser Met Pro Ala Ser Asp
65 70 75 80

Tyr Ser Thr Glu Gln Val Glu Glu Thr Phe Thr Glu Ala Thr Gly Ile
85 90 95

Thr Pro Glu Ile Val Gln Ile Val Gly Ser Gly Asp Ala Arg Thr Leu
100 105 110

Glu Ile Tyr Ser Glu Arg Leu Ser Asp Glu Asp Val Glu Lys Ala Arg
115 120 125

Leu Ala Ile Tyr Glu Glu Tyr Gln Pro Leu Asn Ser Glu Gly Gln Pro
130 135 140

Ser Pro Asp Ala Ile Gly Asn Ser Thr Val Ser Glu Ser Trp Gly Ser
145 150 155 160

Thr Ile Thr Gln Arg Met Val Leu Ala Leu Ile Ala Phe Leu Val Ile
165 170 175

Ala Ala Ile Tyr Ile Ala Phe Arg Leu Glu Arg Glu Met Ala Ile Ala
180 185 190

Ala Met Ala Ala Leu Val Val Asp Gly Ile Val Ile Ala Gly Ile Tyr
 195 200 205

Ala Val Ile Gly Leu Glu Val Ser Pro Ala Thr Val Ile Gly Leu Leu
 210 215 220

Thr Val Leu Thr Phe Ser Ile Tyr Asp Thr Val Val Val Phe Asp Lys
 225 230 235 240

Val Arg Glu Asn Thr Glu Gly Phe Glu Gly Ser Arg Arg Arg Thr Tyr
 245 250 255

Ala Glu Gln Ala Asn Leu Ala Val Asn Gln Thr Phe Met Arg Ser Ile
 260 265 270

Ser Thr Thr Ile Ile Ser Ala Leu Pro Ile Ile Ala Leu Met Val Val
 275 280 285

Ala Val Trp Met Met Gly Val Gly Thr Leu Lys Asp Leu Ala Leu Ile
 290 295 300

Gln Leu Ile Gly Val Ile Glu Gly Thr Phe Ser Ser Val Phe Leu Ala
 305 310 315 320

Thr Pro Leu Leu Val Ser Leu Lys Asn Arg Leu Ser Lys Thr Lys Ala
 325 330 335

His Thr Ala Ser Val Met Lys Leu Arg Asp Gly Gln Ser Thr Leu Ile
 340 345 350

Asp Ala Thr Pro His Thr Asn Ala Asp Ala Phe Ala His Gly Thr Glu
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 Val Ala Gly Phe Asp
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Trp	Phe	Trp	Lys	Ala	Leu	Gly	Gly	Lys	Ser	Gly	Arg	Asn	Gln	Lys	Arg	
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agc	gtg	gca	att	gtc	aat	cag	gta	gaa	aac	cat	gca	gcg	gaa	tta	gac	211
Ser	Val	Ala	Ile	Val	Asn	Gln	Val	Glu	Asn	His	Ala	Ala	Glu	Leu	Asp	
			25					30					35			
gcg	ctg	gat	gat	gtt	gca	ttg	gcg	cag	cgt	gcc	aag	gat	cta	gcc	agt	259
Ala	Leu	Asp	Asp	Val	Ala	Leu	Ala	Gln	Arg	Ala	Lys	Asp	Leu	Ala	Ser	
		40					45					50				
ggc	gga	cg	att	gac	aat	cat	gcg	gaa	ttc	ctc	gcc	att	ttg	ggc	gtg	307
Gly	Gly	Arg	Ile	Asp	Asn	His	Ala	Glu	Phe	Leu	Ala	Ile	Leu	Gly	Val	
	55					60					65					
gca	tcg	cag	cg	aca	ttg	ggg	ctg	aag	ccg	tat	ccg	gtg	caa	tca	cag	355
Ala	Ser	Gln	Arg	Thr	Leu	Gly	Leu	Lys	Pro	Tyr	Pro	Val	Gln	Ser	Gln	
	70				75					80					85	
gcg	gtg	ttg	cgt	ctc	att	gaa	ggc	gat	gtg	gtg	cac	atg	gct	acc	ggc	403
Ala	Val	Leu	Arg	Leu	Ile	Glu	Gly	Asp	Val	Val	His	Met	Ala	Thr	Gly	
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Glu	Gly	Lys	Thr	Leu	Val	Gly	Ala	Met	Ala	Ala	Thr	Gly	Leu	Gly	Leu	
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Met	Gly	Lys	Arg	Val	His	Ser	Ile	Thr	Val	Asn	Asp	Tyr	Leu	Ala	Val	
		120					125					130				
cg	gat	gcc	gaa	tgg	atg	cg	cca	ttg	gtc	gaa	ttt	ttc	ggc	ctg	agc	547
Arg	Asp	Ala	Glu	Trp	Met	Arg	Pro	Leu	Val	Glu	Phe	Phe	Gly	Leu	Ser	
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Tyr	Lys	Ala	Ala	Ile	Val	Tyr	Gly	Pro	Val	Asn	Glu	Ile	Gly	Phe	Asp	
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Tyr	Ala	Thr	Met	Ala	Glu	Lys	Asn	Arg	Ala	Ile	Ile	Asp	Glu	Ile	Ala					
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 35 40 45

Lys Asp Leu Ala Ser Gly Gly Arg Ile Asp Asn His Ala Glu Phe Leu
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Ala Ile Leu Gly Val Ala Ser Gln Arg Thr Leu Gly Leu Lys Pro Tyr
 65 70 75 80

Pro Val Gln Ser Gln Ala Val Leu Arg Leu Ile Glu Gly Asp Val Val
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His Met Ala Thr Gly Glu Gly Lys Thr Leu Val Gly Ala Met Ala Ala
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Thr Gly Leu Gly Leu Met Gly Lys Arg Val His Ser Ile Thr Val Asn
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Asp Tyr Leu Ala Val Arg Asp Ala Glu Trp Met Arg Pro Leu Val Glu
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Phe Phe Gly Leu Ser Val Ala Ser Ile Ser Glu Lys Met Asp Ala Gly
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Glu Arg Arg Gln Ala Tyr Lys Ala Ala Ile Val Tyr Gly Pro Val Asn
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Glu Ile Gly Phe Asp Val Leu Arg Asp Gln Leu Ile Thr Arg Arg Glu
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Asp Ala Val Gln His Gly Ala Asp Val Ala Ile Ile Asp Glu Ala Asp
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Ser Val Leu Val Asp Glu Ala Leu Val Pro Leu Val Leu Ala Gly Asn
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Gln Pro Gly His Ala Pro Arg Gly Lys Ile Thr Asp Val Val Arg Ser
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Leu Lys Glu Asn Asp Asp Tyr Thr Ile Asp Asp Asp Arg Arg Asn Val

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 Ile His Ser Gln Ser Trp Asn Tyr Asn Lys Leu Leu Ala Asp Gln Arg
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 Val Ile Ile Asp Glu Arg Arg Glu Arg Leu Leu Asp Thr Ala Leu Ala
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 Trp Glu Glu Leu Ala Gln His Ala Pro Ala Arg Ala Ala Glu Leu Glu
 625 630 635 640
 Asp Leu Asp Gln Ser Val Arg Glu Gln Ala Ala Arg Asp Ile Met Leu
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 Tyr His Leu Asp Tyr Asn Trp Ser Glu His Leu Ala Leu Met Asp Asp
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 Val Arg Glu Ser Ile His Leu Arg Ala Ile Ala Arg Glu Thr Pro Leu
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 Asp Glu Tyr His Arg Ile Ala Val Arg Glu Phe Lys Asp Leu Ala Gln
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 Arg Ala Val Asp Asp Ala Val Ser Thr Phe Lys Ser Val Thr Ile Asp
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 His Glu Gly Ala His Leu Asp Asp Glu Gly Leu Ala Arg Pro Ser Ala
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 Val Phe Glu Ser Leu
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 Ser Asp Arg Leu Asn Ser Ala Leu Ser Gly Leu Arg Gly Lys Gly Lys
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Thr Leu Glu Asp Phe Leu Asp Gln Met Leu Met Ile Arg Arg Met Gly	
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Ser Glu Val Asn Lys Leu Val Glu Arg Phe Phe Glu Ala Arg Lys Met	
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atg ggt caa atg gct ggc cag ttt ggc atg ggt cct gga tcc cgc agt	1459
Met Gly Gln Met Ala Gly Gln Phe Gly Met Gly Pro Gly Ser Arg Ser	
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Ala Thr Lys Lys Gln Ala Lys Gly Arg Lys Gly Lys Asn Gly Lys Arg	
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aaa cca gcc aag aag ggc cca acc cag cca aag atg cca atg ggc ggt	1555
Lys Pro Ala Lys Lys Gly Pro Thr Gln Pro Lys Met Pro Met Gly Gly	
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Met Pro Gly Met Pro Gly Met Pro Gly Met Gly Gly Ala Gly Met Pro	
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gac ctt gct gaa cta cag aag cag ctt ggt gga gca ggt ggc ggt atg	1651
Asp Leu Ala Glu Leu Gln Lys Gln Leu Gly Gly Ala Gly Gly Gly Met	
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 Gly Gly Leu Gly Gly Gly Leu Pro Gly Met Pro Lys Pro Pro Lys Gly
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atg gag aac ata gat ctc aac aac cta gac ttc ggt aag aag 1741
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Arg Ala Phe Ile Asn Arg Ile Lys Glu Arg Ala Ala Gly Ala Glu Val
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Ser Gln Ala Leu Asn Pro Ala Gln Gln Val Ile Lys Ile Val Asn Glu
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Glu Leu Val Gln Ile Leu Gly Gly Glu Thr Arg Arg Leu Ser Leu Ala
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Lys Asn Pro Pro Thr Val Ile Met Leu Ala Gly Leu Gln Gly Ala Gly
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Lys Thr Thr Leu Ala Gly Lys Leu Ser Lys His Leu Val Lys Gln Gly
 115 120 125

His Thr Pro Met Leu Val Ala Cys Asp Leu Gln Arg Pro Gly Ala Val
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Gln Gln Leu Gln Ile Val Gly Glu Arg Ala Gly Val Thr Thr Phe Ala
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Pro Asp Pro Gly Thr Ser Ile Asp Ser Leu Glu His Glu Met Gly Thr
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Ser His Gly Asp Pro Val Glu Val Ala Arg Ala Gly Ile Glu Glu Ala
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Lys Arg Thr Gln His Asp Ile Val Ile Val Asp Thr Ala Gly Arg Leu
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Gly Ile Asp Glu Thr Leu Met Thr Gln Ala Arg Asn Ile Arg Glu Ala
 210 215 220

Ile Asn Pro Asp Glu Val Leu Phe Val Ile Asp Ser Met Ile Gly Gln
 225 230 235 240

Asp Ala Val Asp Thr Ala Glu Ala Phe Arg Asp Gly Val Asp Phe Thr
 245 250 255
 Gly Val Val Leu Thr Lys Leu Asp Gly Asp Ala Arg Gly Gly Ala Ala
 260 265 270
 Leu Ser Ile Arg Glu Val Thr Gly Lys Pro Ile Met Phe Ala Ser Thr
 275 280 285
 Gly Glu Lys Leu Asp Asp Phe Asp Val Phe His Pro Glu Arg Met Ala
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 Ser Arg Ile Leu Gly Met Gly Asp Val Leu Ser Leu Ile Glu Gln Ala
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 Glu Ala Val Met Asp Gln Glu Lys Ala Glu Val Ala Ala Gln Lys Leu
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 Gly Ser Gly Glu Leu Thr Leu Glu Asp Phe Leu Asp Gln Met Leu Met
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 Ile Arg Arg Met Gly Pro Ile Gly Asn Ile Leu Lys Met Leu Pro Gly
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 Gly Lys Gln Met Ser Gln Met Ala Asp Met Val Asp Glu Lys Gln Leu
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 Asn Pro Lys Ile Leu Asn Ala Ser Arg Arg Lys Arg Ile Ala Asn Gly
 405 410 415
 Ser Gly Val Thr Val Ser Glu Val Asn Lys Leu Val Glu Arg Phe Phe
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 Glu Ala Arg Lys Met Met Gly Gln Met Ala Gly Gln Phe Gly Met Gly
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 Pro Gly Ser Arg Ser Ala Thr Lys Lys Gln Ala Lys Gly Arg Lys Gly
 450 455 460
 Lys Asn Gly Lys Arg Lys Pro Ala Lys Lys Gly Pro Thr Gln Pro Lys
 465 470 475 480
 Met Pro Met Gly Gly Met Pro Gly Met Pro Gly Met Pro Gly Met Gly
 485 490 495
 Gly Ala Gly Met Pro Asp Leu Ala Glu Leu Gln Lys Gln Leu Gly Gly
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 Gly Lys Lys
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Val Thr Asp Phe Ser 1 5																
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Ser Ala Ser Asn Ala Asp Asp Ser Thr Gln Asp Gly Arg Pro Gly Arg 10 15 20																
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Arg Ala Gly Lys Ser Lys Lys Glu Ser Lys Pro Thr Pro Trp Tyr Ile 25 30 35																
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Glu Ile Pro Val Val Val Val Leu Thr Leu Ala Leu Ile Phe Val Leu 40 45 50																
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Gln Thr Phe Val Gly Arg Met Tyr Met Ile Pro Ser Gly Ser Met Glu 55 60 65																
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Pro Thr Leu His Gly Cys Glu Gly Cys Thr Gly Asp Arg Ile Leu Val 70 75 80 85																
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Gly Leu Val Ala Pro Asp Glu Asn Asp Leu Val Lys Arg Ile Ile Ala 135 140 145																
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Thr Gly Gly Gln Thr Val Ser Cys Gln Ala Gly Asp Pro Gly Ile Met 150 155 160 165																
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Val Asp Gly Lys Glu Val Asp Asp Ser Tyr Thr Leu Gln Pro Ala Gln 170 175 180																

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 Phe Pro Ile Asp Glu Thr Ser Gly Ser Thr Glu Cys Gly Gly Asn Tyr
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ttc ggc ccc atc acc gtg cct ggc ggc aac tac ttc atg atg ggt gac 739
 Phe Gly Pro Ile Thr Val Pro Gly Gly Asn Tyr Phe Met Met Gly Asp
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aac cgc acc aac tcc atg gat tcc cgc tac cac ctg ggc gat cag tac 787
 Asn Arg Thr Asn Ser Met Asp Ser Arg Tyr His Leu Gly Asp Gln Tyr
 215 220 225

caa gga acc atc cct gag gaa aac atc aag ggc aaa gtt caa gca att 835
 Gln Gly Thr Ile Pro Glu Glu Asn Ile Lys Gly Lys Val Gln Ala Ile
 230 235 240 245

atc ctg cca ttt agc cga atc ggt ggc gtc gac gac cct gcc atc aaa 883
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 Gly

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 <213> *Corynebacterium glutamicum*

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Leu Ile Phe Val Leu Gln Thr Phe Val Gly Arg Met Tyr Met Ile Pro
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Ser Gly Ser Met Glu Pro Thr Leu His Gly Cys Glu Gly Cys Thr Gly
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Asp Arg Ile Leu Val Glu Lys Val Ser Tyr Tyr Phe Thr Asp Pro Glu
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Pro Gly Asp Val Val Val Phe Lys Gly Thr Asp Ser Trp Asn Val Gly
 100 105 110

Phe Thr Thr Gln Arg Ser Asp Asn Ser Val Ile Arg Gly Leu Gln Asn
 115 120 125

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Met Ser Asn Val Thr
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att tac gcc aca gat tgg tgc cct tac tgc cga tcc ctc ctc aaa ggt 163
Ile Tyr Ala Thr Asp Trp Cys Pro Tyr Cys Arg Ser Leu Leu Lys Gly
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ctc gac ggc caa gag tac gac ctc atc gac gtc gac caa gat gag gaa 211
Leu Asp Gly Gln Glu Tyr Asp Leu Ile Asp Val Asp Gln Asp Glu Glu
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gcc ggc gag tgg gtt aag tca gtc aac gac ggc aac cgc atc gtc cca 259
Ala Gly Glu Trp Val Lys Ser Val Asn Asp Gly Asn Arg Ile Val Pro
40 45 50

acc gtg cgc tac tcc gat ggc acc cac gca act aat ccc cta gct gcg 307
Thr Val Arg Tyr Ser Asp Gly Thr His Ala Thr Asn Pro Leu Ala Ala
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Met Ser Glu Gln Pro																
1 5																
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Ala Ser Ile Lys His Tyr Asp Leu Ile Ile Ile Gly Thr Gly Ser Gly																
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Asn Ser Ile Pro Gly Pro Glu Phe Asp Asp Lys Ser Ile Ala Ile Val																
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Thr Lys Met Tyr Val Tyr Ala Ala Asp Ile Ala Gln Glu Ile Gln Glu																
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Ser Ala Arg Leu Gly Ile Asp Ala Thr Val Asn Ser Val Asp Trp Pro																
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Ser Ile Val Ser Arg Val Phe Asp Lys Arg Ile Asp Leu Ile Ala Gln																

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cgc	tac	tac	acc	aac	gaa	gac	atc	atg	cgc	ctg	gca	cag	cag	cct	gaa	643				
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 Gly Leu Asp Ile Thr Val Lys Ile Gln Asn Tyr Ser Asp Val Ala Tyr
 375 380 385

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 <213> Corynebacterium glutamicum

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 35 40 45

 Val Gly Cys Ile Pro Thr Lys Met Tyr Val Tyr Ala Ala Asp Ile Ala
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 Gln Glu Ile Gln Glu Ser Ala Arg Leu Gly Ile Asp Ala Thr Val Asn
 65 70 75 80

 Ser Val Asp Trp Pro Ser Ile Val Ser Arg Val Phe Asp Lys Arg Ile
 85 90 95

 Asp Leu Ile Ala Gln Gly Gly Glu Ala Tyr Arg Arg Gly Pro Glu Thr
 100 105 110

 Pro Asn Ile Asp Val Tyr Asp Met His Ala Ser Phe Val Asp Ser Lys
 115 120 125

 Thr Ile Ser Thr Gly Ile Ala Gly Gln Glu Gln Leu Ile Ser Gly Thr
 130 135 140

 Asp Ile Val Ile Ala Thr Gly Ser Arg Pro Tyr Ile Pro Glu Ala Ile
 145 150 155 160

 Ala Glu Ser Gly Ala Arg Tyr Tyr Thr Asn Glu Asp Ile Met Arg Leu
 165 170 175

 Ala Gln Gln Pro Glu Ser Leu Val Ile Val Gly Gly Gly Phe Ile Ala
 180 185 190

Leu Glu Phe Ala His Val Phe Glu Ala Leu Gly Thr Lys Val Thr Ile
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 Leu Asn Arg Ser Asp Val Leu Leu Arg Glu Ala Asp Ala Asp Ile Ser
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 Ala Lys Ile Leu Glu Leu Ser Lys Lys Arg Phe Asp Val Arg Leu Ser
 225 230 235 240
 Thr Ala Val Thr Ala Val His Asn Lys Ala Asp Gly Gly Val Lys Ile
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 Ser Thr Asp Thr Gly Asp Asp Ile Glu Ala Asp Ile Leu Leu Val Ala
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 Thr Gly Arg Thr Pro Asn Gly Asn Gln Met Asn Leu Asp Ala Ala Gly
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 Ser Val Glu Gly Val Trp Ala Leu Gly Asp Val Ser Ser Pro Tyr Lys
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 Ala Val Phe Thr Asn Pro Gln Ile Ser Gln Val Gly Met Thr Glu Gln
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 Trp Ala Gly His Leu Leu Leu Ile Val Asn Val Ala Ser Lys Cys Gly
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 Tyr Asp Val Thr Phe Pro Leu Leu Ser Lys Thr Glu Val Asn Gly Glu
 90 95 100

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 Gly Ala His Pro Leu Tyr Lys Val Leu Lys Glu Ala Thr Asp Gly Ser
 105 110 115

gaa atc gag tgg aat ttt gag aaa ttc ctg gta gat gca gaa ggt aat 499
 Glu Ile Glu Trp Asn Phe Glu Lys Phe Leu Val Asp Ala Glu Gly Asn
 120 125 130

acg att aag cgc ttt gct cct cgg acg gaa cca tct gca gct gag gta 547
 Thr Ile Lys Arg Phe Ala Pro Arg Thr Glu Pro Ser Ala Ala Glu Val
 135 140 145

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<211> 159

<212> PRT

<213> Corynebacterium glutamicum

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Met Thr Asn Thr Leu															
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Trp Asn Ser Val Asp Glu Leu Pro Ile His Asp Ser Trp Lys Pro Val															
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 135 140 145

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 170 175 180

gcg gag ccg gat caa ccc ttg gtg gca atc ctg tgg ggt aaa caa gcc 691
 Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu Trp Gly Lys Gln Ala
 185 190 195

caa gag gta cag aaa ttc ctt gga gat acg ccg tgt atc tgc tca gtg 739
 Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro Cys Ile Cys Ser Val
 200 205 210

cac cca tca ccg ctg tcg gcg tcg aga ggc ttt ttt ggc tct aag cct 787
 His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe Phe Gly Ser Lys Pro
 215 220 225

ttt agt cgt gcg aac gaa atc tta agc agc ctc ggt gcc acc gag atc 835
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Phe Arg Ala Phe Ser Tyr Pro Phe Asp Ala Val Lys Val Leu Ile Met
 50 55 60

Gly Gln Asp Pro Tyr Pro Thr Pro Gly His Ala Met Gly Leu Ser Phe
 65 70 75 80

Ser Thr Gln Pro Asp Val Arg Pro Leu Pro Arg Ser Leu Asn Asn Ile
 85 90 95

Phe Lys Glu Leu Val Ser Asp Val Gly Ser Leu Gly Asp Ser Ala Ser
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 Glu Gln Gly Ala Leu Asp Leu Gly Ile Asn Ala Pro Gly Ser Val Ala
 115 120 125
 Gly Thr Gln Val Ala Leu Pro Ala Asp Gly Asp Leu Arg Ala Trp Ser
 130 135 140
 Asn Gln Gly Val Ala Leu Phe Asn Arg Val Leu Thr Val His Pro Gly
 145 150 155 160
 Gln Ala Gly Ser His Lys Gly Lys Gly Trp Glu Ala Val Thr Glu Gln
 165 170 175
 Ala Ile Lys Ala Leu Ala Glu Arg Asp Gln Pro Leu Val Ala Ile Leu
 180 185 190
 Trp Gly Lys Gln Ala Gln Glu Val Gln Lys Phe Leu Gly Asp Thr Pro
 195 200 205
 Cys Ile Cys Ser Val His Pro Ser Pro Leu Ser Ala Ser Arg Gly Phe
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 Val Asp Ala Thr Leu 5

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 Lys Lys Asn Leu Arg Asp Lys Gly Ile Glu Val His Ser His Pro Gly 20

ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act ccc 211
 Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr Pro 35

tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc aga 259
 Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala Arg 40 45 50

gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct cac	307
Val His Ala Tyr Glu Thr Val Lys Asn Asn Val Pro Val Pro Ser His	
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cta aca gga cca gag gat gta gag ctg ccc atc cta gaa atg gag caa	355
Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile Leu Glu Met Glu Gln	
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Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys Ala Pro Gly Glu Lys	
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Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu His Leu Gln Asp Tyr	
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Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala Thr Ser Lys Leu Ser	
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gct cat cta agg ttt ggt gag atc agc atc cac cgc gtg tgg gca gag	547
Ala His Leu Arg Phe Gly Glu Ile Ser Ile His Arg Val Trp Ala Glu	
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Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu Phe Leu Lys Glu Leu	
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Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr Ala Leu Pro His Met	
170 175 180	
gac acg caa aac gtt cgt atg caa ttt aat cgt ttc gga tgg tcc tgg	691
Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg Phe Gly Trp Ser Trp	
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Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro Ser Thr Pro Leu Ile	
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ccc acc aaa gct gac caa ttc cat gag gat tta gca gca tgg cgt gca	787
Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu Ala Ala Trp Arg Ala	
215 220 225	
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Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly Met Arg Glu Leu Trp	
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Ala Thr Gly Ser Met His Asn Arg Val Arg Met Val Val Ala Ser Phe	
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tta acc aag aat ctc cag atc cat tgg cgt cat ggc gaa gaa tgg ttt	931
Leu Thr Lys Asn Leu Gln Ile His Trp Arg His Gly Glu Glu Trp Phe	
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Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser Asn Ala Phe Asn Trp	
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Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser Pro Tyr Phe Arg Ile
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 Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr Tyr
 310 315 320 325
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 Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro Ser Tyr Pro Asp Pro
 330 335 340
 atc gtc gat ctg aaa gaa tcc cgt caa att gct tta gac gcc tac tct 1171
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 Ala Ile Lys
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 35 40 45
 Trp Glu Val Ala Arg Val His Ala Tyr Glu Thr Val Lys Asn Asn Val
 50 55 60
 Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro Ile
 65 70 75 80
 Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu Cys
 85 90 95
 Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu Glu
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 His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser Ala
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 Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile His
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 Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu Leu
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 Phe Leu Lys Glu Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu Tyr
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 Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn Arg
 180 185 190

Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr Pro
 195 200 205
 Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp Leu
 210 215 220
 Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala Gly
 225 230 235 240
 Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg Met
 245 250 255
 Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg His
 260 265 270
 Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala Ser
 275 280 285
 Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala Ser
 290 295 300
 Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp
 305 310 315 320
 Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro
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 Val His Ser His Pro
 1 5
 ggt ttt tta ctc act gaa ccc tgg gaa gtc agt acc gct acc gga act 163
 Gly Phe Leu Leu Thr Glu Pro Trp Glu Val Ser Thr Ala Thr Gly Thr
 10 15 20
 ccc tac aag gta ttt acc cct ttt tct aaa gcc gca tgg gaa gta gcc 211
 Pro Tyr Lys Val Phe Thr Pro Phe Ser Lys Ala Ala Trp Glu Val Ala
 25 30 35
 aga gta cat gca tat gaa act gtt aaa aac aat gtg cct gtc ccc tct 259

Arg	Val	His	Ala	Tyr	Glu	Thr	Val	Lys	Asn	Asn	Val	Pro	Val	Pro	Ser	
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caa	cct	ttt	tgg	tca	aca	acg	tta	gtt	aag	gag	tgt	gct	ccc	ggg	gaa	355
Gln	Pro	Phe	Trp	Ser	Thr	Thr	Leu	Val	Lys	Glu	Cys	Ala	Pro	Gly	Glu	
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Lys	Asn	Ala	Ser	Glu	Lys	Leu	Phe	Asp	Phe	Leu	Glu	His	Leu	Gln	Asp	
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Tyr	Pro	Gln	Ala	Arg	Asp	Ser	Leu	Ala	Arg	Ser	Ala	Thr	Ser	Lys	Leu	
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Ser	Ala	His	Leu	Arg	Phe	Gly	Glu	Ile	Ser	Ile	His	Arg	Val	Trp	Ala	
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Glu	Thr	Ala	Ala	Ile	Asp	Ser	Glu	Gly	Thr	Glu	Leu	Phe	Leu	Lys	Glu	
	135					140					145					
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Leu	Leu	Trp	Arg	Asp	Phe	Ala	Trp	His	Arg	Leu	Tyr	Ala	Leu	Pro	His	
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Trp	Asp	Pro	Ser	Glu	Lys	Asp	Lys	Leu	Asn	Thr	Pro	Ser	Thr	Pro	Leu	
			185					190					195			
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Ile	Pro	Thr	Lys	Ala	Asp	Gln	Phe	His	Glu	Asp	Leu	Ala	Ala	Trp	Arg	
		200					205					210				
gca	gga	aaa	aca	gga	att	ccg	ctg	gtc	gat	gca	ggc	atg	cga	gaa	tta	787
Ala	Gly	Lys	Thr	Gly	Ile	Pro	Leu	Val	Asp	Ala	Gly	Met	Arg	Glu	Leu	
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Trp	Ala	Thr	Gly	Ser	Met	His	Asn	Arg	Val	Arg	Met	Val	Val	Ala	Ser	
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ttt	tta	acc	aag	aat	ctc	cag	atc	cat	tgg	cgt	cat	ggc	gaa	gaa	tgg	883
Phe	Leu	Thr	Lys	Asn	Leu	Gln	Ile	His	Trp	Arg	His	Gly	Glu	Glu	Trp	
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ttt	tgg	gaa	act	ctc	gta	gat	gct	gat	cca	gct	tct	aat	gct	ttc	aac	931
Phe	Trp	Glu	Thr	Leu	Val	Asp	Ala	Asp	Pro	Ala	Ser	Asn	Ala	Phe	Asn	
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tgg	caa	tgg	gct	gcg	ggg	agc	gga	gat	gac	gct	tcg	cct	tat	ttc	cgt	979
Trp	Gln	Trp	Ala	Ala	Gly	Ser	Gly	Asp	Asp	Ala	Ser	Pro	Tyr	Phe	Arg	

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Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe Asp Pro Asp Glu Thr			
295	300	305	
tat att cgt cgc tgg gta ccc gaa tat gga aca cca tca tat ccg gat			1075
Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr Pro Ser Tyr Pro Asp			
310	315	320	325
ccc atc gtc gat ctg aaa gaa tcc cgt caa att gct tta gac gcc tac			1123
Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile Ala Leu Asp Ala Tyr			
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Ser Ala Ile Lys			
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<213> Corynebacterium glutamicum

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35 40 45

Val Pro Val Pro Ser His Leu Thr Gly Pro Glu Asp Val Glu Leu Pro
50 55 60

Ile Leu Glu Met Glu Gln Pro Phe Trp Ser Thr Thr Leu Val Lys Glu
65 70 75 80

Cys Ala Pro Gly Glu Lys Asn Ala Ser Glu Lys Leu Phe Asp Phe Leu
85 90 95

Glu His Leu Gln Asp Tyr Pro Gln Ala Arg Asp Ser Leu Ala Arg Ser
100 105 110

Ala Thr Ser Lys Leu Ser Ala His Leu Arg Phe Gly Glu Ile Ser Ile
115 120 125

His Arg Val Trp Ala Glu Thr Ala Ala Ile Asp Ser Glu Gly Thr Glu
130 135 140

Leu Phe Leu Lys Glu Leu Leu Trp Arg Asp Phe Ala Trp His Arg Leu
145 150 155 160

Tyr Ala Leu Pro His Met Asp Thr Gln Asn Val Arg Met Gln Phe Asn
165 170 175

Arg Phe Gly Trp Ser Trp Asp Pro Ser Glu Lys Asp Lys Leu Asn Thr
180 185 190

Pro Ser Thr Pro Leu Ile Pro Thr Lys Ala Asp Gln Phe His Glu Asp
 195 200 205
 Leu Ala Ala Trp Arg Ala Gly Lys Thr Gly Ile Pro Leu Val Asp Ala
 210 215 220
 Gly Met Arg Glu Leu Trp Ala Thr Gly Ser Met His Asn Arg Val Arg
 225 230 235 240
 Met Val Val Ala Ser Phe Leu Thr Lys Asn Leu Gln Ile His Trp Arg
 245 250 255
 His Gly Glu Glu Trp Phe Trp Glu Thr Leu Val Asp Ala Asp Pro Ala
 260 265 270
 Ser Asn Ala Phe Asn Trp Gln Trp Ala Ala Gly Ser Gly Asp Asp Ala
 275 280 285
 Ser Pro Tyr Phe Arg Ile Phe Asn Pro Val Thr Gln Ala Lys Lys Phe
 290 295 300
 Asp Pro Asp Glu Thr Tyr Ile Arg Arg Trp Val Pro Glu Tyr Gly Thr
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 Pro Ser Tyr Pro Asp Pro Ile Val Asp Leu Lys Glu Ser Arg Gln Ile
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 Ala Leu Asp Ala Tyr Ser Ala Ile Lys
 340 345

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 <223> RXA02476

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 Met Ser Phe Thr Ala
 1 5
 ttt caa aca gcc ctg ctc gtg tgg ttt aga gca aat gcc cgc gat ctt 163
 Phe Gln Thr Ala Leu Leu Val Trp Phe Arg Ala Asn Ala Arg Asp Leu
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 gcg tgg cgt gat ccc aat act tca gca tgg gga att ctc ctt tca gag 211
 Ala Trp Arg Asp Pro Asn Thr Ser Ala Trp Gly Ile Leu Leu Ser Glu
 25 30 35
 gtg atg agc caa caa act ccc gtc gcg cga gtc gag ccg att tgg cgt 259
 Val Met Ser Gln Gln Thr Pro Val Ala Arg Val Glu Pro Ile Trp Arg
 40 45 50
 gag tgg atg gaa aaa tgg ccc act ccg gaa gat ttc gcg aat gcg agc 307

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Thr	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	Gly	Tyr	Pro	Arg	Arg	
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gcg	ctg	agg	ttg	aag	gaa	tgt	gcg	gag	gtg	atc	gtc	gaa	aag	cat	gcc	403
Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	Val	Glu	Lys	His	Ala	
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ggc	gag	gtg	ccg	gat	acg	gtg	gag	gcg	ctg	ctc	gcg	ttg	ccg	ggg	atc	451
Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Gly	Ile	
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ggt	gat	tac	acg	gcg	cgc	gcg	gtc	gcg	gcg	ttt	cat	ttt	ggg	cag	cgc	499
Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	His	Phe	Gly	Gln	Arg	
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Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	Tyr	Gln	Arg	Ala	Val	
	135					140					145					
gcc	gga	cgt	tac	ctt	gcg	ggg	cct	gcg	aaa	aag	caa	gag	ctt	atc	gac	595
Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	Gln	Glu	Leu	Ile	Asp	
150					155				160					165		
gtc	tcc	ctt	ctc	ctt	ccc	aac	act	cac	gcc	cca	gaa	ttc	tct	gcc	gca	643
Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	Glu	Phe	Ser	Ala	Ala	
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Ile	Met	Glu	Leu	Gly	Ala	Leu	Ile	Cys	Thr	Ala	Thr	Ser	Pro	Lys	Cys	
			185					190					195			
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Asp	Thr	Cys	Pro	Leu	Leu	Asp	Gln	Cys	Gln	Trp	Gln	Lys	Leu	Gly	Cys	
	200						205					210				
ccc	tcc	ccg	agt	gaa	gag	gag	ctg	gct	tca	gcg	aaa	aag	cgt	gtg	cag	787
Pro	Ser	Pro	Ser	Glu	Glu	Glu	Leu	Ala	Ser	Ala	Lys	Lys	Arg	Val	Gln	
	215					220					225					
aaa	ttt	gtg	gga	acc	gac	cga	caa	gtc	cgt	ggc	cta	atc	atg	gac	gta	835
Lys	Phe	Val	Gly	Thr	Asp	Arg	Gln	Val	Arg	Gly	Leu	Ile	Met	Asp	Val	
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ctg	cgc	aat	gcc	acc	gca	cct	gtg	cca	cta	tcc	gcg	att	gat	gtc	gtg	883
Leu	Arg	Asn	Ala	Thr	Ala	Pro	Val	Pro	Leu	Ser	Ala	Ile	Asp	Val	Val	
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tgg	cct	gac	gat	gcc	caa	cgc	tcc	cgg	gcg	ctg	ttt	tcg	ctc	att	gag	931
Trp	Pro	Asp	Asp	Ala	Gln	Arg	Ser	Arg	Ala	Leu	Phe	Ser	Leu	Ile	Glu	
			265					270					275			
gac	gga	ctc	gcg	gaa	caa	aat	gag	gcg	ggt	tat	ttc	cac	ctg	cca	cgg	979
Asp	Gly	Leu	Ala	Glu	Gln	Asn	Glu	Ala	Gly	Tyr	Phe	His	Leu	Pro	Arg	
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Ile	Leu	Leu	Ser	Glu	Val	Met	Ser	Gln	Gln	Thr	Pro	Val	Ala	Arg	Val	35	40	45	
Glu	Pro	Ile	Trp	Arg	Glu	Trp	Met	Glu	Lys	Trp	Pro	Thr	Pro	Glu	Asp	50	55	60	
Phe	Ala	Asn	Ala	Ser	Thr	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	65	70	75	80
Gly	Tyr	Pro	Arg	Arg	Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	85	90	95	
Val	Glu	Lys	His	Ala	Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	100	105	110	
Ala	Leu	Pro	Gly	Ile	Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	115	120	125	
His	Phe	Gly	Gln	Arg	Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	130	135	140	
Tyr	Gln	Arg	Ala	Val	Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	145	150	155	160
Gln	Glu	Leu	Ile	Asp	Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	165	170	175	
Glu	Phe	Ser	Ala	Ala	Ile	Met	Glu	Leu	Gly	Ala	Leu	Ile	Cys	Thr	Ala	180	185	190	
Thr	Ser	Pro	Lys	Cys	Asp	Thr	Cys	Pro	Leu	Leu	Asp	Gln	Cys	Gln	Trp	195	200	205	
Gln	Lys	Leu	Gly	Cys	Pro	Ser	Pro	Ser	Glu	Glu	Glu	Leu	Ala	Ser	Ala	210	215	220	
Lys	Lys	Arg	Val	Gln	Lys	Phe	Val	Gly	Thr	Asp	Arg	Gln	Val	Arg	Gly	225	230	235	240
Leu	Ile	Met	Asp	Val	Leu	Arg	Asn	Ala	Thr	Ala	Pro	Val	Pro	Leu	Ser	245	250	255	
Ala	Ile	Asp	Val	Val	Trp	Pro	Asp	Asp	Ala	Gln	Arg	Ser	Arg	Ala	Leu	260	265	270	
Phe	Ser	Leu	Ile	Glu	Asp	Gly	Leu	Ala	Glu	Gln	Asn	Glu	Ala	Gly	Tyr	275	280	285	

Phe His Leu Pro Arg
290

<210> 33
<211> 891
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(868)
<223> RXA00102

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Met Pro Glu Gly Asp
1 5
tcc gta ttc caa ctc tcc cgc aaa ctt caa ttc atg cgc gga aga gaa 163
Ser Val Phe Gln Leu Ser Arg Lys Leu Gln Phe Met Arg Gly Arg Glu
10 15 20
gtg ctg gaa acc tcc ctg cgt gtg cca tca gtg gca ctt cac gat ttc 211
Val Leu Glu Thr Ser Leu Arg Val Pro Ser Val Ala Leu His Asp Phe
25 30 35
acc ggt caa acc gtc aac cgc gta tgg ccc tac gga aaa cac ctc ttc 259
Thr Gly Gln Thr Val Asn Arg Val Trp Pro Tyr Gly Lys His Leu Phe
40 45 50
atg caa ttc ggt gaa gag atc ctc cac acc cac ctc aaa atg gaa ggg 307
Met Gln Phe Gly Glu Glu Ile Leu His Thr His Leu Lys Met Glu Gly
55 60 65
acg tgg gct gtc cac cgc aaa ggc gat cgc tgg cgc aaa cct gga cac 355
Thr Trp Ala Val His Arg Lys Gly Asp Arg Trp Arg Lys Pro Gly His
70 75 80 85
acc gcg agg gta gtg ctt gtg ctg tcg gaa aac atc gag gtg gtg ggg 403
Thr Ala Arg Val Val Leu Val Leu Ser Glu Asn Ile Glu Val Val Gly
90 95 100
cat tcc ctc ggc ttt gtc aga gtg ttc ccc gca aac cgc tac tcc gaa 451
His Ser Leu Gly Phe Val Arg Val Phe Pro Ala Asn Arg Tyr Ser Glu
105 110 115
gag atc gct tac ctc ggc ccc gac gtc ctt gcc gaa gaa ttc gac atc 499
Glu Ile Ala Tyr Leu Gly Pro Asp Val Leu Ala Glu Glu Phe Asp Ile
120 125 130
aac acc gca cgg aac aat att gca tcg aac cct tcc cga aca att ggc 547
Asn Thr Ala Arg Asn Asn Ile Ala Ser Asn Pro Ser Arg Thr Ile Gly
135 140 145
gaa gcc ctc ctc gac caa tcc aac ctc gct gga gta ggc aac gaa tac 595
Glu Ala Leu Leu Asp Gln Ser Asn Leu Ala Gly Val Gly Asn Glu Tyr
150 155 160 165

cgc gct gag atc tgc ttc ctc atg ggc gtc cac ccg gcg aca caa gta 643
 Arg Ala Glu Ile Cys Phe Leu Met Gly Val His Pro Ala Thr Gln Val
 170 175 180

gga tac gtt gac gtc gaa aag gct ctg aag att acc cga aga ctc atg 691
 Gly Tyr Val Asp Val Glu Lys Ala Leu Lys Ile Thr Arg Arg Leu Met
 185 190 195

tgg gaa aat cga aat tcg ccg att cga gtg acc acc ggg gtt cga cgc 739
 Trp Glu Asn Arg Asn Ser Pro Ile Arg Val Thr Thr Gly Val Arg Arg
 200 205 210

gcc ggg gaa tcc acc tat gtg ttt ggg cgt aac aat aaa ccg tgc agg 787
 Ala Gly Glu Ser Thr Tyr Val Phe Gly Arg Asn Asn Lys Pro Cys Arg
 215 220 225

aga tgc cga acc cca atc gtg aaa gcc gag ttg ggg gag cga ata atc 835
 Arg Cys Arg Thr Pro Ile Val Lys Ala Glu Leu Gly Glu Arg Ile Ile
 230 235 240 245

tgg tgg tgt ccg cgc tgc caa ccg cta aac tcg tgaagcatga gactaatact 888
 Trp Trp Cys Pro Arg Cys Gln Pro Leu Asn Ser
 250 255

caa 891

<210> 34

<211> 256

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

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 1 5 10 15

Met Arg Gly Arg Glu Val Leu Glu Thr Ser Leu Arg Val Pro Ser Val
 20 25 30

Ala Leu His Asp Phe Thr Gly Gln Thr Val Asn Arg Val Trp Pro Tyr
 35 40 45

Gly Lys His Leu Phe Met Gln Phe Gly Glu Glu Ile Leu His Thr His
 50 55 60

Leu Lys Met Glu Gly Thr Trp Ala Val His Arg Lys Gly Asp Arg Trp
 65 70 75 80

Arg Lys Pro Gly His Thr Ala Arg Val Val Leu Val Leu Ser Glu Asn
 85 90 95

Ile Glu Val Val Gly His Ser Leu Gly Phe Val Arg Val Phe Pro Ala
 100 105 110

Asn Arg Tyr Ser Glu Glu Ile Ala Tyr Leu Gly Pro Asp Val Leu Ala
 115 120 125

Glu Glu Phe Asp Ile Asn Thr Ala Arg Asn Asn Ile Ala Ser Asn Pro
 130 135 140

Ser Arg Thr Ile Gly Glu Ala Leu Leu Asp Gln Ser Asn Leu Ala Gly

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ttttatcaaa tcggcacacc ggctactaag gttggtgatt																115
Met Pro Glu Gly His																15
gtg att cat cga cta gct ggg gaa ctc acc aag aat ttt ggc gat acc																163
Val Ile His Arg Leu Ala Gly Glu Leu Thr Lys Asn Phe Gly Asp Thr																20
att ttg gac gcc act tca cct caa gga cgc ttt act tct gaa gcg gcg																211
Ile Leu Asp Ala Thr Ser Pro Gln Gly Arg Phe Thr Ser Glu Ala Ala																35
atc atc aac ggt cac cgc atc gcg gtt gcg gag gct tac ggc aag cac																259
Ile Ile Asn Gly His Arg Ile Ala Val Ala Glu Ala Tyr Gly Lys His																45
ctg ttg gtc gag ttc gat gcg gat cac cct gag cac att ttg tat atc																307
Leu Phe Val Glu Phe Asp Ala Asp His Pro Glu His Ile Leu Tyr Ile																65
cat ttg ggg ctg att ggc acg ttg cag ttt gaa cct gcg gaa gaa acc																355
His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro Ala Glu Glu Thr																85
cgc ggg cag att cgc ctg cac ctt tcc gac ggg gag atc gca gct aat																403
Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu Ile Ala Ala Asn																95

ttg cgc gga ccc caa tgg tgc agg ttg atc acc gat gca gag cgc acc 451
 Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp Ala Glu Arg Thr
 105 110 115

 cag gcc att gga aaa ttg ggc gct gat ccg att cgc gat gat gcc gat 499
 Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg Asp Asp Ala Asp
 120 125 130

 ccg gaa cca att cgg att aag gtg cag cgc tca ggg cga agc att ggt 547
 Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly Arg Ser Ile Gly
 135 140 145

 tcg ttg ttg atg gat cag aag ctt ttc gca ggt gtg gga aat atc tac 595
 Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly Val Gly Asn Ile Tyr
 150 155 160 165

 cgt gcg gag aca ctt ttc cgc ctg ggg att tca ccg ttc acc att gga 643
 Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser Pro Phe Thr Ile Gly
 170 175 180

 aaa gac atc acc acg gca cag ttc cga tcc att tgg gcg gat ctt gtt 691
 Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile Trp Ala Asp Leu Val
 185 190 195

 ggg ttg atg aaa gac ggt gtt gtg act ggt cgg att gat act gtg cgc 739
 Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg Ile Asp Thr Val Arg
 200 205 210

 ccg gaa cac aca ccg gag gcg atg ggt agg cca ccg cgg aaa gat gat 787
 Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro Pro Arg Lys Asp Asp
 215 220 225

 cac ggc ggt gag gtt tac acc tat cgg cga acc ggt caa gag tgc ttt 835
 His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr Gly Gln Glu Cys Phe
 230 235 240 245

 ctg tgc gca act ccc atc aag gag cag gtc atg gag ggt cgc aac tta 883
 Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met Glu Gly Arg Asn Leu
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 ttt tgg tgt ccc ggc tgc caa cgc tagacagatt caccttttgc tgt 930
 Phe Trp Cys Pro Gly Cys Gln Arg
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<210> 36

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Pro Glu Gly His Val Ile His Arg Leu Ala Gly Glu Leu Thr Lys
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Asn Phe Gly Asp Thr Ile Leu Asp Ala Thr Ser Pro Gln Gly Arg Phe
 20 25 30

Thr Ser Glu Ala Ala Ile Ile Asn Gly His Arg Ile Ala Val Ala Glu
 35 40 45

Ala Tyr Gly Lys His Leu Phe Val Glu Phe Asp Ala Asp His Pro Glu
50 55 60

His Ile Leu Tyr Ile His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu
65 70 75 80

Pro Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly
85 90 95

Glu Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr
100 105 110

Asp Ala Glu Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile
115 120 125

Arg Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser
130 135 140

Gly Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly
145 150 155 160

Val Gly Asn Ile Tyr Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser
165 170 175

Pro Phe Thr Ile Gly Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile
180 185 190

Trp Ala Asp Leu Val Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg
195 200 205

Ile Asp Thr Val Arg Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro
210 215 220

Pro Arg Lys Asp Asp His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr
225 230 235 240

Gly Gln Glu Cys Phe Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met
245 250 255

Glu Gly Arg Asn Leu Phe Trp Cys Pro Gly Cys Gln Arg
260 265

<210> 37

<211> 635

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(612)

<223> FRXA01670

<400> 37

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His Phe Val Tyr His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro
1 5 10 15

gcg gaa gaa acc cgc ggg cag att cgc ctg cac ctt tcc gac ggg gag 96
Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu
20 25 30

atc gca gct aat ttg cgc gga ccc caa tgg tgc agg ttg atc acc gat 144
 Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp
 35 40 45

gca gag cgc acc cag gcc att gga aaa ttg ggc gct gat ccg att cgc 192
 Ala Glu Arg Thr Gln Ala Ile Gly Lys Leu Gly Ala Asp Pro Ile Arg
 50 55 60

gat gat gcc gat ccg gaa cca att cgg att aag gtg cag cgc tca ggg 240
 Asp Asp Ala Asp Pro Glu Pro Ile Arg Ile Lys Val Gln Arg Ser Gly
 65 70 75 80

cga agc att ggt tgc ttg ttg atg gat cag aag ctt ttc gca ggt gtg 288
 Arg Ser Ile Gly Ser Leu Leu Met Asp Gln Lys Leu Phe Ala Gly Val
 85 90 95

gga aat atc tac cgt gcg gag aca ctt ttc cgc ctg ggg att tca ccg 336
 Gly Asn Ile Tyr Arg Ala Glu Thr Leu Phe Arg Leu Gly Ile Ser Pro
 100 105 110

ttc acc att gga aaa gac atc acc acg gca cag ttc cga tcc att tgg 384
 Phe Thr Ile Gly Lys Asp Ile Thr Thr Ala Gln Phe Arg Ser Ile Trp
 115 120 125

gcg gat ctt gtt ggg ttg atg aaa gac ggt gtt gtg act ggt cgg att 432
 Ala Asp Leu Val Gly Leu Met Lys Asp Gly Val Val Thr Gly Arg Ile
 130 135 140

gat act gtg cgc ccg gaa cac aca ccg gag gcg atg ggt agg cca ccg 480
 Asp Thr Val Arg Pro Glu His Thr Pro Glu Ala Met Gly Arg Pro Pro
 145 150 155 160

cgg aaa gat gat cac ggc ggt gag gtt tac acc tat cgg cga acc ggt 528
 Arg Lys Asp Asp His Gly Gly Glu Val Tyr Thr Tyr Arg Arg Thr Gly
 165 170 175

caa gag tgc ttt ctg tgc gca act ccc atc aag gag cag gtc atg gag 576
 Gln Glu Cys Phe Leu Cys Ala Thr Pro Ile Lys Glu Gln Val Met Glu
 180 185 190

ggt cgc aac tta ttt tgg tgt ccc ggc tgc caa cgc tagacagatt 622
 Gly Arg Asn Leu Phe Trp Cys Pro Gly Cys Gln Arg
 195 200

caccttttgc tgt 635

<210> 38

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 38

His Phe Val Tyr His Leu Gly Leu Ile Gly Thr Leu Gln Phe Glu Pro
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Ala Glu Glu Thr Arg Gly Gln Ile Arg Leu His Leu Ser Asp Gly Glu
 20 25 30

Ile Ala Ala Asn Leu Arg Gly Pro Gln Trp Cys Arg Leu Ile Thr Asp

35					40					45					
Ala	Glu	Arg	Thr	Gln	Ala	Ile	Gly	Lys	Leu	Gly	Ala	Asp	Pro	Ile	Arg
50					55					60					
Asp	Asp	Ala	Asp	Pro	Glu	Pro	Ile	Arg	Ile	Lys	Val	Gln	Arg	Ser	Gly
65					70					75					80
Arg	Ser	Ile	Gly	Ser	Leu	Leu	Met	Asp	Gln	Lys	Leu	Phe	Ala	Gly	Val
				85					90					95	
Gly	Asn	Ile	Tyr	Arg	Ala	Glu	Thr	Leu	Phe	Arg	Leu	Gly	Ile	Ser	Pro
			100					105					110		
Phe	Thr	Ile	Gly	Lys	Asp	Ile	Thr	Thr	Ala	Gln	Phe	Arg	Ser	Ile	Trp
			115				120					125			
Ala	Asp	Leu	Val	Gly	Leu	Met	Lys	Asp	Gly	Val	Val	Thr	Gly	Arg	Ile
130					135					140					
Asp	Thr	Val	Arg	Pro	Glu	His	Thr	Pro	Glu	Ala	Met	Gly	Arg	Pro	Pro
145					150					155					160
Arg	Lys	Asp	Asp	His	Gly	Gly	Glu	Val	Tyr	Thr	Tyr	Arg	Arg	Thr	Gly
				165					170					175	
Gln	Glu	Cys	Phe	Leu	Cys	Ala	Thr	Pro	Ile	Lys	Glu	Gln	Val	Met	Glu
			180					185					190		
Gly	Arg	Asn	Leu	Phe	Trp	Cys	Pro	Gly	Cys	Gln	Arg				
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(958)
 <223> RXA02078

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 gaagcagcgc accaggcatt ccgaaagctt cgaggagtcct gtg cct gaa ctg cct 115
 Val Pro Glu Leu Pro
 1 5
 gaa gtt gag gtg gtg cgc cgc ggt tta gaa gat cat atg gtc ggc cac 163
 Glu Val Glu Val Val Arg Arg Gly Leu Glu Asp His Met Val Gly His
 10 15 20
 acc atc gtg tcc gcc aca gtg ctt cac ccg cgc gca gcc cgc aat caa 211
 Thr Ile Val Ser Ala Thr Val Leu His Pro Arg Ala Ala Arg Asn Gln
 25 30 35
 ctc ggc ggt ggc ccc gaa atc gag gcc aac atc gca ggg ctt agg gtc 259
 Leu Gly Gly Gly Pro Glu Ile Glu Ala Asn Ile Ala Gly Leu Arg Val
 40 45 50

agc gct gcc aag cga cgc ggc aaa ttc ctc tgg ctt gag ctt atc gac	307
Ser Ala Ala Lys Arg Arg Gly Lys Phe Leu Trp Leu Glu Leu Ile Asp	
55 60 65	
gca ccc tcc ggc gaa acc cgt ccc gat tta ggg cta ctg gtt cac ctt	355
Ala Pro Ser Gly Glu Thr Arg Pro Asp Leu Gly Leu Leu Val His Leu	
70 75 80 85	
ggg atg agt gga caa atg ctc atc aaa gaa cca gat gca cca att agt	403
Gly Met Ser Gly Gln Met Leu Ile Lys Glu Pro Asp Ala Pro Ile Ser	
90 95 100	
cca cac ctt cga gcc aaa gtc gag cta gat aat ggc gat gaa gtg tgg	451
Pro His Leu Arg Ala Lys Val Glu Leu Asp Asn Gly Asp Glu Val Trp	
105 110 115	
ttt gtc gat caa cgc acc ttc ggt tat tgg tgg ctc ggc gac cta gtt	499
Phe Val Asp Gln Arg Thr Phe Gly Tyr Trp Trp Leu Gly Asp Leu Val	
120 125 130	
gat gga gta ccc gaa cgc gtc tct cac att gcc aca gat gta ttg gat	547
Asp Gly Val Pro Glu Arg Val Ser His Ile Ala Thr Asp Val Leu Asp	
135 140 145	
gag tct gct gat ttc tct gcg att gcg cgg aat ttg aaa tct cgg aaa	595
Glu Ser Ala Asp Phe Ser Ala Ile Ala Arg Asn Leu Lys Ser Arg Lys	
150 155 160 165	
tcg gag atc aaa cgc ctc ctg ctt aac caa gag atc gtc tcc ggc atc	643
Ser Glu Ile Lys Arg Leu Leu Leu Asn Gln Glu Ile Val Ser Gly Ile	
170 175 180	
gga aat atc tat gcc gat gaa atg ctc tgg caa gca aaa att cac cca	691
Gly Asn Ile Tyr Ala Asp Glu Met Leu Trp Gln Ala Lys Ile His Pro	
185 190 195	
ttg caa cgt gcc gat cga ctg tcc cta gct cgc ttg gaa gaa ctt ctt	739
Leu Gln Arg Ala Asp Arg Leu Ser Leu Ala Arg Leu Glu Glu Leu Leu	
200 205 210	
caa gct ggc aaa gac gtg atg acc aaa gca ctt gct caa ggt ggc acc	787
Gln Ala Gly Lys Asp Val Met Thr Lys Ala Leu Ala Gln Gly Gly Thr	
215 220 225	
tct ttc gac gcg ctc tat gtc aac gtc aat ggc aac tcc ggc tac ttt	835
Ser Phe Asp Ala Leu Tyr Val Asn Val Asn Gly Asn Ser Gly Tyr Phe	
230 235 240 245	
gcg ctg tca ttg aat gct tat gcg caa acc ggg gag ccg tgc gga cgc	883
Ala Leu Ser Leu Asn Ala Tyr Ala Gln Thr Gly Glu Pro Cys Gly Arg	
250 255 260	
tgc gga aca tta atc atc cgg gag agt ttc atg aac cgc ggc tcc cac	931
Cys Gly Thr Leu Ile Ile Arg Glu Ser Phe Met Asn Arg Gly Ser His	
265 270 275	
tac tgc cca aac tgc cag aag cgg cgc tagctgatga gcgaagcttt tga	981
Tyr Cys Pro Asn Cys Gln Lys Arg Arg	
280 285	

<210> 40
 <211> 286
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 40

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His	Met	Val	Gly	His	Thr	Ile	Val	Ser	Ala	Thr	Val	Leu	His	Pro	Arg
			20					25					30		
Ala	Ala	Arg	Asn	Gln	Leu	Gly	Gly	Gly	Pro	Glu	Ile	Glu	Ala	Asn	Ile
		35					40					45			
Ala	Gly	Leu	Arg	Val	Ser	Ala	Ala	Lys	Arg	Arg	Gly	Lys	Phe	Leu	Trp
	50					55					60				
Leu	Glu	Leu	Ile	Asp	Ala	Pro	Ser	Gly	Glu	Thr	Arg	Pro	Asp	Leu	Gly
	65				70					75					80
Leu	Leu	Val	His	Leu	Gly	Met	Ser	Gly	Gln	Met	Leu	Ile	Lys	Glu	Pro
				85					90					95	
Asp	Ala	Pro	Ile	Ser	Pro	His	Leu	Arg	Ala	Lys	Val	Glu	Leu	Asp	Asn
			100					105					110		
Gly	Asp	Glu	Val	Trp	Phe	Val	Asp	Gln	Arg	Thr	Phe	Gly	Tyr	Trp	Trp
		115					120					125			
Leu	Gly	Asp	Leu	Val	Asp	Gly	Val	Pro	Glu	Arg	Val	Ser	His	Ile	Ala
	130					135					140				
Thr	Asp	Val	Leu	Asp	Glu	Ser	Ala	Asp	Phe	Ser	Ala	Ile	Ala	Arg	Asn
	145				150					155					160
Leu	Lys	Ser	Arg	Lys	Ser	Glu	Ile	Lys	Arg	Leu	Leu	Leu	Asn	Gln	Glu
				165					170					175	
Ile	Val	Ser	Gly	Ile	Gly	Asn	Ile	Tyr	Ala	Asp	Glu	Met	Leu	Trp	Gln
			180					185					190		
Ala	Lys	Ile	His	Pro	Leu	Gln	Arg	Ala	Asp	Arg	Leu	Ser	Leu	Ala	Arg
		195					200					205			
Leu	Glu	Glu	Leu	Leu	Gln	Ala	Gly	Lys	Asp	Val	Met	Thr	Lys	Ala	Leu
	210					215					220				
Ala	Gln	Gly	Gly	Thr	Ser	Phe	Asp	Ala	Leu	Tyr	Val	Asn	Val	Asn	Gly
	225				230					235					240
Asn	Ser	Gly	Tyr	Phe	Ala	Leu	Ser	Leu	Asn	Ala	Tyr	Ala	Gln	Thr	Gly
				245					250					255	
Glu	Pro	Cys	Gly	Arg	Cys	Gly	Thr	Leu	Ile	Ile	Arg	Glu	Ser	Phe	Met
			260					265					270		
Asn	Arg	Gly	Ser	His	Tyr	Cys	Pro	Asn	Cys	Gln	Lys	Arg	Arg		
		275					280					285			

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Met Leu Val Asp Ile 5																
gct att gag aac ctc gga gtt att cca gcg gcc tca gct gag ttc agc 163																
Ala Ile Glu Asn Leu Gly Val Ile Pro Ala Ala Ser Ala Glu Phe Ser 20																
tca ggt tta aca gtg ctc acc ggt gag acc ggc gcc gga aag acc atg 211																
Ser Gly Leu Thr Val Leu Thr Gly Glu Thr Gly Ala Gly Lys Thr Met 35																
gta gtg aca ggt tta cgc ctg tta tcc ggc ggt cgc gcc gac gct tca 259																
Val Val Thr Gly Leu Arg Leu Leu Ser Ser Gly Gly Arg Ala Asp Ala Ser 50																
cgc gtg cgc aca gga tcc cct caa gct gtt gtg gag ggg cgc ttt gtt 307																
Arg Val Arg Thr Gly Ser Pro Gln Ala Val Val Glu Gly Arg Phe Val 65																
acg caa ggc gtg ccc tgc gac att gtc gaa cgt gca acc gga atc gtt 355																
Thr Gln Gly Val Pro Cys Asp Ile Val Glu Arg Ala Thr Gly Ile Val 85																
tcg aac gcc gga ggt gcc gca gat gaa aat gga gag ttt tta gct gtc 403																
Ser Asn Ala Gly Gly Ala Ala Asp Glu Asn Gly Glu Phe Leu Ala Val 100																
cgt tcc gtc ggc gcc aac ggc cgt tca aaa gct cat ctc ggt ggt cgc 451																
Arg Ser Val Gly Ala Asn Gly Arg Ser Lys Ala His Leu Gly Gly Arg 115																
tcc gta cct gcg gca acg ctg tcc gag ttc tct gat gag ctg ttg acc 499																
Ser Val Pro Ala Ala Thr Leu Ser Glu Phe Ser Asp Glu Leu Leu Thr 130																
atc cac ggt caa aat gac caa ctc cgg ttg ctc tcc cca gaa cgc caa 547																
Ile His Gly Gln Asn Asp Gln Leu Arg Leu Leu Ser Pro Glu Arg Gln 145																
cta gag gcg ctt gat cgt ttt gat cca gag ctg gcc caa ctg cgc aaa 595																
Leu Glu Ala Leu Asp Arg Phe Asp Pro Glu Leu Ala Gln Leu Arg Lys 165																
aac tac aac gcc aag tac ctc act tgg aag tcc ttg gat aaa gat ctg 643																
Asn Tyr Asn Ala Lys Tyr Leu Thr Trp Lys Ser Leu Asp Lys Asp Leu 180																

cag aag cgc ctg agt agt agg cga gag ctg gct caa gaa gtc gat cgc	691
Gln Lys Arg Leu Ser Ser Arg Arg Glu Leu Ala Gln Glu Val Asp Arg	
185 190 195	
ctg caa ttc gcg att aat gag atc gag gaa gtc tcg cca cag cca ggc	739
Leu Gln Phe Ala Ile Asn Glu Ile Glu Glu Val Ser Pro Gln Pro Gly	
200 205 210	
gaa gac gcc gaa ctg gtt gag cag atc cgc agg ctc cag gac gtg gac	787
Glu Asp Ala Glu Leu Val Glu Gln Ile Arg Arg Leu Gln Asp Val Asp	
215 220 225	
acc ctg cgg gag caa gct gca acc gca ttg gct gcg att gat ggt gcc	835
Thr Leu Arg Glu Gln Ala Ala Thr Ala Leu Ala Ala Ile Asp Gly Ala	
230 235 240 245	
ggc tct ctc agc gac gcc atg ggt ggt tcc ggc ggc ttt gat gaa tcc	883
Gly Ser Leu Ser Asp Ala Met Gly Gly Ser Gly Gly Phe Asp Glu Ser	
250 255 260	
cag gag tca gcc tct gac cag ctc ggc cag gcg gag tcc gcg ctg gca	931
Gln Glu Ser Ala Ser Asp Gln Leu Gly Gln Ala Glu Ser Ala Leu Ala	
265 270 275	
ggc agt gat gac tca aag ctg aaa gat att gcc gtt cag ctt gcg gaa	979
Gly Ser Asp Asp Ser Lys Leu Lys Asp Ile Ala Val Gln Leu Ala Glu	
280 285 290	
atc acc agc cag ctc agc caa gtg tcc atg gaa ttg ggc ggg ttc ctc	1027
Ile Thr Ser Gln Leu Ser Gln Val Ser Met Glu Leu Gly Gly Phe Leu	
295 300 305	
tct gat ctc ccc gca gac ccc caa gca ctc gat gac atg ctc acc cgc	1075
Ser Asp Leu Pro Ala Asp Pro Gln Ala Leu Asp Asp Met Leu Thr Arg	
310 315 320 325	
caa cag caa ttg aaa ctg ctc acg cgt aaa tac gct gca gat att gac	1123
Gln Gln Gln Leu Lys Leu Leu Thr Arg Lys Tyr Ala Ala Asp Ile Asp	
330 335 340	
ggc gtg att gag tgg cag cgg aaa gcc caa atc cgc cta gac agc att	1171
Gly Val Ile Glu Trp Gln Arg Lys Ala Gln Ile Arg Leu Asp Ser Ile	
345 350 355	
gac att tcc tcc gaa gcg ctt gac aag ctg aaa gaa gac gcg aaa aag	1219
Asp Ile Ser Ser Glu Ala Leu Asp Lys Leu Lys Glu Asp Ala Lys Lys	
360 365 370	
gcg cag gcc tcc atg atg cgt gcc gct aag aag ctt tca gct gtc cgt	1267
Ala Gln Ala Ser Met Met Arg Ala Ala Lys Lys Leu Ser Ala Val Arg	
375 380 385	
gca aag gca gca acc aag ttg ggg aca act gtc acc gag gag ctt cag	1315
Ala Lys Ala Ala Thr Lys Leu Gly Thr Thr Val Thr Glu Glu Leu Gln	
390 395 400 405	
ggc ctg gcc atg caa aaa gcc cgc ttt gag gtt gct ttg acc tcc att	1363
Gly Leu Ala Met Gln Lys Ala Arg Phe Glu Val Ala Leu Thr Ser Ile	
410 415 420	

gag gcg tgc gcc agc ggt atc gac cag gtg gaa ttc cag ctc gca gca 1411
 Glu Ala Cys Ala Ser Gly Ile Asp Gln Val Glu Phe Gln Leu Ala Ala
 425 430 435

aat gcc ttt gca cag cct cgt cca ctt gca tcc tct gcg tct ggt ggt 1459
 Asn Ala Phe Ala Gln Pro Arg Pro Leu Ala Ser Ser Ala Ser Gly Gly
 440 445 450

gaa ctt tcc cgc gtt atg ttg gcg ctc gag gtg atc ttg gct gct gga 1507
 Glu Leu Ser Arg Val Met Leu Ala Leu Glu Val Ile Leu Ala Ala Gly
 455 460 465

acc acg ggc acc acc ttg gtg ttc gac gag gtt gat gca ggt gtg ggc 1555
 Thr Thr Gly Thr Thr Leu Val Phe Asp Glu Val Asp Ala Gly Val Gly
 470 475 480 485

gga cgc gca gcg gtg gaa atc ggt cgc cgc ctg gcc cgc ctt gcc acc 1603
 Gly Arg Ala Ala Val Glu Ile Gly Arg Arg Leu Ala Arg Leu Ala Thr
 490 495 500

aaa aac caa gtc atc gtg gtc acc cat ctc cca cag gtc gct gct tac 1651
 Lys Asn Gln Val Ile Val Val Thr His Leu Pro Gln Val Ala Ala Tyr
 505 510 515

gcc gac acg cac ctg cac gtt gcc aag aat gta gga gaa gcc tcc gtg 1699
 Ala Asp Thr His Leu His Val Ala Lys Asn Val Gly Glu Ala Ser Val
 520 525 530

acc tca gga gtg gag tca ctg acc ttc gac cga cgc gtg gaa gag ctc 1747
 Thr Ser Gly Val Glu Ser Leu Thr Phe Asp Arg Arg Val Glu Glu Leu
 535 540 545

tcc cgc atg ctc gct ggc ctc gac gac acc gcc acc ggc cga gcc cac 1795
 Ser Arg Met Leu Ala Gly Leu Asp Asp Thr Ala Thr Gly Arg Ala His
 550 555 560 565

gca acg gag ctg ctc gag cgt gca cag cgt gaa aag gaa gat att aac 1843
 Ala Thr Glu Leu Leu Glu Arg Ala Gln Arg Glu Lys Glu Asp Ile Asn
 570 575 580

gag gag cga gta gaa cca ctt ctc gcc gcc agt gca taagagtttt 1889
 Glu Glu Arg Val Glu Pro Leu Leu Ala Ala Ser Ala
 585 590

cttggaattt ttt 1902

<210> 42

<211> 593

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Ser Ala Glu Phe Ser Ser Gly Leu Thr Val Leu Thr Gly Glu Thr Gly
 20 25 30

Ala Gly Lys Thr Met Val Val Thr Gly Leu Arg Leu Leu Ser Gly Gly
 35 40 45

Arg Ala Asp Ala Ser Arg Val Arg Thr Gly Ser Pro Gln Ala Val Val
 50 55 60
 Glu Gly Arg Phe Val Thr Gln Gly Val Pro Cys Asp Ile Val Glu Arg
 65 70 75 80
 Ala Thr Gly Ile Val Ser Asn Ala Gly Gly Ala Ala Asp Glu Asn Gly
 85 90 95
 Glu Phe Leu Ala Val Arg Ser Val Gly Ala Asn Gly Arg Ser Lys Ala
 100 105 110
 His Leu Gly Gly Arg Ser Val Pro Ala Ala Thr Leu Ser Glu Phe Ser
 115 120 125
 Asp Glu Leu Leu Thr Ile His Gly Gln Asn Asp Gln Leu Arg Leu Leu
 130 135 140
 Ser Pro Glu Arg Gln Leu Glu Ala Leu Asp Arg Phe Asp Pro Glu Leu
 145 150 155 160
 Ala Gln Leu Arg Lys Asn Tyr Asn Ala Lys Tyr Leu Thr Trp Lys Ser
 165 170 175
 Leu Asp Lys Asp Leu Gln Lys Arg Leu Ser Ser Arg Arg Glu Leu Ala
 180 185 190
 Gln Glu Val Asp Arg Leu Gln Phe Ala Ile Asn Glu Ile Glu Glu Val
 195 200 205
 Ser Pro Gln Pro Gly Glu Asp Ala Glu Leu Val Glu Gln Ile Arg Arg
 210 215 220
 Leu Gln Asp Val Asp Thr Leu Arg Glu Gln Ala Ala Thr Ala Leu Ala
 225 230 235 240
 Ala Ile Asp Gly Ala Gly Ser Leu Ser Asp Ala Met Gly Gly Ser Gly
 245 250 255
 Gly Phe Asp Glu Ser Gln Glu Ser Ala Ser Asp Gln Leu Gly Gln Ala
 260 265 270
 Glu Ser Ala Leu Ala Gly Ser Asp Asp Ser Lys Leu Lys Asp Ile Ala
 275 280 285
 Val Gln Leu Ala Glu Ile Thr Ser Gln Leu Ser Gln Val Ser Met Glu
 290 295 300
 Leu Gly Gly Phe Leu Ser Asp Leu Pro Ala Asp Pro Gln Ala Leu Asp
 305 310 315 320
 Asp Met Leu Thr Arg Gln Gln Gln Leu Lys Leu Leu Thr Arg Lys Tyr
 325 330 335
 Ala Ala Asp Ile Asp Gly Val Ile Glu Trp Gln Arg Lys Ala Gln Ile
 340 345 350
 Arg Leu Asp Ser Ile Asp Ile Ser Ser Glu Ala Leu Asp Lys Leu Lys
 355 360 365

Glu Asp Ala Lys Lys Ala Gln Ala Ser Met Met Arg Ala Ala Lys Lys
 370 375 380
 Leu Ser Ala Val Arg Ala Lys Ala Ala Thr Lys Leu Gly Thr Thr Val
 385 390 395 400
 Thr Glu Glu Leu Gln Gly Leu Ala Met Gln Lys Ala Arg Phe Glu Val
 405 410 415
 Ala Leu Thr Ser Ile Glu Ala Cys Ala Ser Gly Ile Asp Gln Val Glu
 420 425 430
 Phe Gln Leu Ala Ala Asn Ala Phe Ala Gln Pro Arg Pro Leu Ala Ser
 435 440 445
 Ser Ala Ser Gly Gly Glu Leu Ser Arg Val Met Leu Ala Leu Glu Val
 450 455 460
 Ile Leu Ala Ala Gly Thr Thr Gly Thr Thr Leu Val Phe Asp Glu Val
 465 470 475 480
 Asp Ala Gly Val Gly Gly Arg Ala Ala Val Glu Ile Gly Arg Arg Leu
 485 490 495
 Ala Arg Leu Ala Thr Lys Asn Gln Val Ile Val Val Thr His Leu Pro
 500 505 510
 Gln Val Ala Ala Tyr Ala Asp Thr His Leu His Val Ala Lys Asn Val
 515 520 525
 Gly Glu Ala Ser Val Thr Ser Gly Val Glu Ser Leu Thr Phe Asp Arg
 530 535 540
 Arg Val Glu Glu Leu Ser Arg Met Leu Ala Gly Leu Asp Asp Thr Ala
 545 550 555 560
 Thr Gly Arg Ala His Ala Thr Glu Leu Leu Glu Arg Ala Gln Arg Glu
 565 570 575
 Lys Glu Asp Ile Asn Glu Glu Arg Val Glu Pro Leu Leu Ala Ala Ser
 580 585 590

Ala

<210> 43
 <211> 1434
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1411)
 <223> RXA01493

<400> 43
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 gcaaccgtta ccttggggga gtctttgcga agctcggcgc atg tcg atg tct aac 115
 Met Ser Met Ser Asn

												1					5	
aac	gac	ttt	gag	cat	gag	tcc	cat	gat	gtt	tct	gca	aag	cag	atc	ttc	163		
Asn	Asp	Phe	Glu	His	Glu	Ser	His	Asp	Val	Ser	Ala	Lys	Gln	Ile	Phe			
				10					15					20				
ggg	ctc	gcg	ttc	ccc	gca	ctg	ggg	ggt	gta	gct	gcg	atg	ccg	ctg	tat	211		
Gly	Leu	Ala	Phe	Pro	Ala	Leu	Gly	Val	Leu	Ala	Ala	Met	Pro	Leu	Tyr			
				25					30					35				
ctc	ttg	ttg	gat	aca	gcg	gtt	gtt	ggc	act	ttg	ggt	ggc	ttc	gaa	ttg	259		
Leu	Leu	Leu	Asp	Thr	Ala	Val	Val	Gly	Thr	Leu	Gly	Gly	Phe	Glu	Leu			
				40					45					50				
gct	gcg	ttg	ggc	gca	gca	aca	aca	att	caa	gct	caa	gtg	aca	aca	cag	307		
Ala	Ala	Leu	Gly	Ala	Ala	Thr	Thr	Ile	Gln	Ala	Gln	Val	Thr	Thr	Gln			
				55					60					65				
ctg	aca	ttc	ttg	tcc	tat	gga	act	acc	gcg	aga	tca	tcg	aga	att	ttc	355		
Leu	Thr	Phe	Leu	Ser	Tyr	Gly	Thr	Thr	Ala	Arg	Ser	Ser	Arg	Ile	Phe			
				70					75					80	85			
gga	atg	ggt	gat	cgc	cgg	gga	gca	att	gcc	gaa	ggt	gtg	caa	gca	acc	403		
Gly	Met	Gly	Asp	Arg	Arg	Gly	Ala	Ile	Ala	Glu	Gly	Val	Gln	Ala	Thr			
				90					95					100				
tgg	gtg	gca	ctc	ttt	gta	ggc	ttg	ggc	atc	tta	acg	ctg	atg	ctc	att	451		
Trp	Val	Ala	Leu	Phe	Val	Gly	Leu	Gly	Ile	Leu	Thr	Leu	Met	Leu	Ile			
				105					110					115				
gga	gcc	ccg	act	ttc	gcg	ttg	tgg	ctc	agt	ggt	gat	gaa	gct	cta	gcc	499		
Gly	Ala	Pro	Thr	Phe	Ala	Leu	Trp	Leu	Ser	Gly	Asp	Glu	Ala	Leu	Ala			
				120					125					130				
caa	gaa	gca	ggg	cat	tgg	ctc	cgg	gtc	gct	gct	ttt	gcg	gtg	cca	cta	547		
Gln	Glu	Ala	Gly	His	Trp	Leu	Arg	Val	Ala	Ala	Phe	Ala	Val	Pro	Leu			
				135					140					145				
att	ctc	atg	atc	atg	gct	ggc	aac	ggt	tgg	tta	aga	ggt	att	caa	aac	595		
Ile	Leu	Met	Ile	Met	Ala	Gly	Asn	Gly	Trp	Leu	Arg	Gly	Ile	Gln	Asn			
				150					155					160	165			
acc	aag	ctg	cca	ctc	tat	ttc	acc	ttg	gcg	gga	gtc	atc	ccc	ggc	gcg	643		
Thr	Lys	Leu	Pro	Leu	Tyr	Phe	Thr	Leu	Ala	Gly	Val	Ile	Pro	Gly	Ala			
				170					175					180				
atc	ttg	att	ccg	ata	ttc	gtg	gct	aag	ttt	gga	ctt	gtg	ggc	tct	gcc	691		
Ile	Leu	Ile	Pro	Ile	Phe	Val	Ala	Lys	Phe	Gly	Leu	Val	Gly	Ser	Ala			
				185					190					195				
tgg	gca	aac	ctc	att	gca	gaa	gca	att	act	gct	tcg	ctg	ttt	ttg	ggt	739		
Trp	Ala	Asn	Leu	Ile	Ala	Glu	Ala	Ile	Thr	Ala	Ser	Leu	Phe	Leu	Gly			
				200					205					210				
gca	ttg	atc	aag	cac	cac	gaa	ggt	tcg	tgg	aag	ccg	agc	tgg	acg	gtg	787		
Ala	Leu	Ile																

tcg ttc cag gtt gct ttt ctt tcc gcg gcc gct gtg gct gca cga ttt	883
Ser Phe Gln Val Ala Phe Leu Ser Ala Ala Ala Val Ala Ala Arg Phe	
250 255 260	
ggc acg gca tcc ttg gcg gcc cac cag gtg ttg ctt cag ctg tgg aat	931
Gly Thr Ala Ser Leu Ala Ala His Gln Val Leu Leu Gln Leu Trp Asn	
265 270 275	
ttc atc aca ttg gtg ctg gat tct cta gct atc gcg gcg cag acc tta	979
Phe Ile Thr Leu Val Leu Asp Ser Leu Ala Ile Ala Ala Gln Thr Leu	
280 285 290	
act ggt gca gcc ctg ggc gct gga act gcg aag gtc gcc cgc agg gtg	1027
Thr Gly Ala Ala Leu Gly Ala Gly Thr Ala Lys Val Ala Arg Arg Val	
295 300 305	
ggt aat cag gtg att aag tac tct ctg att ttc gct ggt ggc tta ggt	1075
Gly Asn Gln Val Ile Lys Tyr Ser Leu Ile Phe Ala Gly Gly Leu Gly	
310 315 320 325	
ttg gtg ttc gtg gtc tta cac tcg tgg att ccg cgt att ttc act cag	1123
Leu Val Phe Val Val Leu His Ser Trp Ile Pro Arg Ile Phe Thr Gln	
330 335 340	
gac gcc gac gtt tta gat gcg att gct tcc ccg tgg tgg atc atg gtc	1171
Asp Ala Asp Val Leu Asp Ala Ile Ala Ser Pro Trp Trp Ile Met Val	
345 350 355	
gcg atg atc att ttg ggt ggc att gtc ttt gct att gat ggt gtg ctg	1219
Ala Met Ile Ile Leu Gly Gly Ile Val Phe Ala Ile Asp Gly Val Leu	
360 365 370	
ttg ggt gct gct gac gcg gtg ttc ctc cga aat gcc tct atc ttg gcg	1267
Leu Gly Ala Ala Asp Ala Val Phe Leu Arg Asn Ala Ser Ile Leu Ala	
375 380 385	
gtt gtg gtc gga ttc tta cca ggc gtc tgg att tcc tat gca tta gat	1315
Val Val Val Gly Phe Leu Pro Gly Val Trp Ile Ser Tyr Ala Leu Asp	
390 395 400 405	
gca ggg ctg aca ggc gtg tgg tgt ggt ttg ctg gcg ttt att ctg atc	1363
Ala Gly Leu Thr Gly Val Trp Cys Gly Leu Leu Ala Phe Ile Leu Ile	
410 415 420	
cga cta ttt gcg gtg att tgg cgg ttt aag tct atg aag tgg gcg cgt	1411
Arg Leu Phe Ala Val Ile Trp Arg Phe Lys Ser Met Lys Trp Ala Arg	
425 430 435	
tagcttcggc gcgtggcaaa cca	1434

<210> 44

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Met Ser Met Ser Asn Asn Asp Phe Glu His Glu Ser His Asp Val Ser

1

5

10

15

Ala Lys Gln Ile Phe Gly Leu Ala Phe Pro Ala Leu Gly Val Leu Ala
 20 25 30
 Ala Met Pro Leu Tyr Leu Leu Leu Asp Thr Ala Val Val Gly Thr Leu
 35 40 45
 Gly Gly Phe Glu Leu Ala Ala Leu Gly Ala Ala Thr Thr Ile Gln Ala
 50 55 60
 Gln Val Thr Thr Gln Leu Thr Phe Leu Ser Tyr Gly Thr Thr Ala Arg
 65 70 75 80
 Ser Ser Arg Ile Phe Gly Met Gly Asp Arg Arg Gly Ala Ile Ala Glu
 85 90 95
 Gly Val Gln Ala Thr Trp Val Ala Leu Phe Val Gly Leu Gly Ile Leu
 100 105 110
 Thr Leu Met Leu Ile Gly Ala Pro Thr Phe Ala Leu Trp Leu Ser Gly
 115 120 125
 Asp Glu Ala Leu Ala Gln Glu Ala Gly His Trp Leu Arg Val Ala Ala
 130 135 140
 Phe Ala Val Pro Leu Ile Leu Met Ile Met Ala Gly Asn Gly Trp Leu
 145 150 155 160
 Arg Gly Ile Gln Asn Thr Lys Leu Pro Leu Tyr Phe Thr Leu Ala Gly
 165 170 175
 Val Ile Pro Gly Ala Ile Leu Ile Pro Ile Phe Val Ala Lys Phe Gly
 180 185 190
 Leu Val Gly Ser Ala Trp Ala Asn Leu Ile Ala Glu Ala Ile Thr Ala
 195 200 205
 Ser Leu Phe Leu Gly Ala Leu Ile Lys His His Glu Gly Ser Trp Lys
 210 215 220
 Pro Ser Trp Thr Val Met Lys Asn Gln Leu Val Leu Gly Arg Asp Leu
 225 230 235 240
 Ile Met Arg Ser Met Ser Phe Gln Val Ala Phe Leu Ser Ala Ala Ala
 245 250 255
 Val Ala Ala Arg Phe Gly Thr Ala Ser Leu Ala Ala His Gln Val Leu
 260 265 270
 Leu Gln Leu Trp Asn Phe Ile Thr Leu Val Leu Asp Ser Leu Ala Ile
 275 280 285
 Ala Ala Gln Thr Leu Thr Gly Ala Ala Leu Gly Ala Gly Thr Ala Lys
 290 295 300
 Val Ala Arg Arg Val Gly Asn Gln Val Ile Lys Tyr Ser Leu Ile Phe
 305 310 315 320
 Ala Gly Gly Leu Gly Leu Val Phe Val Val Leu His Ser Trp Ile Pro
 325 330 335
 Arg Ile Phe Thr Gln Asp Ala Asp Val Leu Asp Ala Ile Ala Ser Pro

340	345	350
Trp Trp Ile Met Val Ala Met Ile Ile Leu Gly Gly Ile Val Phe Ala		
355	360	365
Ile Asp Gly Val Leu Leu Gly Ala Ala Asp Ala Val Phe Leu Arg Asn		
370	375	380
Ala Ser Ile Leu Ala Val Val Val Gly Phe Leu Pro Gly Val Trp Ile		
385	390	395
Ser Tyr Ala Leu Asp Ala Gly Leu Thr Gly Val Trp Cys Gly Leu Leu		
405	410	415
Ala Phe Ile Leu Ile Arg Leu Phe Ala Val Ile Trp Arg Phe Lys Ser		
420	425	430
Met Lys Trp Ala Arg		
435		

<210> 45
 <211> 702
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(679)
 <223> RXA02671

<400> 45
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 agaatgctcc gtggcatcaa aaaccgcttc ggtgccaccg atg aag tcg ggc tgc 115
 Met Lys Ser Gly Cys
 1 5
 ttc gaa caa caa tcc gac ggc atc aaa gaa gtc ccc gat ccc tcc gga 163
 Phe Glu Gln Gln Ser Asp Gly Ile Lys Glu Val Pro Asp Pro Ser Gly
 10 15 20
 ctc ttc ctc tcc cac cgc ggc tct acc cca gac ggc acc gcg gtc acc 211
 Leu Phe Leu Ser His Arg Gly Ser Thr Pro Asp Gly Thr Ala Val Thr
 25 30 35
 gtc gcc atg gat ggc gtg cgc ccg cta tta gcg gag gtt caa agc ttg 259
 Val Ala Met Asp Gly Val Arg Pro Leu Leu Ala Glu Val Gln Ser Leu
 40 45 50
 ctt gtc gac gcc ccc tcc aag aat cca cgc agg gtc gtc acg ggc ctc 307
 Leu Val Asp Ala Pro Ser Lys Asn Pro Arg Arg Val Val Thr Gly Leu
 55 60 65
 gac gcc aat cgg gtc ccc atg gtc ctt gcg gtg tta tcc gca cgc gcc 355
 Asp Ala Asn Arg Val Pro Met Val Leu Ala Val Leu Ser Ala Arg Ala
 70 75 80 85
 gga cgc caa acc caa gga aaa gac gct tac gtg gca acc gtt ggt ggc 403
 Gly Arg Gln Thr Gln Gly Lys Asp Ala Tyr Val Ala Thr Val Gly Gly
 90 95 100

atg aaa gtt ggc gaa cca gca aca gac ctc gct gtc gcg ctc gct act 451
 Met Lys Val Gly Glu Pro Ala Thr Asp Leu Ala Val Ala Leu Ala Thr
 105 110 115

 gcc tcg gct tta gcc aag aaa cca cta cca gat aaa aca gtg gta ctc 499
 Ala Ser Ala Leu Ala Lys Lys Pro Leu Pro Asp Lys Thr Val Val Leu
 120 125 130

 ggt gaa gtc ggc ttg gcc gga gaa atc cgt cgc gtc ccc aac gtt gat 547
 Gly Glu Val Gly Leu Ala Gly Glu Ile Arg Arg Val Pro Asn Val Asp
 135 140 145

 cgc aga cta gcc gag gcg gaa cgt tta ggt tat gaa aaa gca gtc atc 595
 Arg Arg Leu Ala Glu Ala Glu Arg Leu Gly Tyr Glu Lys Ala Val Ile
 150 155 160 165

 ccc gga ggc tca ggc atc aaa caa aca agc ctg aga gtc atc gaa gct 643
 Pro Gly Gly Ser Gly Ile Lys Gln Thr Ser Leu Arg Val Ile Glu Ala
 170 175 180

 tca aca ctt gcc gaa gca ctt gca gca gta agc tta taaagcatga 689
 Ser Thr Leu Ala Glu Ala Leu Ala Ala Val Ser Leu
 185 190

 caccaacaac cac 702

<210> 46

<211> 193

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 46

Met Lys Ser Gly Cys Phe Glu Gln Gln Ser Asp Gly Ile Lys Glu Val
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 Pro Asp Pro Ser Gly Leu Phe Leu Ser His Arg Gly Ser Thr Pro Asp
 20 25 30

 Gly Thr Ala Val Thr Val Ala Met Asp Gly Val Arg Pro Leu Leu Ala
 35 40 45

 Glu Val Gln Ser Leu Leu Val Asp Ala Pro Ser Lys Asn Pro Arg Arg
 50 55 60

 Val Val Thr Gly Leu Asp Ala Asn Arg Val Pro Met Val Leu Ala Val
 65 70 75 80

 Leu Ser Ala Arg Ala Gly Arg Gln Thr Gln Gly Lys Asp Ala Tyr Val
 85 90 95

 Ala Thr Val Gly Gly Met Lys Val Gly Glu Pro Ala Thr Asp Leu Ala
 100 105 110

 Val Ala Leu Ala Thr Ala Ser Ala Leu Ala Lys Lys Pro Leu Pro Asp
 115 120 125

 Lys Thr Val Val Leu Gly Glu Val Gly Leu Ala Gly Glu Ile Arg Arg
 130 135 140

Val Pro Asn Val Asp Arg Arg Leu Ala Glu Ala Glu Arg Leu Gly Tyr
145 150 155 160

Glu Lys Ala Val Ile Pro Gly Gly Ser Gly Ile Lys Gln Thr Ser Leu
165 170 175

Arg Val Ile Glu Ala Ser Thr Leu Ala Glu Ala Leu Ala Ala Val Ser
180 185 190

Leu

<210> 47

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> RXN02291

<400> 47

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ccaccaactt cccagaccac cgcgcagggt tgcagctggc gtg gtg cac ctg ccc 115
Val Val His Leu Pro
1 5

aac ttc ctc ggc ttg gcc gag caa aag gca ctg gtc gcc cag gct cga 163
Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu Val Ala Gln Ala Arg
10 15 20

gac ctt gcg cgt gaa gtt gtg ggc aca ccg ttg gcg atg gtc cga ccc 211
Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu Ala Met Val Arg Pro
25 30 35

aag ctg aaa agt ggt cag atg agt gtc cat atg ttg cat tta gga aag 259
Lys Leu Lys Ser Gly Gln Met Ser Val His Met Leu His Leu Gly Lys
40 45 50

tac tgg gca tcc aat cct tat cgc tat gtg gat gtc gtt gat ggt ttt 307
Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp Val Val Asp Gly Phe
55 60 65

cca gtg cca cca ctg ccg gat tct ttc gtg gac ttg gca cac cga gca 355
Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp Leu Ala His Arg Ala
70 75 80 85

ttg ctg tct gca gga tct tta agc aat tca ctt cag tct tgg tcg gag 403
Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu Gln Ser Trp Ser Glu
90 95 100

gca tat cga gca gaa gcg gca ttg gtg aat tac tac tcg cca gat gct 451
Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr Tyr Ser Pro Asp Ala
105 110 115

tca atg ggc atg cac caa gac gct aat gaa gaa tcg gaa gcc cct gtg 499
Ser Met Gly Met His Gln Asp Ala Asn Glu Glu Ser Glu Ala Pro Val
120 125 130

atc tcc cta tcg atc ggt gat acc gga atc ttt cga ctg ggc ggc act 547
 Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe Arg Leu Gly Gly Thr
 135 140 145

cta aac cgc aat aaa ccg tgg aca gat atc cca cta atg agt ggt gat 595
 Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro Leu Met Ser Gly Asp
 150 155 160 165

ctc atc gtt ttc gga ggt gca aac agg caa gca ttt cat ggc att ccc 643
 Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala Phe His Gly Ile Pro
 170 175 180

tct att gag gcc aat act gca cct gca gga tgc ggg ttg aaa gaa ggg 691
 Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys Gly Leu Lys Glu Gly
 185 190 195

gaa tca aca tca cga tcc gcc aac ttg cac tat aaa act cca ggt aga 739
 Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr Lys Thr Pro Gly Arg
 200 205 210

ggt atg tct cgg ggg tgaaatagcc ccgcaatgtc cca 777
 Gly Met Ser Arg Gly
 215

<210> 48

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 48

Val Val His Leu Pro Asn Phe Leu Gly Leu Ala Glu Gln Lys Ala Leu
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Val Ala Gln Ala Arg Asp Leu Ala Arg Glu Val Val Gly Thr Pro Leu
 20 25 30

Ala Met Val Arg Pro Lys Leu Lys Ser Gly Gln Met Ser Val His Met
 35 40 45

Leu His Leu Gly Lys Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp
 50 55 60

Val Val Asp Gly Phe Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp
 65 70 75 80

Leu Ala His Arg Ala Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu
 85 90 95

Gln Ser Trp Ser Glu Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr
 100 105 110

Tyr Ser Pro Asp Ala Ser Met Gly Met His Gln Asp Ala Asn Glu Glu
 115 120 125

Ser Glu Ala Pro Val Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe
 130 135 140

Arg Leu Gly Gly Thr Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro
 145 150 155 160

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				Val	Val	His	Leu	Pro	5							
				1												
aac	ttc	ctc	ggc	ttg	gcc	gag	caa	aag	gca	ctg	gtc	gcc	cag	gct	cga	163
Asn	Phe	Leu	Gly	Leu	Ala	Glu	Gln	Lys	Ala	Leu	Val	Ala	Gln	Ala	Arg	20
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gac	ctt	gcg	cgt	gaa	gtt	gtg	ggc	aca	ccg	ttg	gcg	atg	gtc	cga	ccc	211
Asp	Leu	Ala	Arg	Glu	Val	Val	Gly	Thr	Pro	Leu	Ala	Met	Val	Arg	Pro	35
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Lys	Leu	Lys	Ser	Gly	Gln	Met	Ser	Val	His	Met	Leu	His	Leu	Gly	Lys	50
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Tyr	Trp	Ala	Ser	Asn	Pro	Tyr	Arg	Tyr	Val	Asp	Val	Val	Asp	Gly	Phe	65
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cca	gtg	cca	cca	ctg	ccg	gat	tct	ttc	gtg	gac	ttg	gca	cac	cga	gca	355
Pro	Val	Pro	Pro	Leu	Pro	Asp	Ser	Phe	Val	Asp	Leu	Ala	His	Arg	Ala	85
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ttg	ctg	tct	gca	gga	tct	tta	agc	aat	tca	ctt	cag	tct	tgg	tcg	gag	403
Leu	Leu	Ser	Ala	Gly	Ser	Leu	Ser	Asn	Ser	Leu	Gln	Ser	Trp	Ser	Glu	95
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gca	tat	cga	gca	gaa	gcg	gca	ttg	gtg	aat	tac	tac	tcg	cca	gat	gct	451
Ala	Tyr	Arg	Ala	Glu	Ala	Ala	Leu	Val	Asn	Tyr	Tyr	Ser	Pro	Asp	Ala	115
																105
tca	atg	ggc	atg	cac	caa	gac	gct	aat	gaa	gaa	tcg	gaa	gcc	cct	gtg	499
Ser	Met	Gly	Met	His	Gln	Asp	Ala	Asn	Glu	Glu	Ser	Glu	Ala	Pro	Val	

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120      125      130
atc tcc cta tcg atc ggt gat acc gga atc ttt cga ctg ggc ggc act 547
Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe Arg Leu Gly Gly Thr
135      140      145

cta aac cgc aat aaa ccg tgg aca gat atc cca cta atg agt ggt gat 595
Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro Leu Met Ser Gly Asp
150      155      160

ctc atc gtt ttc gga ggt gca aac agg caa gca ttt cat ggc att ccc 643
Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala Phe His Gly Ile Pro
170      175      180

tct att gag gcc aat act gca cct gca gga tgc ggg ttg aaa gaa ggg 691
Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys Gly Leu Lys Glu Gly
185      190      195

gaa tca aca tca cga tcc gcc aac ttg cac tat aaa act cca ggt aga 739
Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr Lys Thr Pro Gly Arg
200      205      210

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Gly Met Ser Arg Gly
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<210> 50
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<213> Corynebacterium glutamicum

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Ala Met Val Arg Pro Lys Leu Lys Ser Gly Gln Met Ser Val His Met
35      40      45

Leu His Leu Gly Lys Tyr Trp Ala Ser Asn Pro Tyr Arg Tyr Val Asp
50      55      60

Val Val Asp Gly Phe Pro Val Pro Pro Leu Pro Asp Ser Phe Val Asp
65      70      75      80

Leu Ala His Arg Ala Leu Leu Ser Ala Gly Ser Leu Ser Asn Ser Leu
85      90      95

Gln Ser Trp Ser Glu Ala Tyr Arg Ala Glu Ala Ala Leu Val Asn Tyr
100     105     110

Tyr Ser Pro Asp Ala Ser Met Gly Met His Gln Asp Ala Asn Glu Glu
115     120     125

Ser Glu Ala Pro Val Ile Ser Leu Ser Ile Gly Asp Thr Gly Ile Phe
130     135     140

Arg Leu Gly Gly Thr Leu Asn Arg Asn Lys Pro Trp Thr Asp Ile Pro

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Leu Met Ser Gly Asp	Leu Ile Val Phe Gly Gly Ala Asn Arg Gln Ala					
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Phe His Gly Ile Pro Ser Ile Glu Ala Asn Thr Ala Pro Ala Gly Cys						
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Gly Leu Lys Glu Gly Glu Ser Thr Ser Arg Ser Ala Asn Leu His Tyr						
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Lys Thr Pro Gly Arg Gly Met Ser Arg Gly						
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 Met His Ile Arg Ser Leu Glu Leu Arg Asp Tyr Arg Ser Trp
 1 5 10

cct gaa ctc aaa gtg gat ttg gaa cct gga att aca gtt ttt atc ggc 159
 Pro Glu Leu Lys Val Asp Leu Glu Pro Gly Ile Thr Val Phe Ile Gly
 15 20 25 30

cgc aac ggt ttt ggt aaa acc aac atc gtc gag gcc atc ggc tat ctt 207
 Arg Asn Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu
 35 40 45

gcg cat ttg tca tgc cat cgg gtg tcc tct gat gcg cca ttg gtg cgg 255
 Ala His Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg
 50 55 60

gcg cac gct gaa aac gcc cga gtt tgc gcg gtt gct gtt aat caa ggc 303
 Ala His Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly
 65 70 75

cga gaa ttg gca gct cac ttg ctg atc aaa ccc cat gct gcg aat cag 351
 Arg Glu Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln
 80 85 90

gca agt ttg aat cgc aca aaa gtc agg act ccc cgg gag ctg ctt ggt 399
 Ala Ser Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly
 95 100 105 110

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 Val Val Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys
 115 120 125

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Arg	Gln	Pro	Arg	Met	Ala	Gly	Val	Lys	Ala	Asp	Tyr	Asp	Lys	Val	Leu		
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aaa	caa	agg	aac	gcc	ctg	ctc	aag	acc	gcc	acc	att	gcg	ctt	cgt	cga	591	
Lys	Gln	Arg	Asn	Ala	Leu	Leu	Lys	Thr	Ala	Thr	Ile	Ala	Leu	Arg	Arg		
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Phe	Ala	Leu	Leu	Asn	Glu	Leu	Gly	Pro	Lys	Ile	Tyr	Glu	Ala	Tyr	Thr		
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Thr	Ile	Ala	Pro	Glu	Ser	Arg	Pro	Ala	Ala	Val	Asn	Tyr	Lys	Thr	Thr		
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Ile	Asp	Gln	Gly	Leu	Ser	Gln	Phe	Ser	Glu	Phe	Asp	Ala	Gly	Ile	Ile		
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gaa	gcc	acg	ctg	ctg	aca	gaa	ttg	gca	gcg	aaa	cgt	caa	cga	gaa	atc	879	
Glu	Ala	Thr	Leu	Leu	Thr	Glu	Leu	Ala	Ala	Lys	Arg	Gln	Arg	Glu	Ile		
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gaa	cgc	ggc	tca	agc	ctg	gtc	ggc	ccc	cac	cgc	gat	gat	gtc	gat	tta	927	
Glu	Arg	Gly	Ser	Ser	Leu	Val	Gly	Pro	His	Arg	Asp	Asp	Val	Asp	Leu		
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Met	Leu	Gly	Asp	Gln	Pro	Ala	Lys	Gly	Phe	Ala	Ser	His	Gly	Glu	Thr		
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Trp	Ser	Phe	Ala	Leu	Ser	Leu	Arg	Ile	Ala	Glu	Phe	Asn	Leu	Leu	Lys		
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tcc	gat	ggc	acc	gac	ccg	atc	ctc	atc	ttg	gat	gat	gtg	ttt	tcc	gag	1071	
Ser	Asp	Gly	Thr	Asp	Pro	Ile	Leu	Ile	Leu	Asp	Asp	Val	Phe	Ser	Glu		
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ctc	gac	gcc	ggc	cgt	cgc	gaa	aaa	ctc	gtg	ggc	ata	gcg	caa	gag	gtg	1119	
Leu	Asp	Ala	Gly	Arg	Arg	Glu	Lys	Leu	Val	Gly	Ile	Ala	Gln	Glu	Val		
335					340					345					350		
gaa	cag	gtg	ctc	atc	acc	gct	gca	gtc	cac	gac	gat	ctg	ccg	gag	aat	1167	
Glu	Gln	Val	Leu	Ile	Thr	Ala	Ala	Val	His	Asp	Asp	Leu	Pro	Glu	Asn		
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ctc	aag	aaa	gtg	ctc	act	gcg	cag	cac	acc	gtc	acc	gtc	caa	gac	acc	1215	
Leu	Lys	Lys	Val	Leu	Thr	Ala	Gln	His	Thr	Val	Thr	Val	Gln	Asp	Thr		

370 375 380
 ggc acc ggg cgg att tca ctc ctg gat gtg caa cca tgacagatcc 1261
 Gly Thr Gly Arg Ile Ser Leu Leu Asp Val Gln Pro
 385 390

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Gly Phe Gly Lys Thr Asn Ile Val Glu Ala Ile Gly Tyr Leu Ala His
 35 40 45
 Leu Ser Ser His Arg Val Ser Ser Asp Ala Pro Leu Val Arg Ala His
 50 55 60
 Ala Glu Asn Ala Arg Val Ser Ala Val Ala Val Asn Gln Gly Arg Glu
 65 70 75 80
 Leu Ala Ala His Leu Leu Ile Lys Pro His Ala Ala Asn Gln Ala Ser
 85 90 95
 Leu Asn Arg Thr Lys Val Arg Thr Pro Arg Glu Leu Leu Gly Val Val
 100 105 110
 Lys Thr Val Leu Phe Ala Pro Glu Asp Leu Ala Leu Val Lys Gly Glu
 115 120 125
 Pro Ala Glu Arg Arg Arg Tyr Leu Asp Asp Ile Ile Ala Thr Arg Gln
 130 135 140
 Pro Arg Met Ala Gly Val Lys Ala Asp Tyr Asp Lys Val Leu Lys Gln
 145 150 155 160
 Arg Asn Ala Leu Leu Lys Thr Ala Thr Ile Ala Leu Arg Arg Gly Tyr
 165 170 175
 Gly Thr Glu Glu Gly Ala Ala Ala Leu Ser Thr Leu Asp Thr Trp Asp
 180 185 190
 Gly Gln Leu Ala Arg Leu Gly Ala Glu Val Met Ala Ala Arg Phe Ala
 195 200 205
 Leu Leu Asn Glu Leu Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile
 210 215 220
 Ala Pro Glu Ser Arg Pro Ala Ala Val Asn Tyr Lys Thr Thr Ile Asp
 225 230 235 240
 Gln Gly Leu Ser Gln Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala

245										250					255															
Thr	Leu	Leu	Thr	Glu	Leu	Ala	Ala	Lys	Arg	Gln	Arg	Glu	Ile	Glu	Arg															
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Gly	Asp	Gln	Pro	Ala	Lys	Gly	Phe	Ala	Ser	His	Gly	Glu	Thr	Trp	Ser															
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Phe	Ala	Leu	Ser	Leu	Arg	Ile	Ala	Glu	Phe	Asn	Leu	Leu	Lys	Ser	Asp															
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Gly	Thr	Asp	Pro	Ile	Leu	Ile	Leu	Asp	Asp	Val	Phe	Ser	Glu	Leu	Asp															
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Ala	Gly	Arg	Arg	Glu	Lys	Leu	Val	Gly	Ile	Ala	Gln	Glu	Val	Glu	Gln															
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Val	Leu	Ile	Thr	Ala	Ala	Val	His	Asp	Asp	Leu	Pro	Glu	Asn	Leu	Lys															
		355					360					365																		
Lys	Val	Leu	Thr	Ala	Gln	His	Thr	Val	Thr	Val	Gln	Asp	Thr	Gly	Thr															
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385					390																									

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1				5					10					15						
cca gct gcg gtg aat tac aaa acc acc atc gat caa ggc ctg tcg cag																				96
Pro	Ala	Ala	Val	Asn	Tyr	Lys	Thr	Thr	Ile	Asp	Gln	Gly	Leu	Ser	Gln					
			20					25					30							
ttt tcc gaa ttc gat gcc ggc atc atc gaa gcc acg ctg ctg aca gaa																				144
Phe	Ser	Glu	Phe	Asp	Ala	Gly	Ile	Ile	Glu	Ala	Thr	Leu	Leu	Thr	Glu					
		35				40					45									
ttg gca gcg aaa cgt caa cga gaa atc gaa cgc ggc tca agc ctg gtc																				192
Leu	Ala	Ala	Lys	Arg	Gln	Arg	Glu	Ile	Glu	Arg	Gly	Ser	Ser	Leu	Val					
		50				55					60									
ggc ccc cac cgc gat gat gtc gat tta atg ctc ggc gat cag ccc gcc																				240
Gly	Pro	His	Arg	Asp	Asp	Val	Asp	Leu	Met	Leu	Gly	Asp	Gln	Pro	Ala					
65					70					75					80					

aaa ggc ttt gcc agc cac ggc gag acc tgg tct ttc gcg ctt tca ctg 288
 Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser Phe Ala Leu Ser Leu
 85 90 95

cga att gca gaa ttt aac ctg ctg aaa tcc gat ggc acc gac ccg atc 336
 Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp Gly Thr Asp Pro Ile
 100 105 110

ctc atc ttg gat gat gtg ttt tcc gag ctc gac gcc ggc cgt cgc gaa 384
 Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp Ala Gly Arg Arg Glu
 115 120 125

aaa ctc gtg ggc ata gcg caa gag gtg gaa cag gtg ctc atc acc gct 432
 Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln Val Leu Ile Thr Ala
 130 135 140

gca gtc cac gac gat ctg ccg gag aat ctc aag aaa gtg ctc act gcg 480
 Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys Lys Val Leu Thr Ala
 145 150 155 160

cag cac acc gtc acc gtc caa gac acc ggc acc ggg cgg att tca ctc 528
 Gln His Thr Val Thr Val Gln Asp Thr Gly Thr Gly Arg Ile Ser Leu
 165 170 175

ctg gat gtg caa cca tgacagatcc aattgagcag gca 566
 Leu Asp Val Gln Pro
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<210> 54

<211> 181

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

Gly Pro Lys Ile Tyr Glu Ala Tyr Thr Thr Ile Ala Pro Glu Ser Arg
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 20 25 30

Phe Ser Glu Phe Asp Ala Gly Ile Ile Glu Ala Thr Leu Leu Thr Glu
 35 40 45

Leu Ala Ala Lys Arg Gln Arg Glu Ile Glu Arg Gly Ser Ser Leu Val
 50 55 60

Gly Pro His Arg Asp Asp Val Asp Leu Met Leu Gly Asp Gln Pro Ala
 65 70 75 80

Lys Gly Phe Ala Ser His Gly Glu Thr Trp Ser Phe Ala Leu Ser Leu
 85 90 95

Arg Ile Ala Glu Phe Asn Leu Leu Lys Ser Asp Gly Thr Asp Pro Ile
 100 105 110

Leu Ile Leu Asp Asp Val Phe Ser Glu Leu Asp Ala Gly Arg Arg Glu
 115 120 125

Lys Leu Val Gly Ile Ala Gln Glu Val Glu Gln Val Leu Ile Thr Ala
 130 135 140

Ala Val His Asp Asp Leu Pro Glu Asn Leu Lys Lys Val Leu Thr Ala
145 150 155 160

Gln His Thr Val Thr Val Gln Asp Thr Gly Thr Gly Arg Ile Ser Leu
165 170 175

Leu Asp Val Gln Pro
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<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(754)

<223> RXA01252

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ttccttgtcc aatttttagt tcagataggt agtgtaagac gtg ttt gaa ggc cca 115
Val Phe Glu Gly Pro
1 5

ctc cag gat ctc atc gac gaa ctt tct cgt ctc ccc ggc gtc ggc ccc 163
Leu Gln Asp Leu Ile Asp Glu Leu Ser Arg Leu Pro Gly Val Gly Pro
10 15 20

aaa agt gcc caa cgc atc gca ttt cac ctg ctc aac gta gat cct tcc 211
Lys Ser Ala Gln Arg Ile Ala Phe His Leu Leu Asn Val Asp Pro Ser
25 30 35

gac att acc cgc ctt cag gaa gcc ctc gga ggc gtg cgt gat ggc gtc 259
Asp Ile Thr Arg Leu Gln Glu Ala Leu Gly Gly Val Arg Asp Gly Val
40 45 50

caa ttc tgc cgc atc tgc tgc aac att tcc cgc gaa gaa gtc tgt cgc 307
Gln Phe Cys Arg Ile Cys Cys Asn Ile Ser Arg Glu Glu Val Cys Arg
55 60 65

atc tgc tcc gac tcc gga cgt gac ggc gga aca atc tgt gtc gtc gaa 355
Ile Cys Ser Asp Ser Gly Arg Asp Gly Gly Thr Ile Cys Val Val Glu
70 75 80 85

gaa cca aaa gac atc caa gtt atc gag cgc acc ggc gaa ttc tcc ggc 403
Glu Pro Lys Asp Ile Gln Val Ile Glu Arg Thr Gly Glu Phe Ser Gly
90 95 100

cgc tac cac gtc ctc ggc ggc gcc ctc gac ccg ctg gcc aac atc ggc 451
Arg Tyr His Val Leu Gly Gly Ala Leu Asp Pro Leu Ala Asn Ile Gly
105 110 115

ccc cgc gaa ctc aac att tcc acg ctc ctg cag cgc atc ggc ggc gtc 499
Pro Arg Glu Leu Asn Ile Ser Thr Leu Leu Gln Arg Ile Gly Gly Val
120 125 130

ctg cca gac cgt gag ctc gca gat tcc acg cct gaa aat aag ctt ttc 547

Leu Pro Asp Arg Glu Leu Ala Asp Ser Thr Pro Glu Asn Lys Leu Phe
 135 140 145
 gac gcc acc ccc acc gtc cgc gaa gtc atc ctc gca aca gac ccc aac 595
 Asp Ala Thr Pro Thr Val Arg Glu Val Ile Leu Ala Thr Asp Pro Asn
 150 155 160 165
 acc gaa ggc gaa gcc acc gcc tca tac ctc ggc cgc ctc ttg aaa gac 643
 Thr Glu Gly Glu Ala Thr Ala Ser Tyr Leu Gly Arg Leu Leu Lys Asp
 170 175 180
 ttc cca gat ctg gta att tcc cgc ctc gca tcc gga atg cca cta ggc 691
 Phe Pro Asp Leu Val Ile Ser Arg Leu Ala Ser Gly Met Pro Leu Gly
 185 190 195
 ggc gac ctc gaa ttc gtc gac gaa ctc act ctc tcc cga gca ttg agt 739
 Gly Asp Leu Glu Phe Val Asp Glu Leu Thr Leu Ser Arg Ala Leu Ser
 200 205 210
 ggc cgc ctg cag atc tagccccctcc tttacaggct ggc 777
 Gly Arg Leu Gln Ile
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<210> 56
 <211> 218
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Pro Gly Val Gly Pro Lys Ser Ala Gln Arg Ile Ala Phe His Leu Leu
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 Asn Val Asp Pro Ser Asp Ile Thr Arg Leu Gln Glu Ala Leu Gly Gly
 35 40 45
 Val Arg Asp Gly Val Gln Phe Cys Arg Ile Cys Cys Asn Ile Ser Arg
 50 55 60
 Glu Glu Val Cys Arg Ile Cys Ser Asp Ser Gly Arg Asp Gly Gly Thr
 65 70 75 80
 Ile Cys Val Val Glu Glu Pro Lys Asp Ile Gln Val Ile Glu Arg Thr
 85 90 95
 Gly Glu Phe Ser Gly Arg Tyr His Val Leu Gly Gly Ala Leu Asp Pro
 100 105 110
 Leu Ala Asn Ile Gly Pro Arg Glu Leu Asn Ile Ser Thr Leu Leu Gln
 115 120 125
 Arg Ile Gly Gly Val Leu Pro Asp Arg Glu Leu Ala Asp Ser Thr Pro
 130 135 140
 Glu Asn Lys Leu Phe Asp Ala Thr Pro Thr Val Arg Glu Val Ile Leu
 145 150 155 160
 Ala Thr Asp Pro Asn Thr Glu Gly Glu Ala Thr Ala Ser Tyr Leu Gly

	165		170		175
Arg Leu Leu Lys Asp Phe Pro Asp Leu Val Ile Ser Arg Leu Ala Ser	180		185		190
Gly Met Pro Leu Gly Gly Asp Leu Glu Phe Val Asp Glu Leu Thr Leu	195		200		205
Ser Arg Ala Leu Ser Gly Arg Leu Gln Ile	210		215		

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 <223> RXA01878

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 Met Glu Glu Pro Ser 5
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 ggt gca cag ctg ctc ggc ccg gta gaa atc cgt gcg ctg gca gaa aag 163
 Gly Ala Gln Leu Leu Gly Pro Val Glu Ile Arg Ala Leu Ala Glu Lys 20
 10 15
 ctc gac gtc aca cca act aag aag ttg ggg cag aac ttt gtt cac gat 211
 Leu Asp Val Thr Pro Thr Lys Lys Leu Gly Gln Asn Phe Val His Asp 35
 25 30
 ccc aac acg gtg cgt cgc att gtt gct gcg gca gag ctg acc cca aac 259
 Pro Asn Thr Val Arg Arg Ile Val Ala Ala Ala Glu Leu Thr Pro Asn 50
 40 45
 gac cac gtg gtg gaa gtt ggc cct ggt ctg ggc tct ctg acc ctt gcc 307
 Asp His Val Val Glu Val Gly Pro Gly Leu Gly Ser Leu Thr Leu Ala 65
 55 60
 ctg gtg gaa tct gct gct tca gta act gcg gtg gaa att gat ccc cgt 355
 Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val Glu Ile Asp Pro Arg 85
 70 75 80
 ttg gct gcg gaa ttg ccg gag act ttt cag tgg cgc gcg ccg gcc ctt 403
 Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp Arg Ala Pro Ala Leu 100
 90 95
 gct cac aag ttg agc atc gtg ctg aaa gac gcc ctg aag gtt caa caa 451
 Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala Leu Lys Val Gln Gln 115
 105 110
 tcc gat atg gct gtt caa ccc acc gcc ttg gtg gct aac ttg ccg tac 499
 Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val Ala Asn Leu Pro Tyr 130
 120 125

aac gtc tct gtc cct gtc ttg ttg cac atg atg gag gag ttt ccc acc 547
 Asn Val Ser Val Pro Val Leu Leu His Met Met Glu Glu Phe Pro Thr
 135 140 145

 atc aac aag gtg ctt gtc atg gtg cag gca gag gtt gct gat cgt ttg 595
 Ile Asn Lys Val Leu Val Met Val Gln Ala Glu Val Ala Asp Arg Leu
 150 155 160 165

 gct gcg gat cca gga tcg aag att tat ggt gtg cct agc gtg aag gcg 643
 Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val Pro Ser Val Lys Ala
 170 175 180

 tcc ttc tac ggt cca gtt act cgc gcc ggg tcg att ggt aag aat gtc 691
 Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser Ile Gly Lys Asn Val
 185 190 195

 ttt tgg cca gct cca aag atc gaa tcc ggt ttg gtg aag atc gtg cgc 739
 Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu Val Lys Ile Val Arg
 200 205 210

 gaa gac acc gcg tgg aag cag gac gat gag acg cgt aag aag gtg tgg 787
 Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr Arg Lys Lys Val Trp
 215 220 225

 ccg atc att gat gct gct ttc ttg cag cgc cgt aaa acc cta aga gct 835
 Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg Lys Thr Leu Arg Ala
 230 235 240 245

 gcg ctt tct gga cac tac ggt tct ggc cag gca gct gag gaa gct ttg 883
 Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala Ala Glu Glu Ala Leu
 250 255 260

 cgg gcc gct gat att gat cca acg ctt cgt ggc gaa aag ctt gat gtc 931
 Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly Glu Lys Leu Asp Val
 265 270 275

 act gac tat gtg cgc cta gct ggg gtg ttg cag caa aag gat gag aag 979
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<210> 58

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

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 35 40 45

Glu Leu Thr Pro Asn Asp His Val Val Glu Val Gly Pro Gly Leu Gly
 50 55 60

Ser Leu Thr Leu Ala Leu Val Glu Ser Ala Ala Ser Val Thr Ala Val
 65 70 75 80
 Glu Ile Asp Pro Arg Leu Ala Ala Glu Leu Pro Glu Thr Phe Gln Trp
 85 90 95
 Arg Ala Pro Ala Leu Ala His Lys Leu Ser Ile Val Leu Lys Asp Ala
 100 105 110
 Leu Lys Val Gln Gln Ser Asp Met Ala Val Gln Pro Thr Ala Leu Val
 115 120 125
 Ala Asn Leu Pro Tyr Asn Val Ser Val Pro Val Leu Leu His Met Met
 130 135 140
 Glu Glu Phe Pro Thr Ile Asn Lys Val Leu Val Met Val Gln Ala Glu
 145 150 155 160
 Val Ala Asp Arg Leu Ala Ala Asp Pro Gly Ser Lys Ile Tyr Gly Val
 165 170 175
 Pro Ser Val Lys Ala Ser Phe Tyr Gly Pro Val Thr Arg Ala Gly Ser
 180 185 190
 Ile Gly Lys Asn Val Phe Trp Pro Ala Pro Lys Ile Glu Ser Gly Leu
 195 200 205
 Val Lys Ile Val Arg Glu Asp Thr Ala Trp Lys Gln Asp Asp Glu Thr
 210 215 220
 Arg Lys Lys Val Trp Pro Ile Ile Asp Ala Ala Phe Leu Gln Arg Arg
 225 230 235 240
 Lys Thr Leu Arg Ala Ala Leu Ser Gly His Tyr Gly Ser Gly Gln Ala
 245 250 255
 Ala Glu Glu Ala Leu Arg Ala Ala Asp Ile Asp Pro Thr Leu Arg Gly
 260 265 270
 Glu Lys Leu Asp Val Thr Asp Tyr Val Arg Leu Ala Gly Val Leu Gln
 275 280 285
 Gln Lys Asp Glu Lys
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<210> 59

<211> 872

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(849)

<223> RXA01556

<400> 59

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His Leu Gly His Val Trp Asn Asp Arg Leu Thr Phe Glu Tyr Ser Arg	
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Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe	
35 40 45	
acc gac cgc gtt ccc acc cct ccg ctg cca gct ccg cgt aaa gcg cgc	192
Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg	
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Ala Val Ala Gln Val Leu Val Ser Asn Pro Ala Asp Gln Thr Ser Leu	
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Glu Glu Phe Ala Glu Ile Gln Gly Val Ser Ala Arg Thr Leu Gln Arg	
85 90 95	
cag ttc ctc aaa tcc acg ggc tat tca ttc agc gaa tgg cgt gct gcg	336
Gln Phe Leu Lys Ser Thr Gly Tyr Ser Phe Ser Glu Trp Arg Ala Ala	
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Gln Arg Val Cys Val Ala Ala Ser Leu Leu Ala His Asp Phe Ser Ile	
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Ser Val Val Ala Asn Leu Val Gly Phe Ala Ala Thr Ser Ser Leu Thr	
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Arg Ala Phe Arg Arg His Thr Gly Ala Thr Pro Ser Thr Phe Thr Thr	
145 150 155 160	
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Gly Gln Ile Gly Met Gly Ser Ala Gly His Pro Pro Arg Ile Pro Ala	
165 170 175	
acc acc acg ttt gcc gaa gcg cat cag gac cag cag ctg tgg att tac	576
Thr Thr Thr Phe Ala Glu Ala His Gln Asp Gln Gln Leu Trp Ile Tyr	
180 185 190	
agc gga acc gca acc gtc acc acc ccc ggc tac tgc cga ttc atg gga	624
Ser Gly Thr Ala Thr Val Thr Thr Pro Gly Tyr Cys Arg Phe Met Gly	
195 200 205	
caa ggt gac atg gtg acc atc cct gcc ggc acc caa acc cgc att gac	672
Gln Gly Asp Met Val Thr Ile Pro Ala Gly Thr Gln Thr Arg Ile Asp	
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Val Ala Ala Gly Ser Ile Ala Phe Pro Val Pro Val Gly Leu Asp Glu	
225 230 235 240	
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Trp Gly Met Asp Leu Thr Arg Val Val Ala Val Asn Asn Gln Gln Pro	
245 250 255	
aag cca ctg acc att ttg gaa cag tct gaa tgg tcc aag ctc agc gaa	816

Lys Pro Leu Thr Ile Leu Glu Gln Ser Glu Trp Ser Lys Leu Ser Glu
 260 265 270

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 Glu Leu Leu Asn Thr Pro Val Pro Val Gln Met
 275 280

aaa

872

<210> 60

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 20 25 30

Ser Leu Phe Gly Lys Glu Thr Leu Ser Pro Asp Ile Ala Arg Leu Phe
 35 40 45

Thr Asp Arg Val Pro Thr Pro Pro Leu Pro Ala Pro Arg Lys Ala Arg
 50 55 60

Ala Val Ala Gln Val Leu Val Ser Asn Pro Ala Asp Gln Thr Ser Leu
 65 70 75 80

Glu Glu Phe Ala Glu Ile Gln Gly Val Ser Ala Arg Thr Leu Gln Arg
 85 90 95

Gln Phe Leu Lys Ser Thr Gly Tyr Ser Phe Ser Glu Trp Arg Ala Ala
 100 105 110

Gln Arg Val Cys Val Ala Ala Ser Leu Leu Ala His Asp Phe Ser Ile
 115 120 125

Ser Val Val Ala Asn Leu Val Gly Phe Ala Ala Thr Ser Ser Leu Thr
 130 135 140

Arg Ala Phe Arg Arg His Thr Gly Ala Thr Pro Ser Thr Phe Thr Thr
 145 150 155 160

Gly Gln Ile Gly Met Gly Ser Ala Gly His Pro Pro Arg Ile Pro Ala
 165 170 175

Thr Thr Thr Phe Ala Glu Ala His Gln Asp Gln Gln Leu Trp Ile Tyr
 180 185 190

Ser Gly Thr Ala Thr Val Thr Thr Pro Gly Tyr Cys Arg Phe Met Gly
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Gln Gly Asp Met Val Thr Ile Pro Ala Gly Thr Gln Thr Arg Ile Asp
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 225 230 235 240

<210> 62
 <211> 131
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Leu Ala Arg Glu Leu Lys Glu Glu Leu Leu Cys Asp Ala Thr Val
 50 55 60
 Gly Glu His Leu Thr Thr Thr Glu His Glu Tyr Asp Phe Gly Ile Val
 65 70 75 80
 Val Leu Ser Thr Tyr Phe Cys Thr Leu Asn Asp Ala Glu Pro Gln Leu
 85 90 95
 Thr Glu His Ala Glu Ile Arg Trp Val Ala Pro His Glu Leu Glu Ser
 100 105 110
 Leu Glu Trp Ala Pro Ala Asp Ile Pro Ala Val Lys Leu Leu Val Glu
 115 120 125
 Gln Leu Ala
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 Val Asp Thr Met Lys
 1 5
 ggc gac ggc gat gga tgg gca gca gca ccc aat ggc ggg gca gta tgg 163
 Gly Asp Gly Asp Gly Trp Ala Ala Ala Pro Asn Gly Gly Ala Val Trp
 10 15 20
 ggc aaa aac gga gca gca gga ttg ttg ttg gta gca gat aaa caa atg 211
 Gly Lys Asn Gly Ala Ala Gly Leu Leu Leu Val Ala Asp Lys Gln Met
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Ala Asp Lys Gln Met Leu Met Gln His Arg Ala Ala Trp Thr Asn Asn
      35                40              45

Gly Asp Thr Trp Ala Leu Pro Gly Gly Ala Arg Asp Ser His Glu Thr
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Ala Ala Glu Ser Ala Leu Arg Glu Ala Phe Glu Glu Thr Gly Ile Leu
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Pro Asp Asp Val Glu Val Leu Asp Ser Ile Val Thr Ala Gly Pro Phe
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Pro Ala Asp Pro Glu Arg Pro Glu Leu Ala Gly Asn Trp Thr Tyr Thr

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Lys Leu Leu Asn Thr Thr Glu			
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Phe Ile Val Ser Leu Arg Glu Lys Val Gly Gln Asp Pro Leu Trp Leu			
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Pro Ala Val Thr Ala Val Val Ile Arg Asp Val Pro Pro Gly Ser Pro			
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Phe His Val Val Pro Asp Val Leu Leu Val Lys Arg Ala Asp Thr Gly			
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Glu Trp Thr Pro Pro Thr Gly Ile Cys Asp Pro Asp Glu Gln Pro His			
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gtt gag gcg ttg ctt ggc gtg ggc gcg gtg ggg cct gtg acc tat caa		403	
Val Glu Ala Leu Leu Gly Val Gly Ala Val Gly Pro Val Thr Tyr Gln			
	90 95 100		
aat ggt gat gtg gcg agc tac atg gat acg acc atg cgt tgc gtt gtt		451	
Asn Gly Asp Val Ala Ser Tyr Met Asp Thr Thr Met Arg Cys Val Val			
	105 110 115		
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Ser Gly Asp Ser Asp Glu Pro His Val Gly Asp Asp Glu Asn Val Asp
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 Val Ala Trp Phe Pro Ile Ser Lys Met Pro Val Thr Asn Gln Arg Phe
 135 140 145

cgc atg gtc atc gct gat gcg gtg gca cag ttg aag cat ccg caa ggt 595
 Arg Met Val Ile Ala Asp Ala Val Ala Gln Leu Lys His Pro Gln Gly
 150 155 160 165

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 Tyr Lys Pro Arg Met Gly Tyr Glu Lys Arg Asn Ala Arg
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atttccgtta ggt 657

<210> 66
 <211> 178
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 <213> Corynebacterium glutamicum

<400> 66
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Asp Pro Leu Trp Leu Pro Ala Val Thr Ala Val Val Ile Arg Asp Val
 20 25 30

Pro Pro Gly Ser Pro Phe His Val Val Pro Asp Val Leu Leu Val Lys
 35 40 45

Arg Ala Asp Thr Gly Glu Trp Thr Pro Pro Thr Gly Ile Cys Asp Pro
 50 55 60

Asp Glu Gln Pro His Val Thr Ala Val Arg Glu Val Lys Glu Glu Thr
 65 70 75 80

Gly Leu Asp Val Ser Val Glu Ala Leu Leu Gly Val Gly Ala Val Gly
 85 90 95

Pro Val Thr Tyr Gln Asn Gly Asp Val Ala Ser Tyr Met Asp Thr Thr
 100 105 110

Met Arg Cys Val Val Ser Gly Asp Ser Asp Glu Pro His Val Gly Asp
 115 120 125

Asp Glu Asn Val Asp Val Ala Trp Phe Pro Ile Ser Lys Met Pro Val
 130 135 140

Thr Asn Gln Arg Phe Arg Met Val Ile Ala Asp Ala Val Ala Gln Leu
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Lys His Pro Gln Gly Tyr Lys Pro Arg Met Gly Tyr Glu Lys Arg Asn
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Ala Arg

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																	10						
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Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser Pro Thr Gly Arg Val																	85						
																	70						
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Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala Asp Glu Ala Leu Lys																	100						
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Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro Ala Asp His Leu Pro																	115						
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Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys Tyr Ala Leu Glu Arg																	130						
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Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala His Ser Phe Leu Gly																	145						
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Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val His Glu Ala Val Leu																	165						
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Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg Ser Val Ala Thr Ser																	180						
																	170						

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 Pro Asp Leu Ile Asp Thr Gly Glu Val Leu Ala Gly Thr Pro His Arg
 185 190 195

cca ccc aaa ctg ttc aga ttc caa aga taaattctga cgctcattcc agc 741
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<210> 68

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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 20 25 30

Leu Asn Lys Trp Ala Leu Pro Gly Gly Trp Leu Pro Pro His Glu Glu
 35 40 45

Leu Glu Asp Ala Ala Ala Arg Thr Leu Ala Glu Thr Thr Gly Leu His
 50 55 60

Pro Ser Tyr Leu Glu Gln Leu Tyr Thr Phe Gly Lys Val Asp Arg Ser
 65 70 75 80

Pro Thr Gly Arg Val Ile Ser Val Val Tyr Trp Ala Leu Val Arg Ala
 85 90 95

Asp Glu Ala Leu Lys Ala Ile Pro Gly Glu Asn Val Gln Trp Phe Pro
 100 105 110

Ala Asp His Leu Pro Glu Leu Ala Phe Asp His Asn Asn Ile Val Lys
 115 120 125

Tyr Ala Leu Glu Arg Leu Arg Thr Lys Val Glu Tyr Ser Glu Ile Ala
 130 135 140

His Ser Phe Leu Gly Glu Thr Phe Thr Ile Ala Gln Leu Arg Ser Val
 145 150 155 160

His Glu Ala Val Leu Gly His Lys Leu Asp Ala Ala Asn Phe Arg Arg
 165 170 175

Ser Val Ala Thr Ser Pro Asp Leu Ile Asp Thr Gly Glu Val Leu Ala
 180 185 190

Gly Thr Pro His Arg Pro Pro Lys Leu Phe Arg Phe Gln Arg
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<210> 69

<211> 522

<212> DNA

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 <223> RXA02290

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Leu Phe Glu Ile Leu Thr Leu Val Val Phe Gln Val Gly Val Thr Trp
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Phe Asp Val Ala Lys Val Ala Ala Phe Asn Glu Asp Asp Val Glu Arg
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Leu Leu Asp Asp Leu Gln Ile Phe Arg Asn Arg Arg Lys Ile Asn Ala
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Ala Ile Thr Asn Ala Lys Ala Leu Leu Glu Leu Asn Asp Glu Thr Gly
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Val Lys His Leu Lys Ala Leu Gly Phe Thr His Ile Gly Leu Thr Ser
                        105                        110                        115

ttg agc atc ctc cag cag gcc att ggg gtc aca gag ctg aag gct gcc 499
Leu Ser Ile Leu Gln Gln Ala Ile Gly Val Thr Glu Leu Lys Ala Ala
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<210> 70
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 <213> Corynebacterium glutamicum

<400> 70

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		40					45					50				
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Ile	Glu	Arg	Leu	Met	Glu	Asp	Ala	Gly	Ile	Val	Arg	Asn	Lys	Arg	Lys	
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Lys Gly Gly Leu Val Glu Phe Val Trp Gly Phe Lys Pro Ile Asp Thr
120 125 130

cca cag ccg gag acc ctg gag gag att ccg acg cag tcg ccg gag tca 547
Pro Gln Pro Glu Thr Leu Glu Glu Ile Pro Thr Gln Ser Pro Glu Ser
135 140 145

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Val Ala Leu Ser Lys Ala Leu Lys Lys Glu Gly Phe Ser Phe Val Gly
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ccc acg acg atg ttt gcc ctt atg gaa gcc ata gga atc gtc gac acc 643
Pro Thr Thr Met Phe Ala Leu Met Glu Ala Ile Gly Ile Val Asp Thr
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Ser Phe Arg Ala Ala Phe Ser Gln Phe Asp Pro Glu Leu Val Ala Lys
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Phe Thr Asp Ala Asp Ile Glu Arg Leu Met Glu Asp Ala Gly Ile Val
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Arg Asn Lys Arg Lys Ile Leu Ala Thr Ile Asn Asn Ala Lys Ala Thr
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Leu Gln Leu Arg Glu Lys Gly Gly Leu Val Glu Phe Val Trp Gly Phe
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Ile Trp Pro Arg Gln Thr Arg Lys Thr Ile Asp Ala Ser Phe Glu Gly	
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Gln Asn Ala Pro Pro Val Thr Ala Thr Val His Asp Phe Val Asp Ser
745 750 755

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Ala Cys Thr Asp His Gly Ile Asp Ala Leu Ala Glu Ile Ser Arg Ser
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Ser Arg Pro Asp Met Asp Met Ser Ser Tyr Asp Arg Phe Phe Pro Ala
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 Gly Ala Gly Arg Arg Lys Thr Thr Gly Ile Ile Asp Leu Ile Thr Val
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Ala Thr Pro Phe Arg Ser Asp His Met Asp Glu Ile Ile Thr Met Gln 565	570	575
Cys Gly Pro Val Arg His Arg Met Glu Val Ala Thr Asp Asn Glu Gln 580	585	590
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Ala Gln Ile Thr Ala Glu Val His Lys Ala Leu Glu Ala Gly Asp Arg 625	630	635 640
Cys Leu Val Leu Val Asn Arg Ile Ala Ala Leu Glu Ala Leu Thr Ser 645	650	655
Ser Ile Thr Glu Ser Gly Asp His Thr Val Leu Val Met His Gly Arg 660	665	670
Gln Thr Gln Glu Glu Arg Val His Leu Arg Ala Gln Leu Ala Ser Leu 675	680	685
Ser Glu Lys Gln Asp Pro Phe Val Leu Val Ala Met Asn Lys Val Ala 690	695	700
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Pro Val Ser Phe Lys Gly Leu Val Ile Gln Gln Ile Gly Arg Val Thr 725	730	735
Arg Ala Thr Gly Asp Gln Asn Ala Pro Pro Val Thr Ala Thr Val His 740	745	750
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gcg	gta	acg	tct	cga	gat	ctc	cgc	aat	caa	act	ggg	cat	gat	tca	gaa	1507
Ala 455	Val	Thr	Ser	Arg	Asp	Leu 460	Arg	Asn	Gln	Thr	Gly 465	His	Asp	Ser	Glu	
gac	atg	cgc	agc	tta	ctt	gac	gct	ttg	gtt	gat	cgg	ggc	gtt	cta	aac	1555
Asp	Met	Arg	Ser	Leu	Leu	Asp	Ala	Leu	Val	Asp	Arg	Gly	Val	Leu	Asn	

470	475	480	485	
caa aac tta cag aac caa tat cag ctt gcg aca tcg tct gtg aat gta				1603
Gln Asn Leu Gln Asn Gln Tyr Gln Leu Ala Thr Ser Ser Val Asn Val				
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act caa agc gaa caa gaa gtc tta gat gca atc aat aaa aca act cct				1651
Thr Gln Ser Glu Gln Glu Val Leu Asp Ala Ile Asn Lys Thr Thr Pro				
	505	510	515	
gtc aca att cga gaa att gcc aca aaa aca ggg aaa act gca tcg tct				1699
Val Thr Ile Arg Glu Ile Ala Thr Lys Thr Gly Lys Thr Ala Ser Ser				
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ctt cgg ccg ctg ctt cgt ggc ctt gtt gaa gca ggt ctt gtg gtt gca				1747
Leu Arg Pro Leu Leu Arg Gly Leu Val Glu Ala Gly Leu Val Val Ala				
	535	540	545	
act gct cca cca tca agc cgc aac cga gcg tac ttg aag gct				1789
Thr Ala Pro Pro Ser Ser Arg Asn Arg Ala Tyr Leu Lys Ala				
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Leu Ser Lys Gly Ser Lys Ser Phe Trp Glu Ser Leu Ser Ala Phe Ala				
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Asn Thr Asn Gly Gly Tyr Ile Leu Leu Gly Leu Ser Glu Pro Asp Phe				
	50	55	60	
Thr Pro Val Glu Gly Phe Asp Ser Gln Ala Ser Ile Gln Phe Ile Arg				
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Ala Gly Leu Asn Pro Gln Asp Arg Asp Ala Gln Lys Val Glu Pro Val				
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Pro His His Glu Ile His Glu Met Thr Val Asp Gly Ala Glu Val Val				
	100	105	110	
Leu Val Ser Val Ser Pro Leu Ser Val Asn Gly Pro Cys Tyr Tyr Leu				
	115	120	125	
Pro Val Gly Ile Thr Asn Gly Ser Phe Lys Arg Val Gly Asp Glu Asp				
	130	135	140	
Arg Lys Leu Ser His Leu Glu Ile Tyr Glu Leu Gln Asn Arg Phe Val				
	145	150	155	160

Gln Thr Lys Thr Asp Arg Asn Pro Val Pro Asp Ser Ser Ile Asp Asp
 165 170 175
 Leu Asn Asn Gln Leu Ala Ala Ser Phe Lys Gln Arg Leu Ile Glu Ser
 180 185 190
 Asn Ser Arg Ser Leu Gly Thr Asp Asp Asn Trp Leu Leu Arg Lys Asn
 195 200 205
 Ile Thr Thr Ser Lys Gly Glu Leu Thr Ile Ala Gly Leu Leu Ala Leu
 210 215 220
 Gly Ser Tyr Pro Gln Gln Phe Phe Pro Arg Val Ile Ile Asp Val Ala
 225 230 235 240
 Val His Pro Gly Leu His Lys Ser Pro Ile Gly Thr Ser Ile Arg Phe
 245 250 255
 Glu Asp Arg Lys Ile Cys Glu Gly Asn Leu Leu Glu Met Val Gln Glu
 260 265 270
 Ala Met Ser Ala Ile Lys Arg Asn Leu Arg Val Arg Arg Val Val Glu
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 Gly Leu Ser Gly Lys Asp Val Leu Glu Ile Pro Glu Glu Val Leu Arg
 290 295 300
 Glu Ala Leu Ala Asn Ala Val Leu His Arg Asp Tyr Ser Glu Leu Ala
 305 310 315 320
 Gln Asn Glu Ala Ile His Val Asp Ile Tyr Lys Asp Arg Val Glu Ile
 325 330 335
 Thr Ser Pro Gly Gly Leu Pro Asn Gly Lys Arg Pro Glu Ser Ile Leu
 340 345 350
 Asp Gly Tyr Ser Glu Pro Arg Asn Arg Val Leu Ser Arg Ile Leu Met
 355 360 365
 Asp Ile Pro Trp Thr His Glu Val Gln Gly Val Leu Ala Glu Ser Asn
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 Gly Thr Gly Val Pro Arg Met Phe Asn Leu Met Arg Glu Ala Gly Leu
 385 390 395 400
 Pro Val Pro Asn Phe Lys Ile Asp Ile Ser Ser Val Thr Val Glu Leu
 405 410 415
 Ser Arg His Gly Leu Leu Asp Ala Gln Thr Ser Glu Trp Leu Val Glu
 420 425 430
 Lys Leu Gly Ser Asp Phe Ser Asn Thr Gln Gly Ile Ala Leu Val Leu
 435 440 445
 Ala Lys Glu Leu Gly Ala Val Thr Ser Arg Asp Leu Arg Asn Gln Thr
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															Met Ser Asp Val Glu	5
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aga aca gag ttt gaa att ccg gga gga att cca cct cgt cga aac ggt	163															
Arg Thr Glu Phe Glu Ile Pro Gly Gly Ile Pro Pro Arg Arg Asn Gly																
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ggt caa ggc cgt gca gct gat acc aac gta gat gcg aac ctg aag cct	211															
Gly Gln Gly Arg Ala Ala Asp Thr Asn Val Asp Ala Asn Leu Lys Pro																
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gat gaa tac gat gcg gaa gta aca ctt cgt ccg aag tct ttg act gag	259															
Asp Glu Tyr Asp Ala Glu Val Thr Leu Arg Pro Lys Ser Leu Thr Glu																
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Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu Ser Leu Val Leu Thr																
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Gly Ala Lys Asn Arg Gly Val Val Pro Asp His Val Leu Leu Ser Gly																
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cct cct ggc ctg ggt aag acc acc atg gcg atg att atc gcc cag gag	403															
Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met Ile Ile Ala Gln Glu																
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ttg ggc acc agt ttg cgt atg acc tca ggc cca gcc ttg gaa cgc gca	451															
Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro Ala Leu Glu Arg Ala																

105						110						115						
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Gly	Asp	Leu	Ala	Ala	Met	Leu	Ser	Asn	Leu	Met	Glu	Gly	Asp	Val	Leu			
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Phe	Ile	Asp	Glu	Ile	His	Arg	Ile	Ala	Arg	Pro	Ala	Glu	Glu	Met	Leu			
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Tyr	Met	Ala	Met	Glu	Asp	Phe	Arg	Ile	Asp	Val	Ile	Val	Gly	Lys	Gly			
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cct	ggc	gct	acc	tca	atc	ccg	ctg	gag	atc	cca	ccc	ttt	acc	ctc	gtt	643		
Pro	Gly	Ala	Thr	Ser	Ile	Pro	Leu	Glu	Ile	Pro	Pro	Phe	Thr	Leu	Val			
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Gly	Ala	Thr	Thr	Arg	Ser	Gly	Met	Leu	Thr	Gly	Pro	Leu	Arg	Asp	Arg			
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Phe	Gly	Phe	Thr	Ala	Gln	Met	Glu	Phe	Tyr	Asp	Val	Pro	Asp	Leu	Thr			
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aaa	gtg	gtg	aaa	cga	aca	gct	aag	atc	ctc	gat	gtc	gga	atc	gac	aac	787		
Lys	Val	Val	Lys	Arg	Thr	Ala	Lys	Ile	Leu	Asp	Val	Gly	Ile	Asp	Asn			
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Asp	Ala	Ala	Val	Glu	Ile	Ala	Ser	Arg	Ser	Arg	Gly	Thr	Pro	Arg	Ile			
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gct	aac	cga	ctg	ctt	cgt	cga	gtc	cgt	gac	ttc	gct	gaa	gtt	cat	gcg	883		
Ala	Asn	Arg	Leu	Leu	Arg	Arg	Val	Arg	Asp	Phe	Ala	Glu	Val	His	Ala			
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gat	ggg	cac	atc	acg	atg	ggg	gct	gcc	aat	gct	gcg	ctg	att	gta	ttc	931		
Asp	Gly	His	Ile	Thr	Met	Gly	Ala	Ala	Asn	Ala	Ala	Leu	Ile	Val	Phe			
			265					270					275					
gat	gtc	gat	gaa	gtc	gga	ctc	gat	cgc	ctg	gat	agg	gca	gtg	ctt	gat	979		
Asp	Val	Asp	Glu	Val	Gly	Leu	Asp	Arg	Leu	Asp	Arg	Ala	Val	Leu	Asp			
		280					285					290						
gcc	ttg	atc	cgc	gga	cat	ggc	gga	ggc	cct	gtt	ggc	gtg	aac	aca	ctc	1027		
Ala	Leu	Ile	Arg	Gly	His	Gly	Gly	Gly	Pro	Val	Gly	Val	Asn	Thr	Leu			
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Ala	Val	Ala	Val	Gly	Glu	Glu	Pro	Gly	Thr	Val	Glu	Glu	Val	Cys	Glu			
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ccc	tat	ttg	gtg	cgt	gcc	ggc	atg	att	gca	cga	acc	gga	cgg	gga	cgc	1123		
Pro	Tyr	Leu	Val	Arg	Ala	Gly	Met	Ile	Ala	Arg	Thr	Gly	Arg	Gly	Arg			
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gtg	gca	acc	gca	gct	gca	tgg	aga	cac	ctg	ggg	ctg	gaa	cca	cca	gaa	1171		
Val	Ala	Thr	Ala	Ala	Ala	Trp	Arg	His	Leu	Gly	Leu	Glu	Pro	Pro	Glu			
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 35 40 45
 Lys Ser Leu Thr Glu Phe Ile Gly Gln Pro Lys Val Arg Asp Gln Leu
 50 55 60
 Ser Leu Val Leu Thr Gly Ala Lys Asn Arg Gly Val Val Pro Asp His
 65 70 75 80
 Val Leu Leu Ser Gly Pro Pro Gly Leu Gly Lys Thr Thr Met Ala Met
 85 90 95
 Ile Ile Ala Gln Glu Leu Gly Thr Ser Leu Arg Met Thr Ser Gly Pro
 100 105 110
 Ala Leu Glu Arg Ala Gly Asp Leu Ala Ala Met Leu Ser Asn Leu Met
 115 120 125
 Glu Gly Asp Val Leu Phe Ile Asp Glu Ile His Arg Ile Ala Arg Pro
 130 135 140
 Ala Glu Glu Met Leu Tyr Met Ala Met Glu Asp Phe Arg Ile Asp Val
 145 150 155 160
 Ile Val Gly Lys Gly Pro Gly Ala Thr Ser Ile Pro Leu Glu Ile Pro
 165 170 175
 Pro Phe Thr Leu Val Gly Ala Thr Thr Arg Ser Gly Met Leu Thr Gly
 180 185 190
 Pro Leu Arg Asp Arg Phe Gly Phe Thr Ala Gln Met Glu Phe Tyr Asp
 195 200 205
 Val Pro Asp Leu Thr Lys Val Val Lys Arg Thr Ala Lys Ile Leu Asp
 210 215 220
 Val Gly Ile Asp Asn Asp Ala Ala Val Glu Ile Ala Ser Arg Ser Arg
 225 230 235 240
 Gly Thr Pro Arg Ile Ala Asn Arg Leu Leu Arg Arg Val Arg Asp Phe
 245 250 255
 Ala Glu Val His Ala Asp Gly His Ile Thr Met Gly Ala Ala Asn Ala

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275	280	285
Arg Ala Val Leu Asp Ala Leu Ile Arg Gly His Gly Gly Gly Pro Val		
290	295	300
Gly Val Asn Thr Leu Ala Val Ala Val Gly Glu Glu Pro Gly Thr Val		
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Glu Glu Val Cys Glu Pro Tyr Leu Val Arg Ala Gly Met Ile Ala Arg		
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Thr Gly Arg Gly Arg Val Ala Thr Ala Ala Ala Trp Arg His Leu Gly		
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 <223> RXA00928

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 Met Ile Ala Ser Leu
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cgt ggc act gtt atc aac att ggt ctg agc tct gct gtc att gaa tgc 163
 Arg Gly Thr Val Ile Asn Ile Gly Leu Ser Ser Ala Val Ile Glu Cys
 10 15 20

aat ggc gtg ggc tat gag gtt gtc acc aca ccg aac acc ttg tca cag 211
 Asn Gly Val Gly Tyr Glu Val Val Thr Thr Pro Asn Thr Leu Ser Gln
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ttg gtc cgc ggt gag gaa gca ctg gtg ttg acc acc atg gtg gtc cgc 259
 Leu Val Arg Gly Glu Glu Ala Leu Val Leu Thr Thr Met Val Val Arg
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 Glu Asp Ala Met Lys Leu Tyr Gly Phe Ile Asp Asn Glu Ser Arg Glu
 55 60 65

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 Met Phe Ser Val Leu Gln Thr Val Ser Gly Leu Gly Pro Arg Leu Ala
 70 75 80 85

ttg gca tgt gaa tcg gtg ttg agc cca ctg gag att tct cag gcg atc 403
 Leu Ala Cys Glu Ser Val Leu Ser Pro Leu Glu Ile Ser Gln Ala Ile
 90 95 100

acc aat gcc gat gcc aaa act ttg cag cgg gtt ccg ggt gtg gga aag 451
 Thr Asn Ala Asp Ala Lys Thr Leu Gln Arg Val Pro Gly Val Gly Lys
 105 110 115

cgc atg gca gat cgt ctc atc gtg gag ctt aaa ggc aag gtc gca gct 499
 Arg Met Ala Asp Arg Leu Ile Val Glu Leu Lys Gly Lys Val Ala Ala
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 Phe Ala Ala Gly Val Val Asp Glu Gly Gly Glu Gln Ile Ser Leu Pro
 135 140 145

aac gcg aac att gct tct gag gtg gtt gtg gag cag gtt tct caa gcg 595
 Asn Ala Asn Ile Ala Ser Glu Val Val Val Glu Gln Val Ser Gln Ala
 150 155 160 165

ctg gtg ggg ttg ggc ttt agc gag aag caa tca gat gat gca gtg agc 643
 Leu Val Gly Leu Gly Phe Ser Glu Lys Gln Ser Asp Asp Ala Val Ser
 170 175 180

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 Phe Val Leu Ala Ala Asp Pro Ser Leu Asp Thr Ser Gly Ala Leu Arg
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<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

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 20 25 30

Asn Thr Leu Ser Gln Leu Val Arg Gly Glu Glu Ala Leu Val Leu Thr
 35 40 45

Thr Met Val Val Arg Glu Asp Ala Met Lys Leu Tyr Gly Phe Ile Asp
 50 55 60

Asn Glu Ser Arg Glu Met Phe Ser Val Leu Gln Thr Val Ser Gly Leu
 65 70 75 80

Gly Pro Arg Leu Ala Leu Ala Cys Glu Ser Val Leu Ser Pro Leu Glu
 85 90 95

Ile Ser Gln Ala Ile Thr Asn Ala Asp Ala Lys Thr Leu Gln Arg Val
 100 105 110

Pro Gly Val Gly Lys Arg Met Ala Asp Arg Leu Ile Val Glu Leu Lys
 115 120 125

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Met Phe Gly Ser Ser 1 5																
ttt aag gaa caa aca act aac ccg aga agt caa cga gtt tct tat ttg 163																
Phe Lys Glu Gln Thr Thr Asn Pro Arg Ser Gln Arg Val Ser Tyr Leu 10 15 20																
cgt gtc tct agc acc gat cag aat ctg gct cga caa cgt gaa gct gtt 211																
Arg Val Ser Ser Thr Asp Gln Asn Leu Ala Arg Gln Arg Glu Ala Val 25 30 35																
aac cat tcc ggt cat att gat cgt gag ttc aca gat gag ctt tcc ggt 259																
Asn His Ser Gly His Ile Asp Arg Glu Phe Thr Asp Glu Leu Ser Gly 40 45 50																
ggc gcc aaa tca cac aga cct ggc ttg gaa gac tgc att aat tat ctt 307																
Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp Cys Ile Asn Tyr Leu 55 60 65																
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Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile Asp Arg Leu Ala Arg 70 75 80 85																
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Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg Ile Thr Asp Lys Gly 90 95 100																
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Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr Phe Ala Ala Gly Arg 105 110 115																
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 Glu Phe Glu Arg Ser Ile Ile Arg Glu Arg Gln Ala Glu Gly Ile Ala
 135 140 145
 ctg gca aaa aag gcc ggc aag tat gca ggt cgc cca aaa gcc ctc gac 595
 Leu Ala Lys Lys Ala Gly Lys Tyr Ala Gly Arg Pro Lys Ala Leu Asp
 150 155 160 165
 aag gaa caa ata caa gaa gca aaa gat atg atc gct caa ggt gaa aca 643
 Lys Glu Gln Ile Gln Glu Ala Lys Asp Met Ile Ala Gln Gly Glu Thr
 170 175 180
 aaa tct gct gtc gcc aag cat ttt ggt att aat cgc tcg acc ttg tac 691
 Lys Ser Ala Val Ala Lys His Phe Gly Ile Asn Arg Ser Thr Leu Tyr
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 Glu Tyr Leu Lys Asn Pro Asp
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 <213> Corynebacterium glutamicum

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 35 40 45
 Asp Glu Leu Ser Gly Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp
 50 55 60
 Cys Ile Asn Tyr Leu Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile
 65 70 75 80
 Asp Arg Leu Ala Arg Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg
 85 90 95
 Ile Thr Asp Lys Gly Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr
 100 105 110
 Phe Ala Ala Gly Arg Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile
 115 120 125
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 Ala Glu Gly Ile Ala Leu Ala Lys Lys Ala Gly Lys Tyr Ala Gly Arg
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 Pro Lys Ala Leu Asp Lys Glu Gln Ile Gln Glu Ala Lys Asp Met Ile

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Ala Gln Gly Glu Thr Lys Ser Ala Val Ala Lys His Phe Gly Ile Asn						
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Arg Ser Thr Leu Tyr Glu Tyr Leu Lys Asn Pro Asp						
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				Met Phe Gly Ser Ser		
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Phe Lys Glu Gln Thr Thr Asn Pro Arg Ser Gln Arg Val Ser Tyr Leu						
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cgt gtc tct agc acc gat cag aat ctg gct cga caa cgt gaa gct gtt						211
Arg Val Ser Ser Thr Asp Gln Asn Leu Ala Arg Gln Arg Glu Ala Val						
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aac cat tcc ggt cat att gat cgt gag ttc aca gat gag ctt tcc ggt						259
Asn His Ser Gly His Ile Asp Arg Glu Phe Thr Asp Glu Leu Ser Gly						
	40		45		50	
ggc gcc aaa tca cac aga cct ggc ttg gaa gac tgc att aat tat ctt						307
Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp Cys Ile Asn Tyr Leu						
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cgc gag gat gat gtt ctt gtc gtc gca tcc att gac cga ctt gca cgc						355
Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile Asp Arg Leu Ala Arg						
	70		75		80	85
tcg ctg gtt gat tta cgc gtc atc att gac cgc atc aca gac aaa ggc						403
Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg Ile Thr Asp Lys Gly						
	90		95		100	
gca tcg gtc att ttt ctc aaa gag aat ttg act ttc gct gca ggc cgc						451
Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr Phe Ala Ala Gly Arg						
	105		110		115	
gat gat cct cga gca aac ctc atg ctc ggt att ttg ggc agt ttc gca						499
Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile Leu Gly Ser Phe Ala						
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gaa ttt gaa cgc tca att att cgc gag cgc caa gca gaa ggt att gcc						547
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Leu
150

550

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35 40 45
Asp Glu Leu Ser Gly Gly Ala Lys Ser His Arg Pro Gly Leu Glu Asp
50 55 60
Cys Ile Asn Tyr Leu Arg Glu Asp Asp Val Leu Val Val Ala Ser Ile
65 70 75 80
Asp Arg Leu Ala Arg Ser Leu Val Asp Leu Arg Val Ile Ile Asp Arg
85 90 95
Ile Thr Asp Lys Gly Ala Ser Val Ile Phe Leu Lys Glu Asn Leu Thr
100 105 110
Phe Ala Ala Gly Arg Asp Asp Pro Arg Ala Asn Leu Met Leu Gly Ile
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Met Ser Thr Val His
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gat gag atg ggc gtt atg aat aca aca gtg aag ttt tta cac tcc tcg 163

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Ile	Ala	Arg	Lys	Asn	Gln	Cys	Glu	Phe	Ile	Val	Leu	Ala	Gly	Asp	Val	
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Val	Glu	Ile	Ile	Gly	Ala	Pro	Leu	Leu	His	Lys	Met	Ala	Thr	Ser	Asp	
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Lys	Val	Leu	Ile	Val	Ser	Ala	Ser	Lys	Gly	Asp	Val	Ser	Val	Glu	Glu	

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<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

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Thr	Thr	Asp	His	Arg	Ala	Asp	Leu	Ile	Asp	Leu	Asn	Thr	Val	Glu	Ala
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Ile His Asp His Ile Thr Lys Ala Gln Glu Ile Thr Ile Ile Thr Asp
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Phe Asp Met Asp Gly Ile Ser Ala Gly Val Ile Ala Tyr Ala Gly Leu
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Glu Arg Asn Val Thr Ala Ser Asp Ile Asp Arg Ala Leu Glu Leu Tyr
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Asp His His Met Glu Val Glu Pro Cys Gln Ala Asp Val Val Leu Asn
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<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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Ile	Ser	Glu	Ser	Phe	Ile	Gly	Phe	Thr	Leu	Gly	Pro	Met	Phe	Asn	Ala
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Thr	Arg	Arg	Val	Gly	Gly	Asp	Met	His	Asp	Ser	Phe	Leu	Val	Phe	Ala
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Pro	His	Ala	Ala	Leu	Ala	Ser	Gln	Pro	Ser	Met	Asn	Pro	Asn	Arg	His
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 Ser Lys Ser Ser Tyr Ala Ala Val His Ser Ser Asp Gln Pro Tyr Ala
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 Pro Asp Thr Leu Ser Gly Ser Ala Arg Ser Pro Glu Trp Ala Pro Ile
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 Ala Ala Gly His Glu Tyr Ala Cys Gly Met Arg Phe Asp Asn His Asp
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 Asp Ile Val Thr Phe Val Ala Thr Leu Asp Ala Leu Asp Lys Asn Thr
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 Pro Arg Glu Ala Gln Pro Ala Asp Leu His Leu Val Asp Ile Asp His
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 Ala Arg Pro Val Leu Asp Asn Pro Ser Leu Thr Gln Glu Leu Ser Thr
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 Asp Val Thr Phe Arg Pro Ala Glu Thr Glu Phe Lys Val Met Gly Gln
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 His His Gln His Leu Lys Val Ile Thr His Ser Gly Leu Thr Leu Leu
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 Trp Trp Asn Lys Ala Gln Gln Leu Asp Glu Ile Ala Gln Ser Glu Leu
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                                         Met Asn His Glu Gly
                                         1           5

ctt cgg gta atg ggc att gac cca ggt ctt acc cgt tgt ggc tta tct 163
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Val Val Gln Ala Gly Arg Gly Arg Thr Val Tyr Pro Val Ser Val Gly
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Val Val Arg Thr Pro Pro Asp Ala Glu Leu Ala Glu Arg Leu Leu Arg
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ctc agc aaa gca gtg ggt gag tgg atg gat gag tac acc cca gat gtc 307
Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu Tyr Thr Pro Asp Val
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Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn Val Ser Thr Val Met
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aac act gcg cat gcg gtg ggt gtg ttg atc ttg gct gct gct gaa cgc 403
Asn Thr Ala His Ala Val Gly Val Leu Ile Leu Ala Ala Ala Glu Arg
                        90                      95                      100

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Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu Val Lys Lys Ala Ile
                        105                      110                      115

tcc ggt aat ggt cgc gct gat aag aaa cag atg acg gtc atg atc act 499
Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met Thr Val Met Ile Thr
                        120                      125                      130

cga att ctg ggc ctt ggt gag cca ccc aaa cct gct gac gcc gct gat 547
Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro Ala Asp Ala Ala Asp
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Ala Leu Ser Leu Ala Val Cys His Cys Trp Arg Ala Pro Met Leu Met
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Arg Ala Gln Ser Gln Tyr Ser Glu Gln Glu Leu Glu Lys Arg Arg Arg
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Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser Thr Tyr Asn Ala Glu
                        185                      190                      195

caa gct caa tcc cat gca tcc gat cct gct aaa gcg gct cat ccc agt 739
Gln Ala Gln Ser His Ala Ser Asp Pro Ala Lys Ala Ala His Pro Ser
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786

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 35 40 45
 Glu Arg Leu Leu Arg Leu Ser Lys Ala Val Gly Glu Trp Met Asp Glu
 50 55 60
 Tyr Thr Pro Asp Val Ile Ala Ile Glu Arg Val Phe Glu Arg Gly Asn
 65 70 75 80
 Val Ser Thr Val Met Asn Thr Ala His Ala Val Gly Val Leu Ile Leu
 85 90 95
 Ala Ala Ala Glu Arg Gly Leu Pro Val His Met Tyr Thr Pro Ser Glu
 100 105 110
 Val Lys Lys Ala Ile Ser Gly Asn Gly Arg Ala Asp Lys Lys Gln Met
 115 120 125
 Thr Val Met Ile Thr Arg Ile Leu Gly Leu Gly Glu Pro Pro Lys Pro
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 Ala Asp Ala Ala Asp Ala Leu Ser Leu Ala Val Cys His Cys Trp Arg
 145 150 155 160
 Ala Pro Met Leu Met Arg Ala Gln Ser Gln Tyr Ser Glu Gln Glu Leu
 165 170 175
 Glu Lys Arg Arg Arg Val Gln Gln Gly Lys Leu Gly Lys Ala Lys Ser
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 Thr Tyr Asn Ala Glu Gln Ala Gln Ser His Ala Ser Asp Pro Ala Lys
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 Ala Ala His Pro Ser Gln Phe Gln Arg Thr Asp Thr Asn
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<223> RXA02251

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                                         Val Ala Asp Pro Thr
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act tat cgc ccg gct cca gga aca att cca acg gag ccg ggt gtt tat 163
Thr Tyr Arg Pro Ala Pro Gly Thr Ile Pro Thr Glu Pro Gly Val Tyr
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Lys Phe Arg Asp Glu Asn Arg Arg Val Ile Tyr Val Gly Lys Ala Lys
                        25 30 35
aac ttg cgt tcg ccg ttg tcg aac tat ttc cag gat gtc acc caa ctg 259
Asn Leu Arg Ser Arg Leu Ser Asn Tyr Phe Gln Asp Val Thr Gln Leu
                        40 45 50
cat ccg cgc acc cgc caa atg gtg ttc gca gcg tcg tct gtg gag tgg 307
His Pro Arg Thr Arg Gln Met Val Phe Ala Ala Ser Ser Val Glu Trp
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acc gtg gtg tcc agc gaa gtc gag gcg ctg cag ctg gaa tac acc tgg 355
Thr Val Val Ser Ser Glu Val Glu Ala Leu Gln Leu Glu Tyr Thr Trp
                        70 75 80 85
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Ile Lys Arg Phe Asp Pro Arg Phe Lys Arg Lys Ile Pro Arg Arg
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  20 25 30
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  35 40 45
Asp Val Thr Gln Leu His Pro Arg Thr Arg Gln Met Val Phe Ala Ala
  50 55 60
Ser Ser Val Glu Trp Thr Val Val Ser Ser Glu Val Glu Ala Leu Gln
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Leu Glu Tyr Thr Trp Ile Lys Arg Phe Asp Pro Arg Phe Lys Arg Lys
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Leu Ile Arg Gly Ser
1 5
aac gta aaa tac cgc gac gat aaa acc tat ccc atg ctg gca gta tcc 163
Asn Val Lys Tyr Arg Asp Asp Lys Thr Tyr Pro Met Leu Ala Val Ser
10 15 20
aca ggg gag agg ttc ccg cgc gcg ttc ttc ttc cga ggt ccg cgc cgc 211
Thr Gly Glu Arg Phe Pro Arg Ala Phe Phe Phe Arg Gly Pro Arg Arg
25 30 35
aaa ggt gtg cgc tat ttc gga ccg tat tcc cac gcg tgg gca gtg cgg 259
Lys Gly Val Arg Tyr Phe Gly Pro Tyr Ser His Ala Trp Ala Val Arg
40 45 50
gaa acc ctt gat ctt ctc acc cgc gtt ttc ccc atg cgc acc tgt tca 307
Glu Thr Leu Asp Leu Leu Thr Arg Val Phe Pro Met Arg Thr Cys Ser
55 60 65
aag ggt gtg ttt aac cgc cac gaa agc ctc ggc cgg ccg tgt ttg ttg 355
Lys Gly Val Phe Asn Arg His Glu Ser Leu Gly Arg Pro Cys Leu Leu
70 75 80 85
ggc tat atc gat aaa tgt gcg gcc ccg tgc gtg ggc cgc gtg agc gaa 403
Gly Tyr Ile Asp Lys Cys Ala Ala Pro Cys Val Gly Arg Val Ser Glu
90 95 100
gag gaa cac cgc gaa atc gtt gac ggt ttc acc tct ttc atg gct ggt 451
Glu Glu His Arg Glu Ile Val Asp Gly Phe Thr Ser Phe Met Ala Gly
105 110 115
cac acc gac aaa gtc act cgc aaa ctc aac gcc gac atg atg gct gcg 499
His Thr Asp Lys Val Thr Arg Lys Leu Asn Ala Asp Met Met Ala Ala
120 125 130
gcc gag gaa ctc gat ttc gag cgc gcg gcc cgc ctg cgc gat gat ctg 547
Ala Glu Glu Leu Asp Phe Glu Arg Ala Ala Arg Leu Arg Asp Asp Leu
135 140 145
gaa gcc att gac aag gtc atg gaa aaa cag gcc gtc gtc ctt ggc gat 595
Glu Ala Ile Asp Lys Val Met Glu Lys Gln Ala Val Val Leu Gly Asp
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Gly Thr Asp Ala Asp Ile Ile Ala Phe Ala Thr Asp Gln Leu Glu Ala	
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Ala Val Gln Val Phe Asn Ile Arg Gly Gly Arg Ile Arg Gly Gln Arg	
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Gly Trp Val Val Glu Lys Pro Gly Asp Tyr Ala Gly Leu Leu Val Asp	
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Ala Thr Thr Gln Pro Glu Gly Asp Ala Pro Glu Thr Asp Pro Ala Leu	
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Pro Phe Leu Met Gln Asp Phe Leu Val Gln Phe Tyr Gly Asp Ala Val	
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Glu Arg Ala Glu Thr Glu Ala Lys Glu Asp Ala Ala Val Ile Glu Arg	
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Arg Gly Val Asp Lys His Ser Phe Glu Glu Ala Ala Pro Val Thr Arg	
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Ala Glu Gln Thr Leu Lys Val Leu Glu Glu Leu Arg Gly Ala Gly Val	
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Val Glu Arg Asn Ala Lys Glu Leu Leu Lys Gln His Lys Leu Lys Arg	
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Val Gly Asp Leu Thr Ala Arg Ser Ala Ala Leu Gln Glu Leu Gln Glu	
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Ala Leu Asp Met Glu Gln Ala Pro Leu Arg Ile Glu Cys Thr Asp Ile	
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Ser His Ile Gln Gly Thr Asp Val Val Ala Ser Leu Val Val Phe Glu	
375 380 385	
gat ggt ttg cct cga aaa tcg gac tac cga cgc tat cga gtc aaa gaa	1315
Asp Gly Leu Pro Arg Lys Ser Asp Tyr Arg Arg Tyr Arg Val Lys Glu	
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Thr	Arg	Arg	Arg	Phe	Leu	Arg	His	Asn	Gln	Asp	Lys	Leu	Ala	Val	Pro		
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gaa	gcc	gaa	gag	ttt	gac	ggc	tcg	acc	ttc	agc	gat	gaa	aaa	gtc	gag	1459	
Glu	Ala	Glu	Glu	Phe	Asp	Gly	Ser	Thr	Phe	Ser	Asp	Glu	Lys	Val	Glu		
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Ile	Val	Asp	Gly	Gly	Ala	Pro	Gln	Val	Ala	Ala	Ala	Gln	Glu	Val	Phe		
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gat	gaa	tta	ggc	atc	gtt	gac	gtg	gtg	ctc	att	ggc	cta	gcc	aag	cgc	1603	
Asp	Glu	Leu	Gly	Ile	Val	Asp	Val	Val	Leu	Ile	Gly	Leu	Ala	Lys	Arg		
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Leu	Glu	Glu	Ile	Trp	Leu	Pro	Gly	Asp	Pro	Asp	Pro	Val	Ile	Leu	Pro		
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Arg	Asn	Ser	Gln	Ala	Leu	Phe	Leu	Leu	Gln	Gln	Ile	Arg	Asp	Glu	Ala		
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cac	cgc	ttt	gcc	atc	acc	tac	cac	cgc	cag	caa	cga	tcc	aag	cgc	atg	1747	
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cgt	gtt	tcc	gag	cta	gat	agc	atc	aag	ggc	ctt	ggc	cag	agc	cgt	cgc	1795	
Arg	Val	Ser	Glu	Leu	Asp	Ser	Ile	Lys	Gly	Leu	Gly	Gln	Ser	Arg	Arg		
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Thr	Glu	Leu	Val	Lys	His	Phe	Gly	Ser	Val	Ala	Lys	Leu	Lys	Glu	Ala		
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Ser	Val	Glu	Asp	Ile	Ser	Gln	Val	Lys	Gly	Phe	Gly	Pro	Lys	Leu	Ala		
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Met	Arg	Thr	Cys
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Arg	Pro	Cys	Leu
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Gly	Arg	Val	Ser
			100
Ser	Phe	Met	Ala
			115
Asp	Met	Met	Ala
			130
Leu	Arg	Asp	Asp
			145
Val	Val	Leu	Gly
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Asp	Gln	Leu	Glu
			180
Ile	Arg	Gly	Gln
			195
Gly	Leu	Leu	Val
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Thr	Asp	Pro	Ala
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Tyr	Gly	Asp	Ala
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Ala	Val	Ile	Glu
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Ala	Pro	Val	Thr
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Val	Ala	Pro	Asn
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Arg	Gly	Ala	Gly
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Ala	Leu	Met	Glu
			325

His Lys Leu Lys Arg Val Gly Asp Leu Thr Ala Arg Ser Ala Ala Leu
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 Gln Glu Leu Gln Glu Ala Leu Asp Met Glu Gln Ala Pro Leu Arg Ile
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 Glu Cys Thr Asp Ile Ser His Ile Gln Gly Thr Asp Val Val Ala Ser
 370 375 380
 Leu Val Val Phe Glu Asp Gly Leu Pro Arg Lys Ser Asp Tyr Arg Arg
 385 390 395 400
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 405 410 415
 Ser Ile Ala Glu Ile Thr Arg Arg Arg Phe Leu Arg His Asn Gln Asp
 420 425 430
 Lys Leu Ala Val Pro Glu Ala Glu Glu Phe Asp Gly Ser Thr Phe Ser
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 Asp Glu Lys Val Glu Glu Met Ser Thr Asp Ala Arg Arg Phe Ala Tyr
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 Ala Gln Glu Val Phe Asp Glu Leu Gly Ile Val Asp Val Val Leu Ile
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 Pro Val Ile Leu Pro Arg Asn Ser Gln Ala Leu Phe Leu Leu Gln Gln
 515 520 525
 Ile Arg Asp Glu Ala His Arg Phe Ala Ile Thr Tyr His Arg Gln Gln
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 Arg Ser Lys Arg Met Arg Val Ser Glu Leu Asp Ser Ile Lys Gly Leu
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 Gly Gln Ser Arg Arg Thr Glu Leu Val Lys His Phe Gly Ser Val Ala
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<223> RXN02416

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 Val Arg Gly Ala Arg
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gaa cat aac cta aaa ggc gtg gat att gat ttg cca cgc gac tcg atg 163
 Glu His Asn Leu Lys Gly Val Asp Ile Asp Leu Pro Arg Asp Ser Met
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 Val Val Phe Thr Gly Leu Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe
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gac acc atc ttt gcg gaa ggc cag cgc cgt tac gtg gag tcg ttg tcc 259
 Asp Thr Ile Phe Ala Glu Gly Gln Arg Arg Tyr Val Glu Ser Leu Ser
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agt tac gcc cgc atg ttc ttg ggg cag atg gac aag ccg gac gtg gat 307
 Ser Tyr Ala Arg Met Phe Leu Gly Gln Met Asp Lys Pro Asp Val Asp
 55 60 65

ttg att gat gga tta tcc cca gcg gtc tcc att gac caa aaa tcc acc 355
 Leu Ile Asp Gly Leu Ser Pro Ala Val Ser Ile Asp Gln Lys Ser Thr
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aac cgc aac cct cgg tcc aca gtc ggt acc atc acg gaa gtc tat gac 403
 Asn Arg Asn Pro Arg Ser Thr Val Gly Thr Ile Thr Glu Val Tyr Asp
 90 95 100

tac ctg cgt ctt ctg tac gcc cgc gct ggt acc gca cac tgc cca gtg 451
 Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly Thr Ala His Cys Pro Val
 105 110 115

tgt gat gcc cgc gtg gag cgt caa acc ccc cag cag atg gtg gac caa 499
 Cys Asp Ala Arg Val Glu Arg Gln Thr Pro Gln Gln Met Val Asp Gln
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 Ile Leu Gly Met Glu Glu Gly Leu Lys Phe Gln Ile Leu Ala Pro Val
 135 140 145

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 Val Arg Thr Arg Lys Gly Glu Phe Val Asp Leu Phe Ala Asp Leu Ala
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 Ser Gln Gly Tyr Ser Arg Val Arg Val Asp Gly Glu Val His Gln Leu
 170 175 180

tcg gat cct cca aag cta gaa aag cag atc aag cac gat att gat gtt 691
 Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile Lys His Asp Ile Asp Val
 185 190 195

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Asp Ser Met Glu Thr Ala Leu Arg Leu Ala Asp Gly Val Ala Val Leu	
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Glu Phe Val Gly Leu Glu Glu Asp Asp Pro Asn Arg Leu Arg Arg Phe	
230 235 240 245	
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Ser Glu Lys Met Ser Cys Pro Asn Gly His Ala Leu Thr Val Asp Glu	
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ctg gag cct cgt gct ttt tcc ttc aac tct cct tat ggc gcg tgt cct	931
Leu Glu Pro Arg Ala Phe Ser Phe Asn Ser Pro Tyr Gly Ala Cys Pro	
265 270 275	
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Ala Cys Asp Gly Leu Gly Val Arg Thr Glu Val Asp Ile Asp Leu Ile	
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Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys Ala Val Gln Pro Trp Asn	
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Ser Ser Pro Asn His Ser Tyr Phe Glu Lys Leu Ile Glu Gly Leu Ala	
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Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro Tyr Ser Glu Leu Thr Ala	
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Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser Lys Glu Glu Val Ser Val	
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Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg Ser Trp Thr Ala Pro Phe	
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gaa ggt gtc atg ggc tac ttt gat cgc aag ttg gag cag act gat tcc	1267
Glu Gly Val Met Gly Tyr Phe Asp Arg Lys Leu Glu Gln Thr Asp Ser	
375 380 385	
gaa acc caa aaa gac cga ctg ttg ggc tac acc cgt gaa gtg ccc tgc	1315
Glu Thr Gln Lys Asp Arg Leu Leu Gly Tyr Thr Arg Glu Val Pro Cys	
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Pro Thr Cys Lys Gly Ala Arg Leu Lys Pro Glu Ile Leu Ala Val Arg	
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cta gac tcc gga agc cat gga gcg ttg tcc att gct gga cta acc gcg	1411
Leu Asp Ser Gly Ser His Gly Ala Leu Ser Ile Ala Gly Leu Thr Ala	
425 430 435	
ctg tcg gtg cat gaa gca ttc gag ttt ttg gat aac ctc aca ctg ggc	1459
Leu Ser Val His Glu Ala Phe Glu Phe Leu Asp Asn Leu Thr Leu Gly	
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Lys	Arg	Glu	Glu	Met	Ile	Ala	Gly	Ala	Val	Leu	Lys	Glu	Ile	His	Ala		
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cgc	ctg	aaa	ttc	ctg	ctt	gac	gtg	ggc	ctt	tcc	tac	ctc	acc	ctt	gat	1555	
Arg	Leu	Lys	Phe	Leu	Leu	Asp	Val	Gly	Leu	Ser	Tyr	Leu	Thr	Leu	Asp		
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Arg	Ala	Ala	Gly	Thr	Leu	Ser	Gly	Gly	Glu	Ala	Gln	Arg	Ile	Arg	Leu		
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gct	act	caa	att	ggg	tcc	ggg	ctg	gct	ggg	gtg	ctc	tac	gtc	ttg	gat	1651	
Ala	Thr	Gln	Ile	Gly	Ser	Gly	Leu	Ala	Gly	Val	Leu	Tyr	Val	Leu	Asp		
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gag	cca	tcc	att	ggg	ctg	cac	caa	cgt	gac	aac	cag	cgc	ttg	atc	act	1699	
Glu	Pro	Ser	Ile	Gly	Leu	His	Gln	Arg	Asp	Asn	Gln	Arg	Leu	Ile	Thr		
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acc	ctt	gag	cat	ctc	cga	gat	atc	gga	aac	acg	ctc	att	gtt	gtg	gaa	1747	
Thr	Leu	Glu	His	Leu	Arg	Asp	Ile	Gly	Asn	Thr	Leu	Ile	Val	Val	Glu		
	535					540					545						
cac	gat	gaa	gac	acc	atc	agg	cgc	gca	gat	tgg	ctc	gtg	gat	att	ggg	1795	
His	Asp	Glu	Asp	Thr	Ile	Arg	Arg	Ala	Asp	Trp	Leu	Val	Asp	Ile	Gly		
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cct	cga	gct	ggg	gaa	ttt	ggg	ggc	gaa	gtg	gtc	tac	caa	ggg	gag	cgc	1843	
Pro	Arg	Ala	Gly	Glu	Phe	Gly	Gly	Glu	Val	Val	Tyr	Gln	Gly	Glu	Pro		
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aag	ggc	att	ttg	gac	tgc	gaa	gaa	tcc	ctc	aca	ggg	gct	tac	ttg	tct	1891	
Lys	Gly	Ile	Leu	Asp	Cys	Glu	Glu	Ser	Leu	Thr	Gly	Ala	Tyr	Leu	Ser		
			585					590					595				
ggg	cgt	cga	acc	ctg	ggg	gtt	cct	gat	act	cgc	cgt	gag	atc	gac	aaa	1939	
Gly	Arg	Arg	Thr	Leu	Gly	Val	Pro	Asp	Thr	Arg	Arg	Glu	Ile	Asp	Lys		
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gag	cga	cag	ctc	aag	gtg	gtt	ggg	gct	agg	gaa	aat	aac	ctg	cag	ggc	1987	
Glu	Arg	Gln	Leu	Lys	Val	Val	Gly	Ala	Arg	Glu	Asn	Asn	Leu	Gln	Gly		
	615					620					625						
atc	gat	gtg	aaa	atc	cca	ctg	ggg	gtg	ctg	tgc	tgc	atc	act	ggg	gtg	2035	
Ile	Asp	Val	Lys	Ile	Pro	Leu	Gly	Val	Leu	Cys	Cys	Ile	Thr	Gly	Val		
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tgc	gga	tct	ggg	aaa	tcc	acg	ctg	gtc	aat	cag	att	ttg	gcc	aag	gtt	2083	
Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Val	Asn	Gln	Ile	Leu	Ala	Lys	Val		
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ctg	gcc	aac	aaa	ctc	aac	cgc	gca	cgc	caa	gtg	cct	ggg	cgc	gca	aag	2131	
Leu	Ala	Asn	Lys	Leu	Asn	Arg	Ala	Arg	Gln	Val	Pro	Gly	Arg	Ala	Lys		
			665					670					675				
cgg	gtg	gaa	ggc	ctc	gag	cac	ttg	gat	aag	ttg	gtc	caa	gtg	gat	cag	2179	
Arg	Val	Glu	Gly	Leu	Glu	His	Leu	Asp	Lys	Leu	Val	Gln	Val	Asp	Gln		
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tgc	cca	att	ggg	cgt	act	cca	cgt	tca	aac	cca	gcg	acg	tac	acg	ggg	2227	
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695	700	705	
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gtc cgc ggt tac aag cct ggc cgc ttc tcc ttc aat att aag ggt gga	2323		
Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser Phe Asn Ile Lys Gly Gly			
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cgc tgc gaa gca tgt cag ggc gat ggc acg ctg aag atc gaa atg aac	2371		
Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr Leu Lys Ile Glu Met Asn			
	745	750	755
ttc ctg ccc gac gtg tat gtt ccg tgt gaa gtc tgt gat ggt cag cgc	2419		
Phe Leu Pro Asp Val Tyr Val Pro Cys Glu Val Cys Asp Gly Gln Arg			
	760	765	770
tac aac cgc gag acc ctg gag gtg aag tac aag ggc aaa aac atc gct	2467		
Tyr Asn Arg Glu Thr Leu Glu Val Lys Tyr Lys Gly Lys Asn Ile Ala			
	775	780	785
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Glu Val Leu Gly Met Pro Ile Ser Glu Ala Ala Asp Phe Phe Glu Pro			
	790	795	800
atc acc tca att cac cga tac cta gca acg ctg gtt gat gtc ggc ctt	2563		
Ile Thr Ser Ile His Arg Tyr Leu Ala Thr Leu Val Asp Val Gly Leu			
	810	815	820
ggc tat gtc cgt ttg ggc cag gca gca aca acc ttg tct ggt ggt gaa	2611		
Gly Tyr Val Arg Leu Gly Gln Ala Ala Thr Thr Leu Ser Gly Gly Glu			
	825	830	835
gcc cag cgt gtg aaa ctt gcc gct gag ctg cag aag cgt tcc aac ggt	2659		
Ala Gln Arg Val Lys Leu Ala Ala Glu Leu Gln Lys Arg Ser Asn Gly			
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cgc acc gtt tac atc ctg gat gag cca act act ggt ttg cac ttt gaa	2707		
Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His Phe Glu			
	855	860	865
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Asp Ile Arg Lys Leu Met Met Val Ile Glu Gly Leu Val Asp Lys Gly			
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Asn Ser Val Ile Ile Ile Glu His Asn Leu Asp Val Ile Lys Ala Ala			
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tac acc ggc caa ttc ctt aaa gag ttg ttg taggagaaga tgaggggctt tca	2952		
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Ser	Ser	Leu	Ala	Phe	Asp	Thr	Ile	Phe	Ala	Glu	Gly	Gln	Arg	Arg	Tyr
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Val	Glu	Ser	Leu	Ser	Ser	Tyr	Ala	Arg	Met	Phe	Leu	Gly	Gln	Met	Asp
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Lys	Pro	Asp	Val	Asp	Leu	Ile	Asp	Gly	Leu	Ser	Pro	Ala	Val	Ser	Ile
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Asp	Gln	Lys	Ser	Thr	Asn	Arg	Asn	Pro	Arg	Ser	Thr	Val	Gly	Thr	Ile
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Thr	Glu	Val	Tyr	Asp	Tyr	Leu	Arg	Leu	Leu	Tyr	Ala	Arg	Ala	Gly	Thr
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Ala	His	Cys	Pro	Val	Cys	Asp	Ala	Arg	Val	Glu	Arg	Gln	Thr	Pro	Gln
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Gln	Met	Val	Asp	Gln	Ile	Leu	Gly	Met	Glu	Glu	Gly	Leu	Lys	Phe	Gln
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Ile	Leu	Ala	Pro	Val	Val	Arg	Thr	Arg	Lys	Gly	Glu	Phe	Val	Asp	Leu
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Phe	Ala	Asp	Leu	Ala	Ser	Gln	Gly	Tyr	Ser	Arg	Val	Arg	Val	Asp	Gly
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Glu	Val	His	Gln	Leu	Ser	Asp	Pro	Pro	Lys	Leu	Glu	Lys	Gln	Ile	Lys
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His	Asp	Ile	Asp	Val	Val	Val	Asp	Arg	Leu	Gln	Val	Lys	Ala	Ser	Gln
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Lys	Gln	Arg	Leu	Thr	Asp	Ser	Met	Glu	Thr	Ala	Leu	Arg	Leu	Ala	Asp
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Gly	Val	Ala	Val	Leu	Glu	Phe	Val	Gly	Leu	Glu	Glu	Asp	Asp	Pro	Asn
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Arg	Leu	Arg	Arg	Phe	Ser	Glu	Lys	Met	Ser	Cys	Pro	Asn	Gly	His	Ala
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Leu	Thr	Val	Asp	Glu	Leu	Glu	Pro	Arg	Ala	Phe	Ser	Phe	Asn	Ser	Pro
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Tyr	Gly	Ala	Cys	Pro	Ala	Cys	Asp	Gly	Leu	Gly	Val	Arg	Thr	Glu	Val
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 Ser Glu Leu Thr Ala Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser Lys
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 Asn Leu Thr Leu Gly Lys Arg Glu Glu Met Ile Ala Gly Ala Val Leu
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 465 470 475 480
 Tyr Leu Thr Leu Asp Arg Ala Ala Gly Thr Leu Ser Gly Gly Glu Ala
 485 490 495
 Gln Arg Ile Arg Leu Ala Thr Gln Ile Gly Ser Gly Leu Ala Gly Val
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 Leu Tyr Val Leu Asp Glu Pro Ser Ile Gly Leu His Gln Arg Asp Asn
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 Gln Arg Leu Ile Thr Thr Leu Glu His Leu Arg Asp Ile Gly Asn Thr
 530 535 540
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 Tyr Gln Gly Glu Pro Lys Gly Ile Leu Asp Cys Glu Glu Ser Leu Thr
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 Gly Ala Tyr Leu Ser Gly Arg Arg Thr Leu Gly Val Pro Asp Thr Arg
 595 600 605

Arg Glu Ile Asp Lys Glu Arg Gln Leu Lys Val Val Gly Ala Arg Glu
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 Asn Asn Leu Gln Gly Ile Asp Val Lys Ile Pro Leu Gly Val Leu Cys
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 Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Val Asn Gln
 645 650 655
 Ile Leu Ala Lys Val Leu Ala Asn Lys Leu Asn Arg Ala Arg Gln Val
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 Pro Gly Arg Ala Lys Arg Val Glu Gly Leu Glu His Leu Asp Lys Leu
 675 680 685
 Val Gln Val Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn Pro
 690 695 700
 Ala Thr Tyr Thr Gly Val Phe Asp Lys Val Arg Asn Leu Phe Ala Glu
 705 710 715 720
 Thr Thr Glu Ala Lys Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser Phe
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 Asn Ile Lys Gly Gly Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr Leu
 740 745 750
 Lys Ile Glu Met Asn Phe Leu Pro Asp Val Tyr Val Pro Cys Glu Val
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 Cys Asp Gly Gln Arg Tyr Asn Arg Glu Thr Leu Glu Val Lys Tyr Lys
 770 775 780
 Gly Lys Asn Ile Ala Glu Val Leu Gly Met Pro Ile Ser Glu Ala Ala
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 Asp Phe Phe Glu Pro Ile Thr Ser Ile His Arg Tyr Leu Ala Thr Leu
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 820 825 830
 Leu Ser Gly Gly Glu Ala Gln Arg Val Lys Leu Ala Ala Glu Leu Gln
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 Lys Arg Ser Asn Gly Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr Thr
 850 855 860
 Gly Leu His Phe Glu Asp Ile Arg Lys Leu Met Met Val Ile Glu Gly
 865 870 875 880
 Leu Val Asp Lys Gly Asn Ser Val Ile Ile Ile Glu His Asn Leu Asp
 885 890 895
 Val Ile Lys Ala Ala Asp Trp Ile Val Asp Met Gly Pro Glu Gly Gly
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930

935

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 Ile Thr Glu Val Tyr Asp Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly
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 Thr Ala His Cys Pro Val Cys Asp Ala Arg Val Glu Arg Gln Thr Pro
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 cag cag atg gtg gac caa atc ctt ggc atg gag gag gga ctg aag ttc 240
 Gln Gln Met Val Asp Gln Ile Leu Gly Met Glu Glu Gly Leu Lys Phe
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 caa atc ctt gcg cct gtg gtg cgt acc cgt aaa ggt gag ttc gtt gat 288
 Gln Ile Leu Ala Pro Val Val Arg Thr Arg Lys Gly Glu Phe Val Asp
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 Leu Phe Ala Asp Leu Ala Ser Gln Gly Tyr Ser Arg Val Arg Val Asp
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 Gly Glu Val His Gln Leu Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile
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 aag cac gat att gat gtt gtg gtt gac cgt ctg cag gta aaa gcc agc 432
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 Gln Lys Gln Arg Leu Thr Asp Ser Met Glu Thr Ala Leu Arg Leu Ala
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 Asp Gly Val Ala Val Leu Glu Phe Val Gly Leu Glu Glu Asp Asp Pro
 165 170 175
 aat agg ctt cgt cga ttc tct gaa aag atg agc tgc cct aac ggt cac 576
 Asn Arg Leu Arg Arg Phe Ser Glu Lys Met Ser Cys Pro Asn Gly His
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Pro Tyr Gly Ala Cys Pro Ala Cys Asp Gly Leu Gly Val Arg Thr Glu	
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Val Asp Ile Asp Leu Ile Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys	
225 230 235 240	
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Ala Val Gln Pro Trp Asn Ser Ser Pro Asn His Ser Tyr Phe Glu Lys	
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ctc att gaa ggc ctg gcg aaa gcc ctc gga ttt gat ccg gaa act ccg	816
Leu Ile Glu Gly Leu Ala Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro	
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Tyr Ser Glu Leu Thr Ala Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser	
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Lys Glu Glu Val Ser Val Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg	
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Thr Leu Ile Val Val Glu His Asp Glu Asp Thr Ile Arg Arg Ala Asp	
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Cys Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Val Asn	
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Phe	Asn	Ile	Lys	Gly	Gly	Arg	Cys	Glu	Ala	Cys	Gln	Gly	Asp	Gly	Thr		
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Val	Cys	Asp	Gly	Gln	Arg	Tyr	Asn	Arg	Glu	Thr	Leu	Glu	Val	Lys	Tyr		
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Lys	Gly	Lys	Asn	Ile	Ala	Glu	Val	Leu	Gly	Met	Pro	Ile	Ser	Glu	Ala		
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gcg	gac	ttc	ttt	gag	ccc	atc	acc	tca	att	cac	cga	tac	cta	gca	acg	2256	
Ala	Asp	Phe	Phe	Glu	Pro	Ile	Thr	Ser	Ile	His	Arg	Tyr	Leu	Ala	Thr		
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cag	aag	cgt	tcc	aac	ggg	cgc	acc	gtt	tac	atc	ctc	gat	gag	cca	act	2400	
Gln	Lys	Arg	Ser	Asn	Gly	Arg	Thr	Val	Tyr	Ile	Leu	Asp	Glu	Pro	Thr		
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Thr	Gly	Leu	His	Phe	Glu	Asp	Ile	Arg	Lys	Leu	Met	Met	Val	Ile	Glu		
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ggc	ctg	gtg	gac	aag	ggg	aac	tcc	gtg	atc	atc	atc	gag	cac	aac	ctc	2496	
Gly	Leu	Val	Asp	Lys	Gly	Asn	Ser	Val	Ile	Ile	Ile	Glu	His	Asn	Leu		
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gac	gtg	atc	aag	gct	gcc	gac	tgg	atc	gtg	gac	atg	ggg	cca	gag	ggc	2544	
Asp	Val	Ile	Lys	Ala	Ala	Asp	Trp	Ile	Val	Asp	Met	Gly	Pro	Glu	Gly		
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Gly	Ser	Gly	Gly	Gly	Thr	Val	Val	Ala	Glu	Gly	Thr	Pro	Glu	Gln	Val		
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gct	gaa	gtt	gcg	ggg	tcc	tac	acc	ggc	caa	ttc	ctt	aaa	gag	ttg	ttg	2640	
Ala	Glu	Val	Ala	Gly	Ser	Tyr	Thr	Gly	Gln	Phe	Leu	Lys	Glu	Leu	Leu		
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<213> Corynebacterium glutamicum

<400> 100

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Ile Thr Glu Val Tyr Asp Tyr Leu Arg Leu Leu Tyr Ala Arg Ala Gly	35	40	45
Thr Ala His Cys Pro Val Cys Asp Ala Arg Val Glu Arg Gln Thr Pro	50	55	60
Gln Gln Met Val Asp Gln Ile Leu Gly Met Glu Glu Gly Leu Lys Phe	65	70	75
Gln Ile Leu Ala Pro Val Val Arg Thr Arg Lys Gly Glu Phe Val Asp	85	90	95
Leu Phe Ala Asp Leu Ala Ser Gln Gly Tyr Ser Arg Val Arg Val Asp	100	105	110
Gly Glu Val His Gln Leu Ser Asp Pro Pro Lys Leu Glu Lys Gln Ile	115	120	125
Lys His Asp Ile Asp Val Val Val Asp Arg Leu Gln Val Lys Ala Ser	130	135	140
Gln Lys Gln Arg Leu Thr Asp Ser Met Glu Thr Ala Leu Arg Leu Ala	145	150	155
Asp Gly Val Ala Val Leu Glu Phe Val Gly Leu Glu Glu Asp Asp Pro	165	170	175
Asn Arg Leu Arg Arg Phe Ser Glu Lys Met Ser Cys Pro Asn Gly His	180	185	190
Ala Leu Thr Val Asp Glu Leu Glu Pro Arg Ala Phe Ser Phe Asn Ser	195	200	205
Pro Tyr Gly Ala Cys Pro Ala Cys Asp Gly Leu Gly Val Arg Thr Glu	210	215	220
Val Asp Ile Asp Leu Ile Ile Pro Asp Pro Asp Ala Pro Ala Thr Lys	225	230	235
Ala Val Gln Pro Trp Asn Ser Ser Pro Asn His Ser Tyr Phe Glu Lys	245	250	255
Leu Ile Glu Gly Leu Ala Lys Ala Leu Gly Phe Asp Pro Glu Thr Pro	260	265	270
Tyr Ser Glu Leu Thr Ala Ala Gln Lys Lys Ala Leu Val Tyr Gly Ser	275	280	285
Lys Glu Glu Val Ser Val Arg Tyr Lys Asn Arg Tyr Gly Arg Val Arg	290	295	300
Ser Trp Thr Ala Pro Phe Glu Gly Val Met Gly Tyr Phe Asp Arg Lys	305	310	315
Leu Glu Gln Thr Asp Ser Glu Thr Gln Lys Asp Arg Leu Leu Gly Tyr	325	330	335

Thr Arg Glu Val Pro Cys Pro Thr Cys Lys Gly Ala Arg Leu Lys Pro
 340 345 350
 Glu Ile Leu Ala Val Arg Leu Asp Ser Gly Ser His Gly Ala Leu Ser
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 Ile Ala Gly Leu Thr Ala Leu Ser Val His Glu Ala Phe Glu Phe Leu
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 Asp Asn Leu Thr Leu Gly Lys Arg Glu Glu Met Ile Ala Gly Ala Val
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 Leu Lys Glu Ile His Ala Arg Leu Lys Phe Leu Leu Asp Val Gly Leu
 405 410 415
 Ser Tyr Leu Thr Leu Asp Arg Ala Ala Gly Thr Leu Ser Gly Gly Glu
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 Ala Gln Arg Ile Arg Leu Ala Thr Gln Ile Gly Ser Gly Leu Ala Gly
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 Val Leu Tyr Val Leu Asp Glu Pro Ser Ile Gly Leu His Gln Arg Asp
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 Asn Gln Arg Leu Ile Thr Thr Leu Glu His Leu Arg Asp Ile Gly Asn
 465 470 475 480
 Thr Leu Ile Val Val Glu His Asp Glu Asp Thr Ile Arg Arg Ala Asp
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 Trp Leu Val Asp Ile Gly Pro Arg Ala Gly Glu Phe Gly Gly Glu Val
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 Val Tyr Gln Gly Glu Pro Lys Gly Ile Leu Asp Cys Glu Glu Ser Leu
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 Thr Gly Ala Tyr Leu Ser Gly Arg Arg Thr Leu Gly Val Pro Asp Thr
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 Arg Arg Glu Ile Asp Lys Glu Arg Gln Leu Lys Val Val Gly Ala Arg
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 Glu Asn Asn Leu Gln Gly Ile Asp Val Lys Ile Pro Leu Gly Val Leu
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 Cys Cys Ile Thr Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Val Asn
 580 585 590
 Gln Ile Leu Ala Lys Val Leu Ala Asn Lys Leu Asn Arg Ala Arg Gln
 595 600 605
 Val Pro Gly Arg Ala Lys Arg Val Glu Gly Leu Glu His Leu Asp Lys
 610 615 620
 Leu Val Gln Val Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn
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 Pro Ala Thr Tyr Thr Gly Val Phe Asp Lys Val Arg Asn Leu Phe Ala
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Glu Thr Thr Glu Ala Lys Val Arg Gly Tyr Lys Pro Gly Arg Phe Ser
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 Phe Asn Ile Lys Gly Gly Arg Cys Glu Ala Cys Gln Gly Asp Gly Thr
 675 680 685
 Leu Lys Ile Glu Met Asn Phe Leu Pro Asp Val Tyr Val Pro Cys Glu
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 Val Cys Asp Gly Gln Arg Tyr Asn Arg Glu Thr Leu Glu Val Lys Tyr
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 Lys Gly Lys Asn Ile Ala Glu Val Leu Gly Met Pro Ile Ser Glu Ala
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 Ala Asp Phe Phe Glu Pro Ile Thr Ser Ile His Arg Tyr Leu Ala Thr
 740 745 750
 Leu Val Asp Val Gly Leu Gly Tyr Val Arg Leu Gly Gln Ala Ala Thr
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 Thr Leu Ser Gly Gly Glu Ala Gln Arg Val Lys Leu Ala Ala Glu Leu
 770 775 780
 Gln Lys Arg Ser Asn Gly Arg Thr Val Tyr Ile Leu Asp Glu Pro Thr
 785 790 795 800
 Thr Gly Leu His Phe Glu Asp Ile Arg Lys Leu Met Met Val Ile Glu
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 Gly Leu Val Asp Lys Gly Asn Ser Val Ile Ile Ile Glu His Asn Leu
 820 825 830
 Asp Val Ile Lys Ala Ala Asp Trp Ile Val Asp Met Gly Pro Glu Gly
 835 840 845
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 Met Met Pro Tyr Ile
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 acc gat att gca gcg ctt gaa cat gtg ggt gtg gct gct gct tgg aca 163

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Glu	Lys	Val	Pro	Ala	Phe	Arg	Val	Leu	Arg	Glu	Lys	Arg	Met	Leu	Asp	
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Phe	Arg	Ala	Pro	Ile	Thr	Val	Ile	Thr	Gly	Glu	Asn	Gly	Val	Gly	Lys	
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Ser	Thr	Leu	Leu	Glu	Ala	Ile	Ala	Ile	Asn	Ala	Gly	Phe	Asp	Thr	Ala	
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Thr	Val	Ala	Lys	Ala	His	Lys	Gly	Lys	Glu	Pro	Met	Arg	Gly	Tyr	Phe	
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Leu	Arg	Ala	Glu	Thr	His	Phe	Asn	Val	Ala	Ser	Gly	Tyr	Arg	Asp	Glu	
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Met	His	Ile	Val	Gln	Asn	Ala	Phe	Val	Gly	Lys	Gly	Leu	Tyr	Leu	Met	
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Asp	Glu	Pro	Glu	Ala	Gly	Leu	Ser	Phe	Ile	Arg	Gln	Met	Ala	Ile	Leu	
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Thr	His	Ser	Pro	Val	Leu	Met	Ala	Ile	Pro	Gly	Ala	Glu	Ile	Trp	Glu	
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Phe	Ser	Ala	Ser	Gly	Glu	Leu	His	Arg	Gly	Phe	Asp	Phe	Glu	Val	Thr	
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Thr	Ala	Phe	Arg	Ala	Leu	Arg	Asp	Phe	Phe	Glu	Asp	Pro	Glu	Glu	Ile	
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gct	gag	tac	atg	atg	gac	gtc	atg	atg	gac	aac	aag	ggg	gag	tcc		832
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 35 40 45
 Asn Gly Val Gly Lys Ser Thr Leu Leu Glu Ala Ile Ala Ile Asn Ala
 50 55 60
 Gly Phe Asp Thr Ala Gly Gly Glu His Thr Gly Lys Phe Lys Pro Ser
 65 70 75 80
 Asp Asn Pro Leu Gln Thr Val Ala Lys Ala His Lys Gly Lys Glu Pro
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 Met Arg Gly Tyr Phe Leu Arg Ala Glu Thr His Phe Asn Val Ala Ser
 100 105 110
 Gly Tyr Arg Asp Glu Ala Pro Gly Trp Val Asn Leu His His Met Ser
 115 120 125
 His Gly Glu Ser Val Met His Ile Val Gln Asn Ala Phe Val Gly Lys
 130 135 140
 Gly Leu Tyr Leu Met Asp Glu Pro Glu Ala Gly Leu Ser Phe Ile Arg
 145 150 155 160
 Gln Met Ala Ile Leu Ala Glu Leu Asn Phe Leu Ala Glu Ser Gly Ala
 165 170 175
 Gln Ile Ile Ile Val Thr His Ser Pro Val Leu Met Ala Ile Pro Gly
 180 185 190
 Ala Glu Ile Trp Glu Phe Ser Ala Ser Gly Glu Leu His Arg Gly Phe
 195 200 205
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 Lys Gly Glu Ser

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<223> RXA02731

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                                         Met Ala Phe Ala Ala
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Glu His Pro Val Leu Ser His Ser Glu His Arg Pro Val Gly Glu Ile
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Glu Arg Ser Asp Asp Lys Phe Val Val Val Ser Glu Phe Glu Pro Ala
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Gly Asp Gln Pro Ala Ala Ile Lys Glu Leu Asp Glu Arg Leu Asp Arg
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Gly Glu Arg Asp Val Val Leu Met Gly Ala Thr Gly Thr Gly Lys Ser
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Ala Thr Ala Ala Trp Leu Ile Glu Lys Gln Gln Arg Pro Ala Leu Val
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Gln Leu Leu Pro Asn Asn Ala Val Glu Tyr Phe Val Ser Tyr Tyr Asp
                        105                        110                        115

tac tac cag cca gaa gcg tat atc gcg cag act gat acc tat att gaa 499
Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Gln Thr Asp Thr Tyr Ile Glu
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Lys Asp Ser Ser Ile Asn Glu Asp Val Glu Arg Leu Arg His Ser Ala
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Thr Ser Ser Leu Leu Ser Arg Arg Asp Val Val Val Val Ser Ser Val
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Ser Cys Ile Tyr Gly Leu Gly Thr Pro Gln Ser Tyr Leu Asp Arg Ser
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gtt gtg ttg aac gtg ggg gag gag atc gac cgc gat cgc ttt ttg cgc 691
Val Val Leu Asn Val Gly Glu Glu Ile Asp Arg Asp Arg Phe Leu Arg
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Gly	Ala	Phe	Arg	Val	Lys	Gly	Asp	Thr	Val	Asp	Ile	Ile	Pro	Ala	Tyr	
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Leu	Tyr	Tyr	Ile	His	Pro	Leu	Thr	Gly	Asp	Thr	Ile	Arg	Gln	Val	Asn	
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gag	atc	cgt	att	ttc	cca	gct	acg	cac	tat	gtt	gcg	gga	cct	gag	cgg	931
Glu	Ile	Arg	Ile	Phe	Pro	Ala	Thr	His	Tyr	Val	Ala	Gly	Pro	Glu	Arg	
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Ala	Asp	Leu	Glu	Asn	Arg	Gly	Lys	Leu	Leu	Glu	Ala	Gln	Arg	Leu	Arg	
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Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp	Gly	Arg	Gly	Glu	Gly	
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Thr	Ala	Pro	Ala	Thr	Leu	Ile	Asp	Tyr	Phe	Pro	Glu	Asp	Phe	Leu	Thr	
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Ile	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln	Ile	Gly	Gly	Met	Phe	
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Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Thr	Trp	Glu	Glu	Phe	Asp	
390					395					400					405	
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Glu	Ile	Ala	Ala	Ala	Asp	Gly	Glu	Phe	Val	Glu	Gln	Val	Ile	Arg	Pro	
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Thr	Gly	Leu	Val	Asp	Pro	Lys	Val	Thr	Val	Lys	Pro	Thr	Lys	Gly	Gln	

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tcg atg cag tat gcc atc gag gaa acc gat cga cgc cgt gaa aag cag Ser Met Gln Tyr Ala Ile Glu Glu Thr Asp Arg Arg Arg Glu Lys Gln 585 590 595			1891
gtc gct tat aac aag gaa cac ggc atc gat ccg cag ccg ctt cga aag Val Ala Tyr Asn Lys Glu His Gly Ile Asp Pro Gln Pro Leu Arg Lys 600 605 610			1939
aaa atc gcg gac atc ctc gac cag gtc tat gac aat tcc gct gat gga Lys Ile Ala Asp Ile Leu Asp Gln Val Tyr Asp Asn Ser Ala Asp Gly 615 620 625			1987
gca gga cct tct gcc tct ggc gat gcg gca gtc gtg gct aaa cct gac Ala Gly Pro Ser Ala Ser Gly Asp Ala Ala Val Val Ala Lys Pro Asp 630 635 640 645			2035
gtg tct agc atg ccc gcc aaa gaa gtg caa aag ctt atc gac gac ctc Val Ser Ser Met Pro Ala Lys Glu Val Gln Lys Leu Ile Asp Asp Leu 650 655 660			2083
agc gct cag atg gct gcg gcc gcg cgg gag ctc aag ttc gag ctg gca Ser Ala Gln Met Ala Ala Ala Ala Arg Glu Leu Lys Phe Glu Leu Ala 665 670 675			2131
ggg cgt ctg cga gat gag atc ttc gag ctc aag aag gaa ctg aga ggt Gly Arg Leu Arg Asp Glu Ile Phe Glu Leu Lys Lys Glu Leu Arg Gly 680 685 690			2179

atc aag gat gcc ggc atc taagtcagct tgctcactta aag
 ile lys asp ala gly ile
 695

2220

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 <211> 699
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 104
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 Pro Val Gly Glu Ile Glu Arg Ser Asp Asp Lys Phe Val Val Val Ser
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 Glu Phe Glu Pro Ala Gly Asp Gln Pro Ala Ala Ile Lys Glu Leu Asp
 35 40 45
 Glu Arg Leu Asp Arg Gly Glu Arg Asp Val Val Leu Met Gly Ala Thr
 50 55 60
 Gly Thr Gly Lys Ser Ala Thr Ala Ala Trp Leu Ile Glu Lys Gln Gln
 65 70 75 80
 Arg Pro Ala Leu Val Met Ala Pro Asn Lys Thr Leu Ala Ala Gln Leu
 85 90 95
 Ala Asn Glu Leu Arg Gln Leu Leu Pro Asn Asn Ala Val Glu Tyr Phe
 100 105 110
 Val Ser Tyr Tyr Asp Tyr Tyr Gln Pro Glu Ala Tyr Ile Ala Gln Thr
 115 120 125
 Asp Thr Tyr Ile Glu Lys Asp Ser Ser Ile Asn Glu Asp Val Glu Arg
 130 135 140
 Leu Arg His Ser Ala Thr Ser Ser Leu Leu Ser Arg Arg Asp Val Val
 145 150 155 160
 Val Val Ser Ser Val Ser Cys Ile Tyr Gly Leu Gly Thr Pro Gln Ser
 165 170 175
 Tyr Leu Asp Arg Ser Val Val Leu Asn Val Gly Glu Glu Ile Asp Arg
 180 185 190
 Asp Arg Phe Leu Arg Leu Leu Val Asp Ile Gln Tyr Glu Arg Asn Asp
 195 200 205
 Val Gly Phe Thr Arg Gly Ala Phe Arg Val Lys Gly Asp Thr Val Asp
 210 215 220
 Ile Ile Pro Ala Tyr Glu Glu Leu Ala Val Arg Ile Glu Phe Phe Gly
 225 230 235 240
 Asp Glu Ile Asp Ala Leu Tyr Tyr Ile His Pro Leu Thr Gly Asp Thr
 245 250 255
 Ile Arg Gln Val Asn Glu Ile Arg Ile Phe Pro Ala Thr His Tyr Val

260					265					270					
Ala	Gly	Pro	Glu	Arg	Met	Glu	Lys	Ala	Val	Ala	Asp	Ile	Lys	Ala	Glu
		275					280					285			
Leu	Glu	Val	Arg	Leu	Ala	Asp	Leu	Glu	Asn	Arg	Gly	Lys	Leu	Leu	Glu
		290					295					300			
Ala	Gln	Arg	Leu	Arg	Met	Arg	Thr	Glu	Tyr	Asp	Leu	Glu	Met	Ile	Glu
							310					315			320
Gln	Val	Gly	Phe	Cys	Ser	Gly	Ile	Glu	Asn	Tyr	Ser	Arg	His	Ile	Asp
				325					330					335	
Gly	Arg	Gly	Glu	Gly	Thr	Ala	Pro	Ala	Thr	Leu	Ile	Asp	Tyr	Phe	Pro
				340					345					350	
Glu	Asp	Phe	Leu	Thr	Ile	Ile	Asp	Glu	Ser	His	Val	Thr	Val	Pro	Gln
		355					360					365			
Ile	Gly	Gly	Met	Phe	Glu	Gly	Asp	Met	Ser	Arg	Lys	Arg	Asn	Leu	Val
		370					375					380			
Glu	Phe	Gly	Phe	Arg	Leu	Pro	Ser	Ala	Met	Asp	Asn	Arg	Pro	Leu	Thr
							390					395			400
Trp	Glu	Glu	Phe	Asp	Glu	Arg	Arg	Gly	Gln	Thr	Val	Phe	Met	Ser	Ala
				405					410					415	
Thr	Pro	Gly	Lys	Phe	Glu	Ile	Ala	Ala	Ala	Asp	Gly	Glu	Phe	Val	Glu
				420					425					430	
Gln	Val	Ile	Arg	Pro	Thr	Gly	Leu	Val	Asp	Pro	Lys	Val	Thr	Val	Lys
				435					440					445	
Pro	Thr	Lys	Gly	Gln	Ile	Asp	Asp	Leu	Ile	His	Glu	Ile	Arg	Gln	Arg
							455					460			
Thr	Asp	Lys	Asp	Glu	Arg	Val	Leu	Val	Thr	Thr	Leu	Thr	Lys	Lys	Met
							470					475			480
Ala	Glu	Asp	Leu	Thr	Asp	Tyr	Leu	Leu	Glu	Asn	Gly	Ile	Arg	Val	Arg
									490					495	
Tyr	Leu	His	Ser	Asp	Ile	Asp	Thr	Leu	Gln	Arg	Val	Glu	Leu	Leu	Arg
			500						505					510	
Gln	Leu	Arg	Leu	Gly	Glu	Tyr	Asp	Val	Leu	Val	Gly	Ile	Asn	Leu	Leu
				515			520					525			
Arg	Glu	Gly	Leu	Asp	Leu	Pro	Glu	Val	Ser	Leu	Val	Ala	Ile	Leu	Asp
							535					540			
Ala	Asp	Lys	Glu	Gly	Phe	Leu	Arg	Ser	Thr	Thr	Ser	Leu	Ile	Gln	Thr
							550					555			560
Ile	Gly	Arg	Ala	Ala	Arg	Asn	Val	Ser	Gly	Glu	Val	Ile	Met	Tyr	Ala
				565					570					575	
Asp	Lys	Ile	Thr	Asp	Ser	Met	Gln	Tyr	Ala	Ile	Glu	Glu	Thr	Asp	Arg
				580					585					590	

Arg Arg Glu Lys Gln Val Ala Tyr Asn Lys Glu His Gly Ile Asp Pro
 595 600 605

Gln Pro Leu Arg Lys Lys Ile Ala Asp Ile Leu Asp Gln Val Tyr Asp
 610 615 620

Asn Ser Ala Asp Gly Ala Gly Pro Ser Ala Ser Gly Asp Ala Ala Val
 625 630 635 640

Val Ala Lys Pro Asp Val Ser Ser Met Pro Ala Lys Glu Val Gln Lys
 645 650 655

Leu Ile Asp Asp Leu Ser Ala Gln Met Ala Ala Ala Ala Arg Glu Leu
 660 665 670

Lys Phe Glu Leu Ala Gly Arg Leu Arg Asp Glu Ile Phe Glu Leu Lys
 675 680 685

Lys Glu Leu Arg Gly Ile Lys Asp Ala Gly Ile
 690 695

<210> 105
 <211> 585
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(562)
 <223> RXA00998

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tgaaaatcca accatttttag gccgactaga gtaattaatt atg act tcc cgc gat 115
 Met Thr Ser Arg Asp
 1 5

gat caa ccc caa gat ctg ctt tcg ctt gca gaa ctt gcc gcc acc aga 163
 Asp Gln Pro Gln Asp Leu Leu Ser Leu Ala Glu Leu Ala Ala Thr Arg
 10 15 20

gct tta acc aca gac gaa ctt gaa gca ctc aac aac gcc aat tat ggc 211
 Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn Asn Ala Asn Tyr Gly
 25 30 35

ctc gac cgc aat ctg ggg ctg cgc tac acc acc atc gag ccc ggc cgg 259
 Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr Ile Glu Pro Gly Arg
 40 45 50

gtg gtc agc gaa ctt cac gtg gca tcc aag cac ctg caa gtg gtg ggc 307
 Val Val Ser Glu Leu His Val Ala Ser Lys His Leu Gln Val Val Gly
 55 60 65

ttg gtc aac ggt ggt gtc tac gcc gcc atc gcc gaa tcc act gga tca 355
 Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala Glu Ser Thr Gly Ser
 70 75 80 85

gtc gcc agc atg att tcc gcc cct gga aaa atg gtc gtc ggc atc aac 403

Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met Val Val Gly Ile Asn
 90 95 100

aac aac acc gac ttc att tct gct gtg agc tcc ggt gtc atc gtg gcc 451
 Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser Gly Val Ile Val Ala
 105 110 115

gaa gca acg ccg att cag cta ggt ggc cgc acc cat ctg tgg cag atc 499
 Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr His Leu Trp Gln Ile
 120 125 130

gaa tgc acc cac cgc gga gaa gtc gtc gca cga acc aca ctg cgc acc 547
 Glu Cys Thr His Arg Gly Glu Val Val Ala Arg Thr Thr Leu Arg Thr
 135 140 145

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 Met Val Leu Asn Lys
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<210> 106
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 106
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Leu Ala Ala Thr Arg Ala Leu Thr Thr Asp Glu Leu Glu Ala Leu Asn
 20 25 30

Asn Ala Asn Tyr Gly Leu Asp Arg Asn Leu Gly Leu Arg Tyr Thr Thr
 35 40 45

Ile Glu Pro Gly Arg Val Val Ser Glu Leu His Val Ala Ser Lys His
 50 55 60

Leu Gln Val Val Gly Leu Val Asn Gly Gly Val Tyr Ala Ala Ile Ala
 65 70 75 80

Glu Ser Thr Gly Ser Val Ala Ser Met Ile Ser Ala Pro Gly Lys Met
 85 90 95

Val Val Gly Ile Asn Asn Asn Thr Asp Phe Ile Ser Ala Val Ser Ser
 100 105 110

Gly Val Ile Val Ala Glu Ala Thr Pro Ile Gln Leu Gly Gly Arg Thr
 115 120 125

His Leu Trp Gln Ile Glu Cys Thr His Arg Gly Glu Val Val Ala Arg
 130 135 140

Thr Thr Leu Arg Thr Met Val Leu Asn Lys
 145 150

<210> 107
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> RXN02386

<400> 107

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ttgggtttttc acccgtgaga aaccctgtaa tccacccacc atg gcg gcg ttg gcg 115
 Met Ala Ala Leu Ala
 1 5

gaa aac tat caa aca ccg gcg ccg agt tcg cag gtg gtg gtg tct gtg 163
 Glu Asn Tyr Gln Thr Pro Ala Pro Ser Ser Gln Val Val Val Ser Val
 10 15 20

gtg ggg cac gtg gct aaa ccc ggc ctg gtc acg ctc gct gag ggc tcg 211
 Val Gly His Val Ala Lys Pro Gly Leu Val Thr Leu Ala Glu Gly Ser
 25 30 35

cgg gtg gct gat gcc ctg gcc att gca ggt gcc ttg cca gac gcc gat 259
 Arg Val Ala Asp Ala Leu Ala Ile Ala Gly Ala Leu Pro Asp Ala Asp
 40 45 50

ctg acg gcg ctc aac ttg gcg caa ttg ctt gtc gac ggc acc cag atc 307
 Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly Thr Gln Ile
 55 60 65

cat gtt tta gct atc ggc gag gta caa cct att tcg gtt gat gct gct 355
 His Val Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val Asp Ala Ala
 70 75 80 85

gcg act tct gct tct ggg ttg att tcc ttg aat acc gcc act gtt gct 403
 Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala Thr Val Ala
 90 95 100

gat ttg gtg acg ctg cct ggg gtg ggg gag aag aca gcg cag gcg atc 451
 Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Ile
 105 110 115

att gac ttt cgg gag agc aac ggt ggg ttt agc acc gtg gag gat tta 499
 Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val Glu Asp Leu
 120 125 130

ctg cag gtc aag ggg att ggg ccc tca aag ttt gag cag atc tct gga 547
 Leu Gln Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln Ile Ser Gly
 135 140 145

ttg gtg tcc cca tgattgaggt gcgtttggtt ccc 582
 Leu Val Ser Pro
 150

<210> 108

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

Met Ala Ala Leu Ala Glu Asn Tyr Gln Thr Pro Ala Pro Ser Ser Gln

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Leu Ala Glu Gly Ser Arg Val Ala Asp Ala Leu Ala Ile Ala Gly Ala	35	40	45
Leu Pro Asp Ala Asp Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val	50	55	60
Asp Gly Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile	65	70	75
Ser Val Asp Ala Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn	85	90	95
Thr Ala Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys	100	105	110
Thr Ala Gln Ala Ile Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser	115	120	125
Thr Val Glu Asp Leu Leu Gln Val Lys Gly Ile Gly Pro Ser Lys Phe	130	135	140
Glu Gln Ile Ser Gly Leu Val Ser Pro	145	150	

<210> 109
 <211> 528
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(505)
 <223> FRXA02386

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 Val Ser Val Val Gly
 1 5
 cac gtg gct aaa ccc ggc ctg gtc acg ctc gct gag ggc tcg cgg gtg 163
 His Val Ala Lys Pro Gly Leu Val Thr Leu Ala Glu Gly Ser Arg Val
 10 15 20
 gct gat gcc ctg gcc att gca ggt gcc ttg cca gac gcc gat ctg acg 211
 Ala Asp Ala Leu Ala Ile Ala Gly Ala Leu Pro Asp Ala Asp Leu Thr
 25 30 35
 gcg ctc aac ttg gcg caa ttg ctt gtc gac ggc acc cag atc cat gtt 259
 Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly Thr Gln Ile His Val
 40 45 50
 tta gct atc ggc gag gta caa cct att tcg gtt gat gct gct gcg act 307
 Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val Asp Ala Ala Ala Thr

55	60	65	
tct gct tct ggg ttg att tcc ttg aat acc gcc act gtt gct gat ttg			355
Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala Thr Val Ala Asp Leu			
70	75	80	85
gtg acg ctg cct ggg gtg ggg gag aag aca gcg cag gcg atc att gac			403
Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala Gln Ala Ile Ile Asp			
	90	95	100
ttt cgg gag agc aac ggt ggg ttt agc acc gtg gag gat tta ctg cag			451
Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val Glu Asp Leu Leu Gln			
	105	110	115
gtc aag ggg att ggg ccc tca aag ttt gag cag atc tct gga ttg gtg			499
Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln Ile Ser Gly Leu Val			
	120	125	130
tcc cca tgattgaggt gcgtttgggtt ccc			528
Ser Pro			
135			

<210> 110
 <211> 135
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 110
 Val Ser Val Val Gly His Val Ala Lys Pro Gly Leu Val Thr Leu Ala
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 Glu Gly Ser Arg Val Ala Asp Ala Leu Ala Ile Ala Gly Ala Leu Pro
 20 25 30
 Asp Ala Asp Leu Thr Ala Leu Asn Leu Ala Gln Leu Leu Val Asp Gly
 35 40 45
 Thr Gln Ile His Val Leu Ala Ile Gly Glu Val Gln Pro Ile Ser Val
 50 55 60
 Asp Ala Ala Ala Thr Ser Ala Ser Gly Leu Ile Ser Leu Asn Thr Ala
 65 70 75 80
 Thr Val Ala Asp Leu Val Thr Leu Pro Gly Val Gly Glu Lys Thr Ala
 85 90 95
 Gln Ala Ile Ile Asp Phe Arg Glu Ser Asn Gly Gly Phe Ser Thr Val
 100 105 110
 Glu Asp Leu Leu Gln Val Lys Gly Ile Gly Pro Ser Lys Phe Glu Gln
 115 120 125
 Ile Ser Gly Leu Val Ser Pro
 130 135

<210> 111
 <211> 1785
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1762)

<223> RXN02388

<400> 111

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ggccctcaaa gtttgagcag atctctggat tgggtgtcccc atg att gag gtg cgt 115
 Met Ile Glu Val Arg
 1 5

ttg gtt ccc gtg gcg gct gtg atg tgg atg gct gtc gct gcg ttg att 163
 Leu Val Pro Val Ala Val Met Trp Met Ala Val Ala Ala Leu Ile
 10 15 20

atc aat ggt tcg tgg gtg ttg tcg gtg ggg att gtt ggc atc gcg atc 211
 Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile Val Gly Ile Ala Ile
 25 30 35

att gct gct tgt gtg ttt aaa cac tgg ggt caa gct gtg gtg ata gct 259
 Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln Ala Val Val Ile Ala
 40 45 50

gca ctg ggc gtt ggt gcc gta gtg atg gct gcg ttg aga atc agc agc 307
 Ala Leu Gly Val Gly Ala Val Val Met Ala Ala Leu Arg Ile Ser Ser
 55 60 65

gcg aag gca ttt gaa gca ccg caa acc tgg gtg ggt acc gca gaa acc 355
 Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val Gly Thr Ala Glu Thr
 70 75 80 85

atc aag ttt tta gac agc ggt gat caa cta atc ggt ttg aga gta gaa 403
 Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile Gly Leu Arg Val Glu
 90 95 100

ggc tat cca gcg ccg att cca gtg ttt tac tct ggt agc gac acc att 451
 Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser Gly Ser Asp Thr Ile
 105 110 115

gag aaa gcc tct ctc att gca gtg tcc ggt cgg att aaa cca gat agt 499
 Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg Ile Lys Pro Asp Ser
 120 125 130

ttc cct ggg gtg ggt gat ctg acc att tcc act gaa gac att gat cag 547
 Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr Glu Asp Ile Asp Gln
 135 140 145

ttg gaa ccg acc act ggt tat agc gca tgg gtg aac cag gtg cgt gac 595
 Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val Asn Gln Val Arg Asp
 150 155 160 165

ggg ttt tcc caa gcc gtg gaa gaa acc gtg ggg gag tct tcc cgt gga 643
 Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly Glu Ser Ser Arg Gly
 170 175 180

ctg att cca ggc atg gtg ttg ggg gat acg cgg ttg cag ggg tca att 691
 Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg Leu Gln Gly Ser Ile
 185 190 195

gaa gcc caa acc tat att gat acg ggg ttg tct cac ctg tca gct gtt	739
Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser His Leu Ser Ala Val	
200 205 210	
agt gga agc aat gta gcc att gtg gtg tcc tct gtg gtg gtg ttg tcg	787
Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser Val Val Val Leu Ser	
215 220 225	
tat ttt ctc acc gct ggg cca cgc atc agg gtg gtg gcg tca ttg ctg	835
Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val Val Ala Ser Leu Leu	
230 235 240 245	
tcc tta gtt att ttt gtc tcc ctc gtg ggg ttt gaa cca agt gtg ctt	883
Ser Leu Val Ile Phe Val Ser Leu Val Gly Phe Glu Pro Ser Val Leu	
250 255 260	
cgt gct tcg gtc aca ggc atc gtg ggg ctt ctg gca atc atc aac tct	931
Arg Ala Ser Val Thr Gly Ile Val Gly Leu Leu Ala Ile Ile Asn Ser	
265 270 275	
tct cgg atg gag ccg atg cat ggg ttg agt ctt tcg gtg att tgc tta	979
Ser Arg Met Glu Pro Met His Gly Leu Ser Leu Ser Val Ile Cys Leu	
280 285 290	
ctg ttt tat gat tcc aac ctg gcg gtg cat tac gga ttc tta ctc tcg	1027
Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr Gly Phe Leu Leu Ser	
295 300 305	
tgt gca gca act gct ggc att gtg atg ctt caa cca ctg ctg tac cgt	1075
Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln Pro Leu Leu Tyr Arg	
310 315 320 325	
gcc atc ggt cca cca ctg gcg gtg tgg aaa gta cca gac atc gtg gtg	1123
Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val Pro Asp Ile Val Val	
330 335 340	
cgc gct ttc gcg gtg tcc att gcc gct gat ctg gtg acc atc ccg att	1171
Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu Val Thr Ile Pro Ile	
345 350 355	
atc gct ctg atg gct cgc caa ata tcc ctc gtg gca gtg ctg gcc aac	1219
Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val Ala Val Leu Ala Asn	
360 365 370	
gtg ttg gtt gaa tta gct gtt cca ccc atc acg ttg ctt ggg ttg att	1267
Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr Leu Leu Gly Leu Ile	
375 380 385	
gcc gtg ctg gca agc ctt ctt ccc tgg cca gtg gaa tac cca ctc ttg	1315
Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val Glu Tyr Pro Leu Leu	
390 395 400 405	
aaa atc att gag ccc ttc acc tgg tgg att cat cac gtg gcc aag tgg	1363
Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His His Val Ala Lys Trp	
410 415 420	
tgc caa caa tta ccc aat tcg acg ctg gaa ata agt gct ggt tgg gca	1411
Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile Ser Ala Gly Trp Ala	
425 430 435	
ggg att gcc tgg gcg tgt atg gca gcg gtg tgg gtg gtg gtg att atc	1459

Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp Val Val Val Ile Ile
440 445 450

tac aaa gga tat gtg cgc acc ctt gca gtg tgt tgt gtc tgc ttc ttt 1507
Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys Cys Val Cys Phe Phe
455 460 465

ctt ttc ggc gcg tgg aat aac aga ctg cca gcc caa ata gat ccg aca 1555
Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala Gln Ile Asp Pro Thr
470 475 480 485

gag ctg cgg ttt gtc atc atc gcc gat gat tct gag ctc act gat gtg 1603
Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser Glu Leu Thr Asp Val
490 495 500

ccc gaa cat gca gaa ttg atc atc gtg gaa gac ccc cac ggc agc atg 1651
Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp Pro His Gly Ser Met
505 510 515

tcc gat cgc ccc atc gtc acc aga gaa gga atc cct gtg ctg tat cca 1699
Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile Pro Val Leu Tyr Pro
520 525 530

tac cgc gat ggg gag gtc agc ctt cat att gat ggc acc cag cat gca 1747
Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp Gly Thr Gln His Ala
535 540 545

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Ala Asp Gly Arg Phe
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<210> 112

<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 112

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20 25 30

Val Gly Ile Ala Ile Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln
35 40 45

Ala Val Val Ile Ala Ala Leu Gly Val Gly Ala Val Val Met Ala Ala
50 55 60

Leu Arg Ile Ser Ser Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val
65 70 75 80

Gly Thr Ala Glu Thr Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile
85 90 95

Gly Leu Arg Val Glu Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser
100 105 110

Gly Ser Asp Thr Ile Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg
115 120 125

Ile Lys Pro Asp Ser Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr
 130 135 140
 Glu Asp Ile Asp Gln Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val
 145 150 155 160
 Asn Gln Val Arg Asp Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly
 165 170 175
 Glu Ser Ser Arg Gly Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg
 180 185 190
 Leu Gln Gly Ser Ile Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser
 195 200 205
 His Leu Ser Ala Val Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser
 210 215 220
 Val Val Val Leu Ser Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val
 225 230 235 240
 Val Ala Ser Leu Leu Ser Leu Val Ile Phe Val Ser Leu Val Gly Phe
 245 250 255
 Glu Pro Ser Val Leu Arg Ala Ser Val Thr Gly Ile Val Gly Leu Leu
 260 265 270
 Ala Ile Ile Asn Ser Ser Arg Met Glu Pro Met His Gly Leu Ser Leu
 275 280 285
 Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr
 290 295 300
 Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln
 305 310 315 320
 Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val
 325 330 335
 Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu
 340 345 350
 Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val
 355 360 365
 Ala Val Leu Ala Asn Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr
 370 375 380
 Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val
 385 390 395 400
 Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His
 405 410 415
 His Val Ala Lys Trp Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile
 420 425 430
 Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp
 435 440 445

Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys
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Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala
 465 470 475 480

Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser
 485 490 495

Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp
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Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile
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Pro Val Leu Tyr Pro Tyr Arg Asp Gly Glu Val Ser Leu His Ile Asp
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Gly Thr Gln His Ala Ala Asp Gly Arg Phe
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 <223> FRXA02385

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 Met Ile Glu Val Arg
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ttg gtt ccc gtg gcg gct gtg atg tgg atg gct gtc gct gcg ttg att 163
 Leu Val Pro Val Ala Ala Val Met Trp Met Ala Val Ala Ala Leu Ile
 10 15 20

atc aat ggt tcg tgg gtg ttg tcg gtg ggg att gtt ggc atc gcg atc 211
 Ile Asn Gly Ser Trp Val Leu Ser Val Gly Ile Val Gly Ile Ala Ile
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att gct gct tgt gtg ttt aaa cac tgg ggt caa gct gtg gtg ata gct 259
 Ile Ala Ala Cys Val Phe Lys His Trp Gly Gln Ala Val Val Ile Ala
 40 45 50

gca ctg ggc gtt ggt gcc gta gtg atg gct gcg ttg aga atc agc agc 307
 Ala Leu Gly Val Gly Ala Val Val Met Ala Ala Leu Arg Ile Ser Ser
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gcg aag gca ttt gaa gca ccg caa acc tgg gtg ggt acc gca gaa acc 355
 Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val Gly Thr Ala Glu Thr
 70 75 80 85

atc aag ttt tta gac agc ggt gat caa cta atc ggt ttg aga gta gaa 403
 Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile Gly Leu Arg Val Glu

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Phe	Pro	Gly	Val	Gly	Asp	Leu	Thr	Ile	Ser	Thr	Glu	Asp	Ile	Asp	Gln					
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Ser	Gly	Ser	Asn	Val	Ala	Ile	Val	Val	Ser	Ser	Val	Val	Val	Leu	Ser					
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Tyr	Phe	Leu	Thr	Ala	Gly	Pro	Arg	Ile	Arg	Val	Val	Ala	Ser	Leu	Leu					
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<212> PRT

<213> Corynebacterium glutamicum

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Val	Gly	Ile	Ala	Ile	Ile	Ala	Ala	Cys	Val	Phe	Lys	His	Trp	Gly	Gln
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Leu Arg Ile Ser Ser Ala Lys Ala Phe Glu Ala Pro Gln Thr Trp Val
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 Gly Thr Ala Glu Thr Ile Lys Phe Leu Asp Ser Gly Asp Gln Leu Ile
 85 90 95
 Gly Leu Arg Val Glu Gly Tyr Pro Ala Pro Ile Pro Val Phe Tyr Ser
 100 105 110
 Gly Ser Asp Thr Ile Glu Lys Ala Ser Leu Ile Ala Val Ser Gly Arg
 115 120 125
 Ile Lys Pro Asp Ser Phe Pro Gly Val Gly Asp Leu Thr Ile Ser Thr
 130 135 140
 Glu Asp Ile Asp Gln Leu Glu Pro Thr Thr Gly Tyr Ser Ala Trp Val
 145 150 155 160
 Asn Gln Val Arg Asp Gly Phe Ser Gln Ala Val Glu Glu Thr Val Gly
 165 170 175
 Glu Ser Ser Arg Gly Leu Ile Pro Gly Met Val Leu Gly Asp Thr Arg
 180 185 190
 Leu Gln Gly Ser Ile Glu Ala Gln Thr Tyr Ile Asp Thr Gly Leu Ser
 195 200 205
 His Leu Ser Ala Val Ser Gly Ser Asn Val Ala Ile Val Val Ser Ser
 210 215 220
 Val Val Val Leu Ser Tyr Phe Leu Thr Ala Gly Pro Arg Ile Arg Val
 225 230 235 240
 Val Ala Ser Leu Leu Ser Leu Gly Ile Phe Val Ser Leu Val Gly Phe
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 Glu

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 <223> FRXA02388

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 Ser Val Ile Cys Leu Leu Phe Tyr Asp Ser Asn Leu Ala Val His Tyr
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 Gly Phe Leu Leu Ser Cys Ala Ala Thr Ala Gly Ile Val Met Leu Gln

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cca	gac	atc	gtg	gtg	cgc	gct	ttc	gcg	gtg	tcc	att	gcc	gct	gat	ctg	240				
Pro	Asp	Ile	Val	Val	Arg	Ala	Phe	Ala	Val	Ser	Ile	Ala	Ala	Asp	Leu	80				
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gtg	acc	atc	ccg	att	atc	gct	ctg	atg	gct	cgc	caa	ata	tcc	ctc	gtg	288				
Val	Thr	Ile	Pro	Ile	Ile	Ala	Leu	Met	Ala	Arg	Gln	Ile	Ser	Leu	Val					
85								90				95								
gca	gtg	ctg	gcc	aac	gtg	ttg	gtt	gaa	tta	gct	gtt	cca	ccc	atc	acg	336				
Ala	Val	Leu	Ala	Asn	Val	Leu	Val	Glu	Leu	Ala	Val	Pro	Pro	Ile	Thr					
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Leu	Leu	Gly	Leu	Ile	Ala	Val	Leu	Ala	Ser	Leu	Leu	Pro	Trp	Pro	Val					
115								120				125								
gaa	tac	cca	ctc	ttg	aaa	atc	att	gag	ccc	ttc	acc	tgg	tgg	att	cat	432				
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165								170				175								
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180								185				190								
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Cys	Val	Cys	Phe	Phe	Leu	Phe	Gly	Ala	Trp	Asn	Asn	Arg	Leu	Pro	Ala					
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Gln	Ile	Asp	Pro	Thr	Glu	Leu	Arg	Phe	Val	Ile	Ile	Ala	Asp	Asp	Ser					
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Glu	Leu	Thr	Asp	Val	Pro	Glu	His	Ala	Glu	Leu	Ile	Ile	Val	Glu	Asp	240				
225								230				235								
ccc	cac	ggc	agc	atg	tcc	gat	cgc	ccc	atc	gtc	acc	aga	gaa	gga	atc	768				
Pro	His	Gly	Ser	Met	Ser	Asp	Arg	Pro	Ile	Val	Thr	Arg	Glu	Gly	Ile					
245								250				255								
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Pro	Val	Leu	Tyr	Pro	Tyr	Arg	Asp	Gly	Glu	Val	Ser	Leu	His	Ile	Asp					
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<213> Corynebacterium glutamicum

<400> 116

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 35 40 45

Pro Leu Leu Tyr Arg Ala Ile Gly Pro Pro Leu Ala Val Trp Lys Val
 50 55 60

Pro Asp Ile Val Val Arg Ala Phe Ala Val Ser Ile Ala Ala Asp Leu
 65 70 75 80

Val Thr Ile Pro Ile Ile Ala Leu Met Ala Arg Gln Ile Ser Leu Val
 85 90 95

Ala Val Leu Ala Asn Val Leu Val Glu Leu Ala Val Pro Pro Ile Thr
 100 105 110

Leu Leu Gly Leu Ile Ala Val Leu Ala Ser Leu Leu Pro Trp Pro Val
 115 120 125

Glu Tyr Pro Leu Leu Lys Ile Ile Glu Pro Phe Thr Trp Trp Ile His
 130 135 140

His Val Ala Lys Trp Cys Gln Gln Leu Pro Asn Ser Thr Leu Glu Ile
 145 150 155 160

Ser Ala Gly Trp Ala Gly Ile Ala Trp Ala Cys Met Ala Ala Val Trp
 165 170 175

Val Val Val Ile Ile Tyr Lys Gly Tyr Val Arg Thr Leu Ala Val Cys
 180 185 190

Cys Val Cys Phe Phe Leu Phe Gly Ala Trp Asn Asn Arg Leu Pro Ala
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Gln Ile Asp Pro Thr Glu Leu Arg Phe Val Ile Ile Ala Asp Asp Ser
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Glu Leu Thr Asp Val Pro Glu His Ala Glu Leu Ile Ile Val Glu Asp
 225 230 235 240

Pro His Gly Ser Met Ser Asp Arg Pro Ile Val Thr Arg Glu Gly Ile
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<223> RXA01975
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Leu Ser His His Thr 5																
cac ctc aat aac tac atc acg agc ttg agt gat aac gct gat ctc cgt 163																
His Leu Asn Asn Tyr Ile Thr Ser Leu Ser Asp Asn Ala Asp Leu Arg 20																
gaa aaa gtc acc gca acc gta gac gct ttc cgc cat acc gtc atg gat 211																
Glu Lys Val Thr Ala Thr Val Asp Ala Phe Arg His Thr Val Met Asp 35																
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Asp Phe Asp Tyr Ile Ser Asp Gln Gln Val Leu Leu Tyr Gly Asp Val 50																
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Gln Ser Gly Lys Thr Ser His Met Leu Gly Ile Ile Ala Asp Cys Leu 65																
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Asp Ser Thr Phe His Thr Ile Val Ile Leu Thr Ser Pro Asn Thr Arg 85																
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Leu Val Gln Gln Thr Tyr Asp Arg Val Val Ala Gln Ala Phe Pro Asp Thr 100																
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Leu Val Cys Asp Arg Asp Gly Tyr Asn Asp Phe Arg Ala Asn Gln Lys 115																
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Ser Leu Thr Pro Arg Lys Ser Ile Val Val Val Gly Lys Ile Pro Ala 130																
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Val Leu Gly Asn Trp Leu Arg Val Phe Asn Asp Ser Gly Ala Leu Ser 145																
gga cac cct gta ctc att att gat gac gaa gca gat gcg aca agt ctc 595																
Gly His Pro Val Leu Ile Ile Asp Asp Glu Ala Asp Ala Thr Ser Leu 165																
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Asn Thr Lys Val Asn Gln Ser Asp Val Ser Thr Ile Asn His Gln Leu																

170										175					180					
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gcg	gaa	cat	gtg	ctt	cac	ttc	gca	cct	ggt	gag	agc	tac	atc	ggt	ggt	787				
Ala	Glu	His	Val	Leu	His	Phe	Ala	Pro	Gly	Glu	Ser	Tyr	Ile	Gly	Gly					
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caa	ctt	ttc	ttt	tct	gag	ctc	aac	aac	cct	tat	cta	cga	ctt	ttc	gct	835				
Gln	Leu	Phe	Phe	Ser	Glu	Leu	Asn	Asn	Pro	Tyr	Leu	Arg	Leu	Phe	Ala					
230					235					240					245					
aat	acc	caa	ttt	gac	gag	gat	tct	cgc	ttc	agc	gac	gcc	att	tac	acc	883				
Asn	Thr	Gln	Phe	Asp	Glu	Asp	Ser	Arg	Phe	Ser	Asp	Ala	Ile	Tyr	Thr					
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Tyr	Leu	Leu	Thr	Ala	Ala	Leu	Phe	Lys	Leu	Arg	Gly	Glu	Ser	Leu	Cys					
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Thr	Met	Leu	Ile	His	Pro	Ser	His	Thr	Ala	Ser	Ser	His	Arg	Asp	Phe					
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gcg	caa	gaa	gcc	cgc	ctc	caa	ctc	act	ttc	gcc	ttc	gag	cga	ttc	tat	1027				
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	295					300					305									
gaa	cca	atg	att	cag	cac	aat	ttc	caa	cgt	gct	tat	gaa	cag	ctc	gca	1075				
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310					315					320					325					
caa	act	gac	agc	aac	ctg	cca	ccc	ttg	aga	aaa	att	ctt	aac	att	ctt	1123				
Gln	Thr	Asp	Ser	Asn	Leu	Pro	Pro	Leu	Arg	Lys	Ile	Leu	Asn	Ile	Leu					
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Pro	Thr	Val	Glu	Glu	Asp	Trp	Ala	Asp	Gly	Tyr	Asn	Ile	Ile	Val	Gly					
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	375					380					385									
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Phe	Tyr	Val	Arg	Glu	Ser	Lys	Arg	Pro	Gln	Ala	Asp	Thr	Leu	Trp	Gln					
390					395					400					405					
cac	gcc	cgc	atg	ttt	ggc	tac	aaa	cgc	cac	aaa	gac	acc	atg	cgt	gtg	1363				
His	Ala	Arg	Met	Phe	Gly	Tyr	Lys	Arg	His	Lys	Asp	Thr	Met	Arg	Val					
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Phe Met Pro Ala Thr Ile Ala Gln Thr Phe Gln Glu Val Tyr Leu Gly	
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aac gaa gct att aaa aat cag ctc gat cat ggc acg cat atc aac gac	1459
Asn Glu Ala Ile Lys Asn Gln Leu Asp His Gly Thr His Ile Asn Asp	
440 445 450	
att cgg gtc att tta ggt gat ggc gtc gca cct act cgt gcc aat gtt	1507
Ile Arg Val Ile Leu Gly Asp Gly Val Ala Pro Thr Arg Ala Asn Val	
455 460 465	
ctc gac aaa cgc aaa gtt gga aac ctc agc ggt ggc gtc aac tac ttt	1555
Leu Asp Lys Arg Lys Val Gly Asn Leu Ser Gly Gly Val Asn Tyr Phe	
470 475 480 485	
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Ala Ala Asp Pro Arg Ile Lys Asn Val Glu Ala Leu Asp Lys Lys Leu	
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Leu Ala Tyr Leu Asp Lys His Gly Glu Asp Ser Thr Ile Gly Met Arg	
505 510 515	
gcg ata atc acc att ctc aac gcc ttt act gta gac ccc aac gat ctc	1699
Ala Ile Ile Thr Ile Leu Asn Ala Phe Thr Val Asp Pro Asn Asp Leu	
520 525 530	
gac ctc gcg acc ttc aag gct gcg ctc ctt gac ttt gaa cgc aac caa	1747
Asp Leu Ala Thr Phe Lys Ala Ala Leu Leu Asp Phe Glu Arg Asn Gln	
535 540 545	
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Pro His Leu Thr Ala Arg Met Val Leu Arg Thr Asn Arg Lys Val Asn	
550 555 560 565	
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Gln Gly Thr Gly Ala Leu Leu Ser Pro Thr Asp Gln Ala Leu Ser Arg	
570 575 580	
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Ala Glu Val Ala His Pro Leu Leu Ile Leu Tyr Arg Ile Glu Gly Val	
585 590 595	
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Asn Asp Ala Ala Ala Gln Arg Gly Glu Pro Thr Trp Ser Ser Asp Pro	
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Ile Trp Val Pro Asn Ile Lys Leu Pro Gly Gln Arg Gln Phe Trp Cys	
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Val Asp Gly	
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<211> 632

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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His	Thr	Val	Met	Asp	Asp	Phe	Asp	Tyr	Ile	Ser	Asp	Gln	Gln	Val	Leu	35	40	45	
Leu	Tyr	Gly	Asp	Val	Gln	Ser	Gly	Lys	Thr	Ser	His	Met	Leu	Gly	Ile	50	55	60	
Ile	Ala	Asp	Cys	Leu	Asp	Ser	Thr	Phe	His	Thr	Ile	Val	Ile	Leu	Thr	65	70	75	80
Ser	Pro	Asn	Thr	Arg	Leu	Val	Gln	Gln	Thr	Tyr	Asp	Arg	Val	Ala	Gln	85	90	95	
Ala	Phe	Pro	Asp	Thr	Leu	Val	Cys	Asp	Arg	Asp	Gly	Tyr	Asn	Asp	Phe	100	105	110	
Arg	Ala	Asn	Gln	Lys	Ser	Leu	Thr	Pro	Arg	Lys	Ser	Ile	Val	Val	Val	115	120	125	
Gly	Lys	Ile	Pro	Ala	Val	Leu	Gly	Asn	Trp	Leu	Arg	Val	Phe	Asn	Asp	130	135	140	
Ser	Gly	Ala	Leu	Ser	Gly	His	Pro	Val	Leu	Ile	Ile	Asp	Asp	Glu	Ala	145	150	155	160
Asp	Ala	Thr	Ser	Leu	Asn	Thr	Lys	Val	Asn	Gln	Ser	Asp	Val	Ser	Thr	165	170	175	
Ile	Asn	His	Gln	Leu	Thr	Ser	Ile	Arg	Asp	Leu	Ala	Thr	Gly	Cys	Ile	180	185	190	
Tyr	Leu	Gln	Val	Thr	Gly	Thr	Pro	Gln	Ala	Val	Leu	Leu	Gln	Ser	Asp	195	200	205	
Asp	Ser	Asn	Trp	Ala	Ala	Glu	His	Val	Leu	His	Phe	Ala	Pro	Gly	Glu	210	215	220	
Ser	Tyr	Ile	Gly	Gly	Gln	Leu	Phe	Phe	Ser	Glu	Leu	Asn	Asn	Pro	Tyr	225	230	235	240
Leu	Arg	Leu	Phe	Ala	Asn	Thr	Gln	Phe	Asp	Glu	Asp	Ser	Arg	Phe	Ser	245	250	255	
Asp	Ala	Ile	Tyr	Thr	Tyr	Leu	Leu	Thr	Ala	Ala	Leu	Phe	Lys	Leu	Arg	260	265	270	
Gly	Glu	Ser	Leu	Cys	Thr	Met	Leu	Ile	His	Pro	Ser	His	Thr	Ala	Ser	275	280	285	
Ser	His	Arg	Asp	Phe	Ala	Gln	Glu	Ala	Arg	Leu	Gln	Leu	Thr	Phe	Ala	290	295	300	
Phe	Glu	Arg	Phe	Tyr	Glu	Pro	Met	Ile	Gln	His	Asn	Phe	Gln	Arg	Ala				

305						310						315						320
Tyr	Glu	Gln	Leu	Ala	Gln	Thr	Asp	Ser	Asn	Leu	Pro	Pro	Leu	Arg	Lys			
				325					330					335				
Ile	Leu	Asn	Ile	Leu	Gly	Gly	Met	Glu	Asp	Asp	Phe	Ser	Ile	His	Ile			
				340					345					350				
Val	Asn	Ser	Asp	Asn	Pro	Thr	Val	Glu	Glu	Asp	Trp	Ala	Asp	Gly	Tyr			
				355					360					365				
Asn	Ile	Ile	Val	Gly	Gly	Asn	Ser	Leu	Gly	Arg	Gly	Leu	Thr	Phe	Asn			
				370					375					380				
Asn	Leu	Gln	Thr	Val	Phe	Tyr	Val	Arg	Glu	Ser	Lys	Arg	Pro	Gln	Ala			
				385					390					395				
Asp	Thr	Leu	Trp	Gln	His	Ala	Arg	Met	Phe	Gly	Tyr	Lys	Arg	His	Lys			
				405					410					415				
Asp	Thr	Met	Arg	Val	Phe	Met	Pro	Ala	Thr	Ile	Ala	Gln	Thr	Phe	Gln			
				420					425					430				
Glu	Val	Tyr	Leu	Gly	Asn	Glu	Ala	Ile	Lys	Asn	Gln	Leu	Asp	His	Gly			
				435					440					445				
Thr	His	Ile	Asn	Asp	Ile	Arg	Val	Ile	Leu	Gly	Asp	Gly	Val	Ala	Pro			
				450					455					460				
Thr	Arg	Ala	Asn	Val	Leu	Asp	Lys	Arg	Lys	Val	Gly	Asn	Leu	Ser	Gly			
				465					470					475				
Gly	Val	Asn	Tyr	Phe	Ala	Ala	Asp	Pro	Arg	Ile	Lys	Asn	Val	Glu	Ala			
				485					490					495				
Leu	Asp	Lys	Lys	Leu	Leu	Ala	Tyr	Leu	Asp	Lys	His	Gly	Glu	Asp	Ser			
				500					505					510				
Thr	Ile	Gly	Met	Arg	Ala	Ile	Ile	Thr	Ile	Leu	Asn	Ala	Phe	Thr	Val			
				515					520					525				
Asp	Pro	Asn	Asp	Leu	Asp	Leu	Ala	Thr	Phe	Lys	Ala	Ala	Leu	Leu	Asp			
				530					535					540				
Phe	Glu	Arg	Asn	Gln	Pro	His	Leu	Thr	Ala	Arg	Met	Val	Leu	Arg	Thr			
				545					550					555				
Asn	Arg	Lys	Val	Asn	Gln	Gly	Thr	Gly	Ala	Leu	Leu	Ser	Pro	Thr	Asp			
				565					570					575				
Gln	Ala	Leu	Ser	Arg	Ala	Glu	Val	Ala	His	Pro	Leu	Leu	Ile	Leu	Tyr			
				580					585					590				
Arg	Ile	Glu	Gly	Val	Asn	Asp	Ala	Ala	Ala	Gln	Arg	Gly	Glu	Pro	Thr			
				595					600					605				
Trp	Ser	Ser	Asp	Pro	Ile	Trp	Val	Pro	Asn	Ile	Lys	Leu	Pro	Gly	Gln			
				610					615					620				
Arg	Gln	Phe	Trp	Cys	Val	Asp	Gly											
				625					630									

<400> 119																
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atctcgcgga gctcgcgcgtc gaagaacccg agactcggca										gtg Val 1	ctt Leu	gcc Ala	gac Asp	gac Asp 5	115	
gtg	gtg	gtc	gtc	gcg	gag	ttc	cgg	gat	cgc	atc	tac	ccc	ggc	ctg	gtg	163
Val	Val	Val	Val	Ala	Glu	Phe	Arg	Asp	Arg	Ile	Tyr	Pro	Gly	Leu	Val	
				10						15		20				
gag	aca	ggc	agg	gtt	gag	cgg	ggc	ggc	gac	aag	ccg	ttc	cac	acg	gtc	211
Glu	Thr	Gly	Arg	Val	Glu	Arg	Gly	Gly	Asp	Lys	Pro	Phe	His	Thr	Val	
				25						30		35				
gtc	aac	gct	gag	aac	tac	cac	gcg	ctg	gag	atg	ctg	acc	tat	acg	cac	259
Val	Asn	Ala	Glu	Asn	Tyr	His	Ala	Leu	Glu	Met	Leu	Thr	Tyr	Thr	His	
				40						45		50				
cgg	cat	tcc	atc	gac	gcc	atc	tac	atc	gac	ccg	ccg	tac	aac	acc	ggg	307
Arg	His	Ser	Ile	Asp	Ala	Ile	Tyr	Ile	Asp	Pro	Pro	Tyr	Asn	Thr	Gly	
				55						60		65				
gcg	agg	gac	tgg	aag	tac	gac	aac	gat	tac	gtc	gcg	agt	gat	gac	gac	355
Ala	Arg	Asp	Trp	Lys	Tyr	Asp	Asn	Asp	Tyr	Val	Ala	Ser	Asp	Asp	Asp	
				70						75		80				85
tat	cga	cac	tcg	aaa	tgg	ctg	gcg	ttc	atg	gag	cga	cgg	ttg	aag	atc	403
Tyr	Arg	His	Ser	Lys	Trp	Leu	Ala	Phe	Met	Glu	Arg	Arg	Leu	Lys	Ile	
				90						95		100				
tgt	cgg	gag	ctc	atg	cgt	agc	gat	gct	act	ctt	gtg	gca	cct	atc	gat	451
Cys	Arg	Glu	Leu	Met	Arg	Ser	Asp	Ala	Thr	Leu	Val	Ala	Pro	Ile	Asp	
				105						110		115				
gag	cat	gaa	gta	aac	cgt	ttg	ggc	gtg	ttg	cta	gat	cag	ctc	ttc	ccg	499
Glu	His	Glu	Val	Asn	Arg	Leu	Gly	Val	Leu	Leu	Asp	Gln	Leu	Phe	Pro	
				120						125		130				
gaa	tct	acg	cgg	caa	ctc	gtc	aca	att	gtc	aac	aac	cct	aaa	ggc	gtt	547
Glu	Ser	Thr	Arg	Gln	Leu	Val	Thr	Ile	Val	Asn	Asn	Pro	Lys	Gly	Val	
				135						140		145				
act	cag	gga	tat	ctt	tcg	agg	gtc	gaa	gag	tat	gcg	ttc	ttt	gta	ttt	595
Thr	Gln	Gly	Tyr	Leu	Ser	Arg	Val	Glu	Glu	Tyr	Ala	Phe	Phe	Val	Phe	
				150						155		160				165
ggg	cct	gac	gcg	cga	atc	ggg	tcg	gtc	gat	gac	gac	ctt	ctg	acg	cat	643
Gly	Pro	Asp	Ala	Arg	Ile	Gly	Ser	Val	Asp	Asp	Asp	Leu	Leu	Thr	His	

170										175					180					
cga	gac	atg	gcc	gat	gct	gaa	ggg	gaa	ctg	cag	agg	cct	cga	tg	aag	691				
Arg	Asp	Met	Ala	Asp	Ala	Glu	Gly	Glu	Leu	Gln	Arg	Pro	Arg	Trp	Lys					
			185					190					195							
ggg	ctc	ttg	cgg	tcg	ggc	gac	gac	tcg	ctt	cga	gct	gac	cgt	aaa	gat	739				
Gly	Leu	Leu	Arg	Ser	Gly	Asp	Asp	Ser	Leu	Arg	Ala	Asp	Arg	Lys	Asp					
		200					205					210								
atg	ttc	tat	ccg	gtg	tg	ttc	gat	gag	tcg	act	ggg	cga	ctc	agc	cac	787				
Met	Phe	Tyr	Pro	Val	Trp	Phe	Asp	Glu	Ser	Thr	Gly	Arg	Leu	Ser	His					
	215					220					225									
gcg	ggc	gaa	gca	ttg	cca	ctt	gac	gaa	act	cct	gac	ttc	agt	ccg	cag	835				
Ala	Gly	Glu	Ala	Leu	Pro	Leu	Asp	Glu	Thr	Pro	Asp	Phe	Ser	Pro	Gln					
230					235					240					245					
gat	ggc	ctg	acg	ccg	atc	tg	cct	att	agg	cgg	gac	atg	aag	gag	ggg	883				
Asp	Gly	Leu	Thr	Pro	Ile	Trp	Pro	Ile	Arg	Arg	Asp	Met	Lys	Glu	Gly					
				250					255					260						
cct	acc	cgg	gca	gcg	cca	cgc	cgt	tcg	atc	ctt	gac	tac	gcg	cta	cac	931				
Pro	Thr	Arg	Ala	Ala	Pro	Arg	Arg	Ser	Ile	Leu	Asp	Tyr	Ala	Leu	His					
			265					270					275							
cct	cat	ctg	tgaagagcca	ccaaacctgg	gac											963				
Pro	His	Leu																		
		280																		

<210> 120

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

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Tyr	Pro	Gly	Leu	Val	Glu	Thr	Gly	Arg	Val	Glu	Arg	Gly	Gly	Asp	Lys
			20					25					30		
Pro	Phe	His	Thr	Val	Val	Asn	Ala	Glu	Asn	Tyr	His	Ala	Leu	Glu	Met
		35					40					45			
Leu	Thr	Tyr	Thr	His	Arg	His	Ser	Ile	Asp	Ala	Ile	Tyr	Ile	Asp	Pro
		50				55					60				
Pro	Tyr	Asn	Thr	Gly	Ala	Arg	Asp	Trp	Lys	Tyr	Asp	Asn	Asp	Tyr	Val
65					70					75					80
Ala	Ser	Asp	Asp	Asp	Tyr	Arg	His	Ser	Lys	Trp	Leu	Ala	Phe	Met	Glu
				85					90					95	
Arg	Arg	Leu	Lys	Ile	Cys	Arg	Glu	Leu	Met	Arg	Ser	Asp	Ala	Thr	Leu
			100					105					110		
Val	Ala	Pro	Ile	Asp	Glu	His	Glu	Val	Asn	Arg	Leu	Gly	Val	Leu	Leu
		115					120					125			

Asp Gln Leu Phe Pro Glu Ser Thr Arg Gln Leu Val Thr Ile Val Asn
 130 135 140
 Asn Pro Lys Gly Val Thr Gln Gly Tyr Leu Ser Arg Val Glu Glu Tyr
 145 150 155 160
 Ala Phe Phe Val Phe Gly Pro Asp Ala Arg Ile Gly Ser Val Asp Asp
 165 170 175
 Asp Leu Leu Thr His Arg Asp Met Ala Asp Ala Glu Gly Glu Leu Gln
 180 185 190
 Arg Pro Arg Trp Lys Gly Leu Leu Arg Ser Gly Asp Asp Ser Leu Arg
 195 200 205
 Ala Asp Arg Lys Asp Met Phe Tyr Pro Val Trp Phe Asp Glu Ser Thr
 210 215 220
 Gly Arg Leu Ser His Ala Gly Glu Ala Leu Pro Leu Asp Glu Thr Pro
 225 230 235 240
 Asp Phe Ser Pro Gln Asp Gly Leu Thr Pro Ile Trp Pro Ile Arg Arg
 245 250 255
 Asp Met Lys Glu Gly Pro Thr Arg Ala Ala Pro Arg Arg Ser Ile Leu
 260 265 270
 Asp Tyr Ala Leu His Pro His Leu
 275 280

<210> 121

<211> 441

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(418)

<223> RXA02236

<400> 121

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ccttttgtca ctaaaaacca cacgataacg gaggaacccc gtg gcc ctt cca cag 115
 Val Ala Leu Pro Gln
 1 5

ttg act gat gag cag cgc aag gca gcg ctt gct aag gca gca gag gca 163
 Leu Thr Asp Glu Gln Arg Lys Ala Ala Leu Ala Lys Ala Ala Glu Ala
 10 15 20

cgc aag gca cgc gca gag ctc aaa gag aac ctg aag cgc ggc aac act 211
 Arg Lys Ala Arg Ala Glu Leu Lys Glu Asn Leu Lys Arg Gly Asn Thr
 25 30 35

aac ctc agg gaa gtt ctg gac aag gct gag tct gac gag atc atc ggc 259
 Asn Leu Arg Glu Val Leu Asp Lys Ala Glu Ser Asp Glu Ile Ile Gly
 40 45 50

aag acc aag gtc tcc gct ctc ctc gag gct ctc cct aag gtt ggc aag 307

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<210> 122
<211> 106
<212> PRT
<213> Corynebacterium glutamicum
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<400> 122
Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Lys Ala Ala Leu Ala
  1          5          10          15

Lys Ala Ala Glu Ala Arg Lys Ala Arg Ala Glu Leu Lys Glu Asn Leu
          20          25          30

Lys Arg Gly Asn Thr Asn Leu Arg Glu Val Leu Asp Lys Ala Glu Ser
          35          40          45

Asp Glu Ile Ile Gly Lys Thr Lys Val Ser Ala Leu Leu Glu Ala Leu
  50          55          60

Pro Lys Val Gly Lys Val Lys Ala Lys Glu Ile Met Asp Glu Leu Gly
  65          70          75          80

Ile Ala Gln Thr Arg Arg Leu Arg Gly Leu Gly Asp Arg Gln Arg Arg
          85          90          95

Ala Leu Leu Glu Arg Phe Gly Phe Glu Asp
          100          105

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<210> 123
<211> 720
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(697)
<223> RXN01795
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<400> 123
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caacttcgct gaatacggtg tcccacaatt ccgcgaacgt gtg ctc att gtt ggc 115
Val Leu Ile Val Gly
1 5
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att cgc cgt gac acc ggc ttt gat ttc aag cac cca gct cct acc cat 163
 Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His Pro Ala Pro Thr His
 10 15 20

ggc cct cgc ggt gac atg ccg tat aag act gcc ggc gaa gcg ctc aaa 211
 Gly Pro Arg Gly Asp Met Pro Tyr Lys Thr Ala Gly Glu Ala Leu Lys
 25 30 35

ggc gtg aag gat gtc ccc aca aac aac aac cac atg aag atc atg cct 259
 Gly Val Lys Asp Val Pro Thr Asn Asn Asn His Met Lys Ile Met Pro
 40 45 50

cgc acc gtt gaa gtg ctt aag cgc atc cct gag ggc gaa aac ttc acc 307
 Arg Thr Val Glu Val Leu Lys Arg Ile Pro Glu Gly Glu Asn Phe Thr
 55 60 65

gcg atc ccc aaa gat gac ccc tac tac gtc aag ggc atg att agt cac 355
 Ala Ile Pro Lys Asp Asp Pro Tyr Tyr Val Lys Gly Met Ile Ser His
 70 75 80 85

gtt tac cgt cgc ttg cac cgt gat gag cca tcc aaa acc ctt atc gcc 403
 Val Tyr Arg Arg Leu His Arg Asp Glu Pro Ser Lys Thr Leu Ile Ala
 90 95 100

ggt ggc ggc ggg ggt aca tgg gga tac cat tat gaa aaa aat cga gca 451
 Gly Gly Gly Gly Gly Thr Trp Gly Tyr His Tyr Glu Lys Asn Arg Ala
 105 110 115

ttg acc aac cgc gag ccg gct aga att caa tcg ttc ccc gat gac ttt 499
 Leu Thr Asn Arg Glu Arg Ala Arg Ile Gln Ser Phe Pro Asp Asp Phe
 120 125 130

gag ttt ttg gga tca aac acc gaa gtc cgc cgc caa atc ggt aat gct 547
 Glu Phe Leu Gly Ser Asn Thr Glu Val Arg Arg Gln Ile Gly Asn Ala
 135 140 145

gtt cct cct gta ggt atg cac gct gtg ggt gag cga ctg atg aac ctg 595
 Val Pro Pro Val Gly Met His Ala Val Gly Glu Arg Leu Met Asn Leu
 150 155 160 165

tac acc ggg aat tac act ccc gtc gat cta gag gaa cag cac gcg tac 643
 Tyr Thr Gly Asn Tyr Thr Pro Val Asp Leu Glu Glu Gln His Ala Tyr
 170 175 180

ctg cag acg ctc tcc att aag gaa cgt ctc gcg ctg gct gat cag gaa 691
 Leu Gln Thr Leu Ser Ile Lys Glu Arg Leu Ala Leu Ala Asp Gln Glu
 185 190 195

gct gat taagtagata tatgaagccc acc 720
 Ala Asp

<210> 124

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 124

Val Leu Ile Val Gly Ile Arg Arg Asp Thr Gly Phe Asp Phe Lys His
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<400> 125
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accaacgatt caagccttat cagttttgta caggaaaata gtg caa aaa tgg ggt 115
                                         Val Gln Lys Trp Gly
                                         1                               5
tta agc ttc gtg gag agg att gtc atc gtg aac aac gtg caa cag ttt 163
Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn Asn Val Gln Gln Phe
                        10                        15                        20
cat cga ttt ttt gat gat tcc gca gtc tat tat ccc tgc ttc gtc ccg 211
His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr Pro Cys Phe Val Pro

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25										30					35					
ctt	gac	cga	gcc	atc	ggc	gaa	cac	ttt	gat	cgt	cag	aac	aaa	ccg	atg	259				
Leu	Asp	Arg	Ala	Ile	Gly	Glu	His	Phe	Asp	Arg	Gln	Asn	Lys	Pro	Met					
		40					45					50								
tcc	aga	ttc	atc	gga	acg	ctc	att	ctg	ccg	tta	gcc	aaa	ctg	gaa	gaa	307				
Ser	Arg	Phe	Ile	Gly	Thr	Leu	Ile	Leu	Pro	Leu	Ala	Lys	Leu	Glu	Glu					
	55					60					65									
gcc	gcc	caa	tac	acc	ggc	gat	gaa	gtc	ctt	cgc	gtg	tcg	gca	gta	atc	355				
Ala	Ala	Gln	Tyr	Thr	Gly	Asp	Glu	Val	Leu	Arg	Val	Ser	Ala	Val	Ile					
70					75					80					85					
agt	act	gat	ggg	ctc	gct	gat	ctg	cga	agg	gat	ttt	tac	gaa	ctc	ccc	403				
Ser	Thr	Asp	Gly	Leu	Ala	Asp	Leu	Arg	Arg	Asp	Phe	Tyr	Glu	Leu	Pro					
				90					95					100						
aac	atc	gac	atc	gcc	tcg	gtg	gaa	atc	aag	ctg	gtc	ggc	gca	gcc	ctc	451				
Asn	Ile	Asp	Ile	Ala	Ser	Val	Glu	Ile	Lys	Leu	Val	Gly	Ala	Ala	Leu					
			105					110					115							
acc	aac	acc	gct	tgg	ttg	gga	gat	gtg	gaa	aaa	ctc	atc	caa	caa	cat	499				
Thr	Asn	Thr	Ala	Trp	Leu	Gly	Asp	Val	Glu	Lys	Leu	Ile	Gln	Gln	His					
		120					125					130								
cgc	aac	act	ttc	gta	tgg	gtt	gag	att	ccg	aca	gcc	ctg	gtc	acc	gca	547				
Arg	Asn	Thr	Phe	Val	Trp	Val	Glu	Ile	Pro	Thr	Ala	Leu	Val	Thr	Ala					
	135					140					145									
gat	att	gtc	cga	aaa	ctc	cgc	cac	atg	gga	gct	ggc	ctg	aaa	tac	aga	595				
Asp	Ile	Val	Arg	Lys	Leu	Arg	His	Met	Gly	Ala	Gly	Leu	Lys	Tyr	Arg					
150					155					160					165					
act	gga	ggt	gat	agg	gaa	gag	ctc	ttc	ccc	tca	ccg	cag	gac	ttg	gtc	643				
Thr	Gly	Gly	Asp	Arg	Glu	Glu	Leu	Phe	Pro	Ser	Pro	Gln	Asp	Leu	Val					
				170					175					180						
act	gtg	ctg	cgc	acc	gcc	atc	gat	gct	gca	ttg	ccg	ttt	aaa	ctc	act	691				
Thr	Val	Leu	Arg	Thr	Ala	Ile	Asp	Ala	Ala	Leu	Pro	Phe	Lys	Leu	Thr					
			185				190						195							
gca	ggc	ctg	cat	cgt	gct	ctc	agg	tat	cgt	gac	gag	aaa	acc	ggc	cga	739				
Ala	Gly	Leu	His	Arg	Ala	Leu	Arg	Tyr	Arg	Asp	Glu	Lys	Thr	Gly	Arg					
		200					205					210								
ctt	cac	ttc	gga	ttc	ctc	aac	att	gca	gcc	gcc	gtg	gcg	aca	ctt	cgt	787				
Leu	His	Phe	Gly	Phe	Leu	Asn	Ile	Ala	Ala	Ala	Val	Ala	Thr	Leu	Arg					
		215				220					225									
gct	gga	aaa	ggc	gag	gca	gag	gca	ctg	aag	atc	ctt	gaa	ggc	gat	gat	835				
Ala	Gly	Lys	Gly	Glu	Ala	Glu	Ala	Leu	Lys	Ile	Leu	Glu	Gly	Asp	Asp					
230					235					240					245					
gcc	gct	ccg	ctt	att	cac	gca	cta	caa	agc	ggc	gaa	aac	tgg	cgg	gat	883				
Ala	Ala	Pro	Leu	Ile	His	Ala	Leu	Gln	Ser	Gly	Glu	Asn	Trp	Arg	Asp					
				250					255					260						
tcc	ttc	cgc	agc	ttc	agt	acc	tgc	aat	gtt	gtt	gaa	cca	ctc	aac	act	931				
Ser	Phe	Arg	Ser	Phe	Ser	Thr	Cys	Asn	Val	Val	Glu	Pro	Leu	Asn	Thr					
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973

996

<210> 126

<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 126

Val Gln Lys Trp Gly Leu Ser Phe Val Glu Arg Ile Val Ile Val Asn
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Asn Val Gln Gln Phe His Arg Phe Phe Asp Asp Ser Ala Val Tyr Tyr
20 25 30

Pro Cys Phe Val Pro Leu Asp Arg Ala Ile Gly Glu His Phe Asp Arg
35 40 45

Gln Asn Lys Pro Met Ser Arg Phe Ile Gly Thr Leu Ile Leu Pro Leu
50 55 60

Ala Lys Leu Glu Glu Ala Ala Gln Tyr Thr Gly Asp Glu Val Leu Arg
65 70 75 80

Val Ser Ala Val Ile Ser Thr Asp Gly Leu Ala Asp Leu Arg Arg Asp
85 90 95

Phe Tyr Glu Leu Pro Asn Ile Asp Ile Ala Ser Val Glu Ile Lys Leu
100 105 110

Val Gly Ala Ala Leu Thr Asn Thr Ala Trp Leu Gly Asp Val Glu Lys
115 120 125

Leu Ile Gln Gln His Arg Asn Thr Phe Val Trp Val Glu Ile Pro Thr
130 135 140

Ala Leu Val Thr Ala Asp Ile Val Arg Lys Leu Arg His Met Gly Ala
145 150 155 160

Gly Leu Lys Tyr Arg Thr Gly Gly Asp Arg Glu Glu Leu Phe Pro Ser
165 170 175

Pro Gln Asp Leu Val Thr Val Leu Arg Thr Ala Ile Asp Ala Ala Leu
180 185 190

Pro Phe Lys Leu Thr Ala Gly Leu His Arg Ala Leu Arg Tyr Arg Asp
195 200 205

Glu Lys Thr Gly Arg Leu His Phe Gly Phe Leu Asn Ile Ala Ala Ala
210 215 220

Val Ala Thr Leu Arg Ala Gly Lys Gly Glu Ala Glu Ala Leu Lys Ile
225 230 235 240

Leu Glu Gly Asp Asp Ala Ala Pro Leu Ile His Ala Leu Gln Ser Gly
245 250 255

Glu Asn Trp Arg Asp Ser Phe Arg Ser Phe Ser Thr Cys Asn Val Val
 260 265 270

Glu Pro Leu Asn Thr Leu Ile Asp Leu Asp Val Leu Ala Glu Gly Asp
 275 280 285

Val His Pro
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<210> 127

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN02988

<400> 127

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acggtaaaca cgcacaagat aaaacattgc gagatttttc atg agt aca aaa ccc 115
 Met Ser Thr Lys Pro
 1 5

act att gtg tcc aca ttt tct ggt tgc ggt ggc ctc gat ctt ggc ctc 163
 Thr Ile Val Ser Thr Phe Ser Gly Cys Gly Gly Leu Asp Leu Gly Leu
 10 15 20

caa gag gtc gga ttc gac ccc att tgg gcc aac gac ttc tca gaa gaa 211
 Gln Glu Val Gly Phe Asp Pro Ile Trp Ala Asn Asp Phe Ser Glu Glu
 25 30 35

gca gtc caa acc tat aag cac aac atc ggt gac cac att gtt cac ggc 259
 Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp His Ile Val His Gly
 40 45 50

gac atc act gaa att gat ccg ttt act gat gac acc atc cct gac ggc 307
 Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp Thr Ile Pro Asp Gly
 55 60 65

gat ctc gtc acc ggc ggc ttc ccg tgc cag gac ttc tcc atg atc tgg 355
 Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp Phe Ser Met Ile Trp
 70 75 80 85

aag cgt cct gga ctc gac ggc aag cgt ggc acc ctg tac caa aac ttc 403
 Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr Leu Tyr Gln Asn Phe
 90 95 100

cgt gac ttt gtt gca gca aag aag cct aaa gcc ttt atc gca gaa aac 451
 Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala Phe Ile Ala Glu Asn
 105 110 115

gtg aag ggc cta ctc act gct aac cag cac aag gct att aag acc ata 499
 Val Lys Gly Leu Leu Thr Ala Asn Gln His Lys Ala Ile Lys Thr Ile
 120 125 130

ttg aag acc tcg aag ctg ttg agc ctg gct aca tcg tca agc ctc gcc 547

Leu Lys Thr Ser Lys Leu Leu Ser Leu Ala Thr Ser Ser Ser Leu Ala
 135 140 145
 tgt aca act tcg ctg aat acg gtg tcc cac aat tcc gcg aac gtg tgc 595
 Cys Thr Thr Ser Leu Asn Thr Val Ser His Asn Ser Ala Asn Val Cys
 150 155 160 165
 tca ttg ttg gca ttc gcc gtg aca ccg gct ttg att tca agc acc cag 643
 Ser Leu Leu Ala Phe Ala Val Thr Pro Ala Leu Ile Ser Ser Thr Gln
 170 175 180
 ctc cta ccc atg gcc ctc gcg gtg aca tgc cgt ata aga ctg ccg gcg 691
 Leu Leu Pro Met Ala Leu Ala Val Thr Cys Arg Ile Arg Leu Pro Ala
 185 190 195
 aag cgc tca aag gcg tgaaggatgt cccacaaac aac 729
 Lys Arg Ser Lys Ala
 200

<210> 128

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Ser Thr Lys Pro Thr Ile Val Ser Thr Phe Ser Gly Cys Gly Gly
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 20 25 30
 Asp Phe Ser Glu Glu Ala Val Gln Thr Tyr Lys His Asn Ile Gly Asp
 35 40 45
 His Ile Val His Gly Asp Ile Thr Glu Ile Asp Pro Phe Thr Asp Asp
 50 55 60
 Thr Ile Pro Asp Gly Asp Leu Val Thr Gly Gly Phe Pro Cys Gln Asp
 65 70 75 80
 Phe Ser Met Ile Trp Lys Arg Pro Gly Leu Asp Gly Lys Arg Gly Thr
 85 90 95
 Leu Tyr Gln Asn Phe Arg Asp Phe Val Ala Ala Lys Lys Pro Lys Ala
 100 105 110
 Phe Ile Ala Glu Asn Val Lys Gly Leu Leu Thr Ala Asn Gln His Lys
 115 120 125
 Ala Ile Lys Thr Ile Leu Lys Thr Ser Lys Leu Leu Ser Leu Ala Thr
 130 135 140
 Ser Ser Ser Leu Ala Cys Thr Thr Ser Leu Asn Thr Val Ser His Asn
 145 150 155 160
 Ser Ala Asn Val Cys Ser Leu Leu Ala Phe Ala Val Thr Pro Ala Leu
 165 170 175
 Ile Ser Ser Thr Gln Leu Leu Pro Met Ala Leu Ala Val Thr Cys Arg
 180 185 190

Ile Arg Leu Pro Ala Lys Arg Ser Lys Ala
 195 200

<210> 129

<211> 588

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(565)

<223> RXN00127

<400> 129

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gaagccgccca acattggcgc ggcttgattt agatttaccg gtg tgg acg ttg tgc 115
 Val Trp Thr Leu Ser
 1 5

ccg tat gac ggc ccg cat cgc aac gtg ctc att gcg ctg aag gag cac 163
 Pro Tyr Asp Gly Pro His Arg Asn Val Leu Ile Ala Leu Lys Glu His
 10 15 20

ggc cgt gca gac ctt gtg gcg ttt gtg ggc gcg gtg gtg ggg gcg tgc 211
 Gly Arg Ala Asp Leu Val Ala Phe Val Gly Ala Val Val Gly Ala Ser
 25 30 35

ata agc tat ctg gcg gct cag ggg gaa att gag cac gac atc acg ctg 259
 Ile Ser Tyr Leu Ala Ala Gln Gly Glu Ile Glu His Asp Ile Thr Leu
 40 45 50

gtt ccg gcg ccc acc cgc gcc acc tcg cga cgc cgg cgg ggc ggc gat 307
 Val Pro Ala Pro Thr Arg Ala Thr Ser Arg Arg Arg Arg Gly Gly Asp
 55 60 65

ccg gtt gag cgg gtg tgc aat gca tca cgc tta tcg acg ttt ccc tgc 355
 Pro Val Glu Arg Val Cys Asn Ala Ser Arg Leu Ser Thr Phe Pro Cys
 70 75 80 85

ctt caa atc tca tcc cgc aca cca gac tcc gtc ggt caa act gcg caa 403
 Leu Gln Ile Ser Ser Arg Thr Pro Asp Ser Val Gly Gln Thr Ala Gln
 90 95 100

cag cga aga ctc aat atg cga gtg gag tta gtc cga caa cct cgg ggt 451
 Gln Arg Arg Leu Asn Met Arg Val Glu Leu Val Arg Gln Pro Arg Gly
 105 110 115

tct gtc ttg atc atc gac gat gtg gta aca acg ggg gca act att tcc 499
 Ser Val Leu Ile Ile Asp Asp Val Val Thr Thr Gly Ala Thr Ile Ser
 120 125 130

gca tct gca aac gtt ctt cgc gca gcg ggt gtg cag gtc aga gga gct 547
 Ala Ser Ala Asn Val Leu Arg Ala Ala Gly Val Gln Val Arg Gly Ala
 135 140 145

tta act tat tgc caa gcg tgatctttgga tataaaaggg gcc 588
 Leu Thr Tyr Cys Gln Ala
 150 155

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Ala	Leu	Lys	Glu	His	Gly	Arg	Ala	Asp	Leu	Val	Ala	Phe	Val	Gly	Ala	
			20					25					30			
Val	Val	Gly	Ala	Ser	Ile	Ser	Tyr	Leu	Ala	Ala	Gln	Gly	Glu	Ile	Glu	
		35					40					45				
His	Asp	Ile	Thr	Leu	Val	Pro	Ala	Pro	Thr	Arg	Ala	Thr	Ser	Arg	Arg	
	50					55					60					
Arg	Arg	Gly	Gly	Asp	Pro	Val	Glu	Arg	Val	Cys	Asn	Ala	Ser	Arg	Leu	
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Ser	Thr	Phe	Pro	Cys	Leu	Gln	Ile	Ser	Ser	Arg	Thr	Pro	Asp	Ser	Val	
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Gly	Gln	Thr	Ala	Gln	Gln	Arg	Arg	Leu	Asn	Met	Arg	Val	Glu	Leu	Val	
			100					105					110			
Arg	Gln	Pro	Arg	Gly	Ser	Val	Leu	Ile	Ile	Asp	Asp	Val	Val	Thr	Thr	
		115					120					125				
Gly	Ala	Thr	Ile	Ser	Ala	Ser	Ala	Asn	Val	Leu	Arg	Ala	Ala	Gly	Val	
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Gln	Val	Arg	Gly	Ala	Leu	Thr	Tyr	Cys	Gln	Ala						
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<223> RXN02938
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                                         Met Arg Asn Tyr Pro
                                         1                               5

gat tta ccg cat gat ttc cca ggt caa aac aca gag ctc acc ccc gca 163
Asp Leu Pro His Asp Phe Pro Gly Gln Asn Thr Glu Leu Thr Pro Ala
                        10                               15                               20

aag gca ccc gtg tgg atg cac cga ctc tta gac cgc atc cac acc ggc 211

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Lys	Ala	Pro	Val	Trp	Met	His	Arg	Leu	Leu	Asp	Arg	Ile	His	Thr	Gly		
			25					30					35				
cgc	atg	gcc	aac	ccg	ctg	gac	ggg	gcg	gaa	acg	ctc	ggc	gac	aca	gac	259	
Arg	Met	Ala	Asn	Pro	Leu	Asp	Gly	Ala	Glu	Thr	Leu	Gly	Asp	Thr	Asp		
		40					45					50					
tcc	gaa	aag	cgc	gct	gcc	gtg	ctc	atg	cta	ttt	tct	ggc	tcg	gaa	acc	307	
Ser	Glu	Lys	Arg	Ala	Ala	Val	Leu	Met	Leu	Phe	Ser	Gly	Ser	Glu	Thr		
	55					60					65						
tcc	ttt	gac	ctg	ccc	aat	gac	gcc	tcc	gtg	ctg	ctg	acg	cac	cgc	acc	355	
Ser	Phe	Asp	Leu	Pro	Asn	Asp	Ala	Ser	Val	Leu	Leu	Thr	His	Arg	Thr		
70					75				80						85		
ccg	acg	atg	cgt	tcc	cat	gca	ggg	cag	att	gcc	ttt	ccc	ggg	ggc	cga	403	
Pro	Thr	Met	Arg	Ser	His	Ala	Gly	Gln	Ile	Ala	Phe	Pro	Gly	Gly	Arg		
				90				95						100			
atc	gac	ccc	acc	gat	act	aac	gcc	gtg	gac	tgc	gcc	ttc	cgc	gag	gcc	451	
Ile	Asp	Pro	Thr	Asp	Thr	Asn	Ala	Val	Asp	Cys	Ala	Phe	Arg	Glu	Ala		
			105					110					115				
tgg	gaa	gaa	acc	ggg	ctg	gat	cgc	cgc	acc	gca	acc	cca	tta	gcc	cag	499	
Trp	Glu	Glu	Thr	Gly	Leu	Asp	Arg	Arg	Thr	Ala	Thr	Pro	Leu	Ala	Gln		
	120						125					130					
ctc	aac	gag	gtg	cac	atc	cgt	gcc	acc	gga	tac	ccc	gtc	tac	cca	atc	547	
Leu	Asn	Glu	Val	His	Ile	Arg	Ala	Thr	Gly	Tyr	Pro	Val	Tyr	Pro	Ile		
	135					140					145						
ctt	gga	cac	tgg	cac	acc	cca	tca	ccc	gtc	gcc	gtg	gcc	agc	cca	cac	595	
Leu	Gly	His	Trp	His	Thr	Pro	Ser	Pro	Val	Ala	Val	Ala	Ser	Pro	His		
150					155				160						165		
gaa	acc	gac	gaa	gtt	ttg	gac	gcc	cca	ctc	tac	gac	ctc	atc	gac	ccc	643	
Glu	Thr	Asp	Glu	Val	Leu	Asp	Ala	Pro	Leu	Tyr	Asp	Leu	Ile	Asp	Pro		
				170				175						180			
aaa	aac	cgc	ctc	atg	gtc	ggc	tgg	cgc	gaa	tgg	cac	gga	cca	gcg	ttt	691	
Lys	Asn	Arg	Leu	Met	Val	Gly	Trp	Arg	Glu	Trp	His	Gly	Pro	Ala	Phe		
			185					190					195				
cga	atc	aac	gac	tac	atc	atc	tgg	gga	ttc	acc	ggc	gga	cta	ctc	tcc	739	
Arg	Ile	Asn	Asp	Tyr	Ile	Ile	Trp	Gly	Phe	Thr	Gly	Gly	Leu	Leu	Ser		
		200					205					210					
gcg	atc	ctc	gac	acc	gcc	ggc	tgg	gcc	acc	gaa	tgg	gac	acc	gac	cgc	787	
Ala	Ile	Leu	Asp	Thr	Ala	Gly	Trp	Ala	Thr	Glu	Trp	Asp	Thr	Asp	Arg		
	215					220					225						
atc	ttc	gac	ctg	gaa	aat	aca	ttg	tca	aca	tct	cgc	aac	aat	gag	cgt	835	
Ile	Phe	Asp	Leu	Glu	Asn	Thr	Leu	Ser	Thr	Ser	Arg	Asn	Asn	Glu	Arg		
230					235					240					245		
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Met	Arg																

<210> 132

<211> 247
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 132

Met	Arg	Asn	Tyr	Pro	Asp	Leu	Pro	His	Asp	Phe	Pro	Gly	Gln	Asn	Thr
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Glu	Leu	Thr	Pro	Ala	Lys	Ala	Pro	Val	Trp	Met	His	Arg	Leu	Leu	Asp
			20					25					30		
Arg	Ile	His	Thr	Gly	Arg	Met	Ala	Asn	Pro	Leu	Asp	Gly	Ala	Glu	Thr
		35					40					45			
Leu	Gly	Asp	Thr	Asp	Ser	Glu	Lys	Arg	Ala	Ala	Val	Leu	Met	Leu	Phe
	50					55					60				
Ser	Gly	Ser	Glu	Thr	Ser	Phe	Asp	Leu	Pro	Asn	Asp	Ala	Ser	Val	Leu
65					70					75					80
Leu	Thr	His	Arg	Thr	Pro	Thr	Met	Arg	Ser	His	Ala	Gly	Gln	Ile	Ala
				85					90					95	
Phe	Pro	Gly	Gly	Arg	Ile	Asp	Pro	Thr	Asp	Thr	Asn	Ala	Val	Asp	Cys
			100					105					110		
Ala	Phe	Arg	Glu	Ala	Trp	Glu	Glu	Thr	Gly	Leu	Asp	Arg	Arg	Thr	Ala
		115					120					125			
Thr	Pro	Leu	Ala	Gln	Leu	Asn	Glu	Val	His	Ile	Arg	Ala	Thr	Gly	Tyr
		130				135					140				
Pro	Val	Tyr	Pro	Ile	Leu	Gly	His	Trp	His	Thr	Pro	Ser	Pro	Val	Ala
145					150					155					160
Val	Ala	Ser	Pro	His	Glu	Thr	Asp	Glu	Val	Leu	Asp	Ala	Pro	Leu	Tyr
				165					170					175	
Asp	Leu	Ile	Asp	Pro	Lys	Asn	Arg	Leu	Met	Val	Gly	Trp	Arg	Glu	Trp
			180					185					190		
His	Gly	Pro	Ala	Phe	Arg	Ile	Asn	Asp	Tyr	Ile	Ile	Trp	Gly	Phe	Thr
		195					200					205			
Gly	Gly	Leu	Leu	Ser	Ala	Ile	Leu	Asp	Thr	Ala	Gly	Trp	Ala	Thr	Glu
	210					215					220				
Trp	Asp	Thr	Asp	Arg	Ile	Phe	Asp	Leu	Glu	Asn	Thr	Leu	Ser	Thr	Ser
225					230					235					240
Arg	Asn	Asn	Glu	Arg	Met	Arg									
				245											

<210> 133
 <211> 597
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS

<222> (83)..(574)

<223> RXN03102

<400> 133

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gtcggagaat ctggcggggc ga gtg gtg gag ctg ttg aaa tcg cgc ggt gaa 112
 Val Val Glu Leu Leu Lys Ser Arg Gly Glu
 1 5 10

acg ctg gcg ttt tgt gaa tcc ctc acc gcc ggc ctt gcc agt gcg acg 160
 Thr Leu Ala Phe Cys Glu Ser Leu Thr Ala Gly Leu Ala Ser Ala Thr
 15 20 25

atc gca gag atc ccc ggc gcc tca gtg gta ctt aaa ggc ggg ctg gtc 208
 Ile Ala Glu Ile Pro Gly Ala Ser Val Val Leu Lys Gly Gly Leu Val
 30 35 40

acc tat gcc acc gag ctt aag gtt gcg ctt gcc ggt gtg ccg cag gag 256
 Thr Tyr Ala Thr Glu Leu Lys Val Ala Leu Ala Gly Val Pro Gln Glu
 45 50 55

ctt atc gac gcg cac ggc gtt gtt tcc ccg cag tgc gcc cgt gcg atg 304
 Leu Ile Asp Ala His Gly Val Val Ser Pro Gln Cys Ala Arg Ala Met
 60 65 70

gca acg ggg gcc gca cac aga tgc cag gca gat tgg gcg gtt tcg ctc 352
 Ala Thr Gly Ala Ala His Arg Cys Gln Ala Asp Trp Ala Val Ser Leu
 75 80 85 90

acg ggc gtt gct ggc ccc agc aaa caa gat ggt cat ccg gtg ggg gaa 400
 Thr Gly Val Ala Gly Pro Ser Lys Gln Asp Gly His Pro Val Gly Glu
 95 100 105

gtg tgg atc gga gtg gct ggt cct gcg cat ttt ggg gcg tcg gga aca 448
 Val Trp Ile Gly Val Ala Gly Pro Ala His Phe Gly Ala Ser Gly Thr
 110 115 120

att gac gcg tat cgt gcg ttt gaa agt gaa caa cag gta ata ttg gct 496
 Ile Asp Ala Tyr Arg Ala Phe Glu Ser Glu Gln Gln Val Ile Leu Ala
 125 130 135

gaa ttg gga cgg cat cat att aga gag tct gct gtg cag caa agc ttt 544
 Glu Leu Gly Arg His His Ile Arg Glu Ser Ala Val Gln Gln Ser Phe
 140 145 150

cgc ctg ctg att gac cat att gag tcg cag tgactcaagt ttccaggtaa act 597
 Arg Leu Leu Ile Asp His Ile Glu Ser Gln
 155 160

<210> 134

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 134

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Ser Leu Thr Ala Gly Leu Ala Ser Ala Thr Ile Ala Glu Ile Pro Gly

20					25					30					
Ala	Ser	Val	Val	Leu	Lys	Gly	Gly	Leu	Val	Thr	Tyr	Ala	Thr	Glu	Leu
		35					40					45			
Lys	Val	Ala	Leu	Ala	Gly	Val	Pro	Gln	Glu	Leu	Ile	Asp	Ala	His	Gly
		50					55					60			
Val	Val	Ser	Pro	Gln	Cys	Ala	Arg	Ala	Met	Ala	Thr	Gly	Ala	Ala	His
		65					70					75			80
Arg	Cys	Gln	Ala	Asp	Trp	Ala	Val	Ser	Leu	Thr	Gly	Val	Ala	Gly	Pro
				85					90					95	
Ser	Lys	Gln	Asp	Gly	His	Pro	Val	Gly	Glu	Val	Trp	Ile	Gly	Val	Ala
			100					105					110		
Gly	Pro	Ala	His	Phe	Gly	Ala	Ser	Gly	Thr	Ile	Asp	Ala	Tyr	Arg	Ala
		115					120					125			
Phe	Glu	Ser	Glu	Gln	Gln	Val	Ile	Leu	Ala	Glu	Leu	Gly	Arg	His	His
		130					135					140			
Ile	Arg	Glu	Ser	Ala	Val	Gln	Gln	Ser	Phe	Arg	Leu	Leu	Ile	Asp	His
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Ile	Glu	Ser	Gln												

<210> 135

<211> 933

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(910)

<223> RXN03118

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gtctcgcgct ggctgatcag gaagctgatt aagtagatat atg aag ccc acc gtt 115
 Met Lys Pro Thr Val
 1 5

aat gtt gtg ttc aat gcg cat cac ccc aaa gat acg cag ccg ttg gat 163
 Asn Val Val Phe Asn Ala His His Pro Lys Asp Thr Gln Pro Leu Asp
 10 15 20

aag ttc ttc gat aaa gaa ctt aaa gac aca cat cat ctc gat ata acg 211
 Lys Phe Phe Asp Lys Glu Leu Lys Asp Thr His His Leu Asp Ile Thr
 25 30 35

gtg ggt tat atc agt gag aaa tca cta caa tat ttg ctt ctt att gca 259
 Val Gly Tyr Ile Ser Glu Lys Ser Leu Gln Tyr Leu Leu Leu Ile Ala
 40 45 50

ggc act tac ccc gac ctc acc att aca ctt acc tgt gga atg cac gct 307
 Gly Thr Tyr Pro Asp Leu Thr Ile Thr Leu Thr Cys Gly Met His Ala

55	60	65	
cgt gaa ggc atg act gct gcc caa ctg cat cat gcg cga gtg ctc cat			355
Arg Glu Gly Met Thr Ala Ala Gln Leu His His Ala Arg Val Leu His			
70	75	80	85
gac tac tta agc gac cat gat cga ggc ggg gtg ttc gtt att ccc cga			403
Asp Tyr Leu Ser Asp His Asp Arg Gly Gly Val Phe Val Ile Pro Arg			
	90	95	100
ttg cgt tat cac ggg aaa atc tat ctt ttc cac aag aac cag cac aca			451
Leu Arg Tyr His Gly Lys Ile Tyr Leu Phe His Lys Asn Gln His Thr			
	105	110	115
gat cct att gct tat atc ggt agc gct aac ctc tca gcc atc gtt cct			499
Asp Pro Ile Ala Tyr Ile Gly Ser Ala Asn Leu Ser Ala Ile Val Pro			
	120	125	130
ggg tac acc tct aca ttc gag ccc ggc gtc atc tta gac ccc gca cct			547
Gly Tyr Thr Ser Thr Phe Glu Pro Gly Val Ile Leu Asp Pro Ala Pro			
	135	140	145
gaa gat ctc gtg ctt cat ctc aac cgt gat gtc gta ccc cta tgt gtc			595
Glu Asp Leu Val Leu His Leu Asn Arg Asp Val Val Pro Leu Cys Val			
	150	155	160
ccc att gac acc gcg cat gtc ccc atc att aaa gat caa gaa tcc ccg			643
Pro Ile Asp Thr Ala His Val Pro Ile Ile Lys Asp Gln Glu Ser Pro			
	170	175	180
atg aag cac gtc gct gaa gca aca gct gtg tcc acc tct gat gtt gtt			691
Met Lys His Val Ala Glu Ala Thr Ala Val Ser Thr Ser Asp Val Val			
	185	190	195
gcc atc atg tcc agc cca ttt act tat agt ttt gac ctt aaa ctc aaa			739
Ala Ile Met Ser Ser Pro Phe Thr Tyr Ser Phe Asp Leu Lys Leu Lys			
	200	205	210
gcc act gcc agc agc aac ctc aat gct cat aac tca ggc ggt ggc gcg			787
Ala Thr Ala Ser Ser Asn Leu Asn Ala His Asn Ser Gly Gly Gly Ala			
	215	220	225
cgc aaa cag aaa aac ggt agc ttc ctt gca cgc aat tgg tat gag ggc			835
Arg Lys Gln Lys Asn Gly Ser Phe Leu Ala Arg Asn Trp Tyr Glu Gly			
	230	235	240
gaa atc att gtc ggt gtc gag aca aca aga ctc cca ggt tac cca caa			883
Glu Ile Ile Val Gly Val Glu Thr Thr Arg Leu Pro Gly Tyr Pro Gln			
	250	255	260
aac aaa tcc gaa ttc act gcg ggt cac tgatgacggc tggtcatttg ttt			933
Asn Lys Ser Glu Phe Thr Ala Gly His			
	265	270	

<210> 136

<211> 270

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Lys Pro Thr Val Asn Val Val Phe Asn Ala His His Pro Lys Asp
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 Thr Gln Pro Leu Asp Lys Phe Phe Asp Lys Glu Leu Lys Asp Thr His
 20 25 30
 His Leu Asp Ile Thr Val Gly Tyr Ile Ser Glu Lys Ser Leu Gln Tyr
 35 40 45
 Leu Leu Leu Ile Ala Gly Thr Tyr Pro Asp Leu Thr Ile Thr Leu Thr
 50 55 60
 Cys Gly Met His Ala Arg Glu Gly Met Thr Ala Ala Gln Leu His His
 65 70 75 80
 Ala Arg Val Leu His Asp Tyr Leu Ser Asp His Asp Arg Gly Gly Val
 85 90 95
 Phe Val Ile Pro Arg Leu Arg Tyr His Gly Lys Ile Tyr Leu Phe His
 100 105 110
 Lys Asn Gln His Thr Asp Pro Ile Ala Tyr Ile Gly Ser Ala Asn Leu
 115 120 125
 Ser Ala Ile Val Pro Gly Tyr Thr Ser Thr Phe Glu Pro Gly Val Ile
 130 135 140
 Leu Asp Pro Ala Pro Glu Asp Leu Val Leu His Leu Asn Arg Asp Val
 145 150 155 160
 Val Pro Leu Cys Val Pro Ile Asp Thr Ala His Val Pro Ile Ile Lys
 165 170 175
 Asp Gln Glu Ser Pro Met Lys His Val Ala Glu Ala Thr Ala Val Ser
 180 185 190
 Thr Ser Asp Val Val Ala Ile Met Ser Ser Pro Phe Thr Tyr Ser Phe
 195 200 205
 Asp Leu Lys Leu Lys Ala Thr Ala Ser Ser Asn Leu Asn Ala His Asn
 210 215 220
 Ser Gly Gly Gly Ala Arg Lys Gln Lys Asn Gly Ser Phe Leu Ala Arg
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<211> 1263

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1240)

<223> RXN02989

<400> 137

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Leu Asp Ala Ala Leu Ala Leu Ile Glu Lys Asp Phe Gly Lys Gly Ala
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Val Met Arg Leu Gly Asp Glu Asn Arg Pro Pro Ile Gln Thr Ile Ser
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Ser Gly Asn Thr Ala Ile Asp Ile Ala Leu Gly Ile Gly Gly Phe Pro
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Arg Gly Arg Ile Val Glu Val Tyr Gly Pro Glu Ser Ser Gly Lys Thr
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Ala Ala Phe Ile Asp Ala Glu His Ala Leu Asp Pro Asp Tyr Ala Arg
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Lys Leu Gly Val Asp Thr Asp Ala Leu Leu Val Ser Gln Pro Asp Thr
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Gly	Lys	Tyr	Ala	Ala	Ala	Ser	Asp	Glu	Leu	Thr	Asp	Asp	Pro	Val	Glu	
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<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Val	Arg	Ser	Gly	Ala	Ile	Asp	Ile	Ile	Val	Ile	Asp	Ser	Val	Ala	Ala	145	150	155	160
Leu	Thr	Pro	Lys	Ala	Glu	Ile	Glu	Gly	Glu	Met	Gly	Asp	Ser	His	Val	165	170	175	
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Glu	Lys	Ile	Gly	Val	Met	Phe	Gly	Ser	Pro	Glu	Thr	Thr	Thr	Gly	Gly	210	215	220	
Lys	Ala	Leu	Lys	Phe	Tyr	Ala	Ser	Val	Arg	Cys	Asp	Ile	Arg	Arg	Ile	225	230	235	240
Gln	Thr	Leu	Lys	Asp	Gly	Gln	Asp	Ala	Ile	Gly	Asn	Arg	Thr	Arg	Leu	245	250	255	
Lys	Val	Val	Lys	Asn	Lys	Val	Ser	Pro	Pro	Phe	Lys	Ile	Ala	Glu	Phe	260	265	270	
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Asp	Asp	Pro	Val	Glu	Leu	Val	Pro	Asn	Val	Asp	Phe	Asp	Asp	Glu	Ala	355	360	365	
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Thr Pro Gln Asp Arg Tyr Thr Asp Glu Tyr Gly Ile Glu Arg Val Asn																
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Lys Asp Glu Pro Gly Leu Val Asp Lys Leu Arg Asp Lys His Asp Trp																
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Ser Gly Leu Gly Trp Met Ala Asn Leu Arg Phe Gly Val Ser Arg Met																
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Asp Leu Val Ala Leu Ile Val Leu Leu Leu Ala Met Gly Val Ala Phe																
170 175 180																

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cag gca gca ctg ctt ggc gca atc ggt ttt gag gtg gtc aag cag gtt 883
 Gln Ala Ala Leu Leu Gly Ala Ile Gly Phe Glu Val Val Lys Gln Val
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 Arg Leu Ala Thr Val Pro Ala Pro Glu Pro Ala Ile Ile Arg Val Arg
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 His Glu Ile Asp Pro Gly Glu Glu Val Ser Gln Ser Ala Arg Lys Val
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<400> 140

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Val	Thr	Ala	Leu	Trp	Ser	Gly	Leu	Gly	Trp	Met	Ala	Asn	Leu	Arg	Phe
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Met	Gly	Val	Ala	Phe	Gly	Ile	Thr	Ala	Leu	Gly	Ala	Ser	Gly	Leu	Thr
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Pro	Ala	Gly	Ala	Ala	Phe	Gly	Pro	Ile	Ile	Gly	Ile	Met	Val	Val	Leu
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Tyr	Leu	Ile	Trp	Arg	Ile	Leu	Met	Tyr	Cys	Ser	Ala	Trp	Ala	Ala	Thr
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 Arg Ala Glu Ala Lys Gln Ile Ser Gln Glu His Thr Tyr Glu Lys Asp
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 Ser Val Lys Leu Arg Met Ala Asp Phe Arg Ile Glu Ser Arg Ser Tyr
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 Phe Arg Leu Ala Arg Tyr Pro Gly Glu Val Gly Pro Ile Arg Leu Val
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Glu	Ala	Pro	Gln	Asp	Val	Ala	Leu	Ser	Met	Trp	Cys	Ala	Thr	Gln	Asp					
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Leu	Asp	Ser	Leu	Asp	Trp	Ala	Asp	Trp	Phe	Ala	Glu	Asn	Gly	Glu	Thr					
	275					280					285									
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<212> PRT

<213> Corynebacterium glutamicum

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Leu	Thr	Gln	Lys	Glu	Val	Glu	Ile	Ser	Leu	Gly	Ala	Thr	Ile	Gly	Ile
		35					40						45		
Ser	Leu	Trp	Asn	Leu	Ala	Arg	Gly	Ile	Asp	Asp	Arg	Pro	Val	Glu	Pro
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Leu	Leu	Thr	Arg	Gln	Gln	Val	Asp	Ala	Ala	Ile	Ile	Arg	Ser	Ala	Glu
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 Glu Ala Pro Gln Asp Val Ala Leu Ser Met Trp Cys Ala Thr Gln Asp
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 225 230 235 240
 Gly Val Val Ser Val Arg Phe Glu Thr Arg Ser Thr Thr Lys Gly Arg
 245 250 255
 Thr Lys Ser Phe Ser Met Asp Asp Pro Asp Leu Thr Pro Ala Asp Pro
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 Leu Asp Ser Leu Asp Trp Ala Asp Trp Phe Ala Glu Asn Gly Glu Thr
 275 280 285
 Gly Asp Asp Glu
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(433)
 <223> RXN02985

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 Met Arg Leu Glu Ser
 1 5

tat gcc atg gct aag aaa gta gac acc tcg aac gct acc ccc gct cta 163
 Tyr Ala Met Ala Lys Lys Val Asp Thr Ser Asn Ala Thr Pro Ala Leu
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gcc ctt ctt acg gag agg cag att cct ttt gag ctg gat gtt cat gat 211
 Ala Leu Leu Thr Glu Arg Gln Ile Pro Phe Glu Leu Asp Val His Asp
 25 30 35

gta gat cca aaa tca tca aag ggc ttt gca ttg gat gcc tct gaa gta 259
 Val Asp Pro Lys Ser Ser Lys Gly Phe Ala Leu Asp Ala Ser Glu Val

40 45 50
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 Met Gly Val Glu Pro Glu Val Val Phe Lys Thr Leu Met Ala Asp Ile
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 Asp Gly Glu His Val Val Ala Ile Val Pro Ala Ser Arg Thr Leu Asn
 70 75 80 85
 ctc aag cag ttg gct aag gct gga aaa ggt aag cat gca aac atg atg 403
 Leu Lys Gln Leu Ala Lys Ala Gly Lys Gly Lys His Ala Asn Met Met
 90 95 100
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 35 40 45
 Asp Ala Ser Glu Val Met Gly Val Glu Pro Glu Val Val Phe Lys Thr
 50 55 60
 Leu Met Ala Asp Ile Asp Gly Glu His Val Val Ala Ile Val Pro Ala
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 Ser Arg Thr Leu Asn Leu Lys Gln Leu Ala Lys Ala Gly Lys Gly Lys
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 His Ala Asn Met Met Asp Arg Ser Arg Ala Gln Val Val Thr Gly
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Val Phe Leu Asp Glu
1 5

tct gca att ctc cag gag cga atc tac gtc agc gca ggg cga cgc ggg 163
Ser Ala Ile Leu Gln Glu Arg Ile Tyr Val Ser Ala Gly Arg Arg Gly
10 15 20

tgg tcc ctg att atc gcc ccg gat gat gtt ctt ctg gct acc gat ggt 211
Trp Ser Leu Ile Ile Ala Pro Asp Asp Val Leu Leu Ala Thr Asp Gly
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Val Tyr Ala Asp Ile Ala Asp His Ser
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Leu Ala Thr Asp Gly Val Tyr Ala Asp Ile Ala Asp His Ser
35 40 45

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<212> DNA
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<223> RXS00061

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Val Thr Glu Lys Thr
1 5

gac cag acc tta atg ctt atc gac ggc cac tcg atg gct ttc cgc gca 163
Asp Gln Thr Leu Met Leu Ile Asp Gly His Ser Met Ala Phe Arg Ala
10 15 20

ttc ttt gct ttg ccg gct gag aat ttc tcc acg tcg ggc ggg cag gcc 211
Phe Phe Ala Leu Pro Ala Glu Asn Phe Ser Thr Ser Gly Gly Gln Ala
25 30 35

acc aat gct gtc tat ggc ttt ctc tcg atg ctg tcc acg ttg ttg aag 259
Thr Asn Ala Val Tyr Gly Phe Leu Ser Met Leu Ser Thr Leu Leu Lys
40 45 50

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Asp	Glu	Gln	Pro	Thr	His	Val	Ala	Val	Ala	Phe	Asp	Val	Gly	Arg	Lys	
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Thr	Phe	Arg	Thr	Asp	Met	Phe	Pro	Ala	Tyr	Lys	Ala	Gln	Arg	Glu	Ala	
	70				75					80					85	
acg	cca	cct	gag	ttt	aag	ggc	cag	gtg	gaa	atc	ctc	aag	gag	gtg	ttg	403
Thr	Pro	Pro	Glu	Phe	Lys	Gly	Gln	Val	Glu	Ile	Leu	Lys	Glu	Val	Leu	
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Ser	Thr	Leu	Gly	Ile	Thr	Thr	Ile	Glu	Lys	Ile	Asp	Phe	Glu	Ala	Asp	
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Asp	Val	Ile	Ala	Thr	Leu	Ser	Val	Ala	Ala	Lys	Pro	Leu	Gly	Phe	Lys	
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Thr	Leu	Ile	Val	Thr	Gly	Asp	Arg	Asp	Ser	Phe	Gln	Leu	Val	Asn	Asp	
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acc	acc	acg	gtg	ttg	tat	ccg	atg	aag	ggc	gtg	tct	gtg	ctg	cac	cgt	595
Thr	Thr	Thr	Val	Leu	Tyr	Pro	Met	Lys	Gly	Val	Ser	Val	Leu	His	Arg	
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Phe	Thr	Pro	Glu	Ala	Val	Glu	Glu	Lys	Tyr	Gly	Leu	Thr	Pro	Arg	Gln	
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Tyr	Pro	Glu	Phe	Ala	Ala	Leu	Arg	Gly	Asp	Pro	Ser	Asp	Asn	Leu	Pro	
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Asn	Ile	Pro	Gly	Val	Gly	Glu	Lys	Thr	Ala	Thr	Lys	Trp	Ile	Ala	Gln	
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Tyr	Glu	Thr	Leu	Asp	Asn	Leu	Leu	Asp	His	Ala	Asp	Glu	Ile	Lys	Gly	
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Lys	Val	Gly	Ala	Ser	Leu	Arg	Glu	Arg	Ile	Glu	Gln	Val	Arg	Met	Asn	
	230				235					240					245	
cgc	aag	ctc	acg	gag	atg	gtg	aag	gat	ctg	gag	ctg	ccg	ctt	ggt	ccg	883
Arg	Lys	Leu	Thr	Glu	Met	Val	Lys	Asp	Leu	Glu	Leu	Pro	Leu	Gly	Pro	
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gac	gat	ttt	gag	atg	aag	cct	gtg	cag	gtt	gcg	gag	gtt	gcg	gcg	aag	931
Asp	Asp	Phe	Glu	Met	Lys	Pro	Val	Gln	Val	Ala	Glu	Val	Ala	Ala	Lys	
			265					270					275			
ttt	gac	gat	ctg	gag	ttt	ggt	acc	aat	ttg	cgt	gag	cgg	gtg	ctg	gcg	979
Phe	Asp	Asp	Leu	Glu	Phe	Gly	Thr	Asn	Leu	Arg	Glu	Arg	Val	Leu	Ala	
		280					285					290				
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Val	Val	Lys	Ala	Glu	Gly	Ser	Ala	Ala	Pro	Val	Glu	Glu	Val	Glu	Ala	
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gaa	cag	gtt	gtc	gtc	gat	acg	caa	tct	ttg	gcg	caa	tggt	ctg	cct	gct	1075
Glu	Gln	Val	Val	Val	Asp	Thr	Gln	Ser	Leu	Ala	Gln	Trp	Leu	Pro	Ala	
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Arg	Ala	Gly	Gln	Ala	Leu	Ala	Leu	Ala	Leu	Ala	Gly	Val	Ala	Lys	Pro	
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gct	gct	ggc	gac	acg	tat	gcg	cta	gcg	att	gcg	gat	acc	aag	cgc	cat	1171
Ala	Ala	Gly	Asp	Thr	Tyr	Ala	Leu	Ala	Ile	Ala	Asp	Thr	Lys	Arg	His	
			345					350					355			
gcg	gtg	ttg	gtt	gat	gtg	gct	gat	att	tca	gcg	gag	gat	gaa	aag	gcg	1219
Ala	Val	Leu	Val	Asp	Val	Ala	Asp	Ile	Ser	Ala	Glu	Asp	Glu	Lys	Ala	
		360					365						370			
ctg	gcc	acg	tggt	ttg	gcg	tcg	gaa	gat	cca	aag	atg	ctg	cac	ggc	gct	1267
Leu	Ala	Thr	Trp	Leu	Ala	Ser	Glu	Asp	Pro	Lys	Met	Leu	His	Gly	Ala	
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aag	gcc	gcc	tat	cat	atg	ctc	gct	ggg	cgc	ggg	ttt	gag	ctg	cac	ggc	1315
Lys	Ala	Ala	Tyr	His	Met	Leu	Ala	Gly	Arg	Gly	Phe	Glu	Leu	His	Gly	
390					395				400						405	
gtg	gtg	cat	gac	acg	gcg	atc	gcg	gca	tac	ttg	ctg	cgt	ccg	ggc	caa	1363
Val	Val	His	Asp	Thr	Ala	Ile	Ala	Ala	Tyr	Leu	Leu	Arg	Pro	Gly	Gln	
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cgc	acc	tat	gag	ctt	gcc	gac	gtc	tac	cag	cgg	cat	ctt	caa	cga	cag	1411
Arg	Thr	Tyr	Glu	Leu	Ala	Asp	Val	Tyr	Gln	Arg	His	Leu	Gln	Arg	Gln	
			425					430					435			
ttg	tct	aca	aac	gac	aat	ggc	ggc	cag	ctc	acg	ctg	ctc	gac	gca	gct	1459
Leu	Ser	Thr	Asn	Asp	Asn	Gly	Gly	Gln	Leu	Thr	Leu	Leu	Asp	Ala	Ala	
		440					445					450				
gat	gac	caa	tcg	ctt	gtt	gat	gat	gtc	att	gca	atc	ctt	gag	ctg	tct	1507
Asp	Asp	Gln	Ser	Leu	Val	Asp	Asp	Val	Ile	Ala	Ile	Leu	Glu	Leu	Ser	
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gaa	gaa	ttg	acc	aaa	cag	ctt	cag	gag	att	caa	gct	ttt	gag	ctt	tac	1555
Glu	Glu	Leu	Thr	Lys	Gln	Leu	Gln	Glu	Ile	Gln	Ala	Phe	Glu	Leu	Tyr	
470					475					480					485	
cat	gac	ctg	gaa	att	ccg	ctg	tcg	gga	att	ctg	gcg	cgc	atg	gag	gcc	1603
His	Asp	Leu	Glu	Ile	Pro	Leu	Ser	Gly	Ile	Leu	Ala	Arg	Met	Glu	Ala	
				490					495					500		
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Ile	Gly	Ile	Ala	Val	Asp	Val	Ala	Thr	Leu	Glu	Glu	Gln	Leu	Lys	Thr	
			505					510					515			
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Phe	Ile	Gly	Gln	Val	Ala	Gln	Glu	Glu	Glu	Ala	Ala	Arg	Glu	Leu	Ala	
		520					525					530				
gag	gat	cca	acc	ctg	aat	ctc	tcg	agc	ccg	aag	cag	ctg	caa	gtg	gtg	1747
Glu	Asp	Pro	Thr	Leu	Asn	Leu	Ser	Ser	Pro	Lys	Gln	Leu	Gln	Val	Val	

535	540	545	
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tac tct acg gct gcc gcg gaa att gaa gcc cta gcg atc aag aat ccg Tyr Ser Thr Ala Ala Glu Ile Glu Ala Leu Ala Ile Lys Asn Pro 570 575 580			1843
cac cca ttc cta gat cac ctg ttg gca cac cgt cag tac caa aag atg His Pro Phe Leu Asp His Leu Leu Ala His Arg Gln Tyr Gln Lys Met 585 590 595			1891
aag acc act ctg gaa ggt ctc atc cgt gag gtg gct cct gat ggc cgt Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val Ala Pro Asp Gly Arg 600 605 610			1939
att cac acc acc ttc aac cag acg gtg gcg tct acg gga cgt ttg tca Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser Thr Gly Arg Leu Ser 615 620 625			1987
tcc act gat ccc aac ctg caa aac att cct gtg cgc act gag gct ggc Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Glu Ala Gly 630 635 640 645			2035
cga aag att cgt tcg gga ttc gtc gta ggc gag ggg tat gaa acc ttg Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu Gly Tyr Glu Thr Leu 650 655 660			2083
ctg act gcc gac tat tcg cag att gaa atg cgc gtg atg gct cac ctt Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg Val Met Ala His Leu 665 670 675			2131
tcc cag gac cca ggc ttg att gag gcg tac cgc gaa ggc gaa gac ctg Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg Glu Gly Glu Asp Leu 680 685 690			2179
cac aat tac gtg ggt tcc aag gtg ttt aat gtg ccc atc gat ggc gtg His Asn Tyr Val Gly Ser Lys Val Phe Asn Val Pro Ile Asp Gly Val 695 700 705			2227
acc cct gag ctg cgt cgc cag gtc aag gcc atg tct tac ggt ctg gtg Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met Ser Tyr Gly Leu Val 710 715 720 725			2275
tac ggc ttg tcc gcg ttt ggt ttg tct cag cag ctg agc att cct gct Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln Leu Ser Ile Pro Ala 730 735 740			2323
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gta cag cgc tac ctc cgg gag atc gtg gag gag gct cga aaa gct ggc Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu Ala Arg Lys Ala Gly 760 765 770			2419
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tcg gat aac cgt gtc gct cgt gaa aac gct gaa cgt gcc gca ctg aac 2515
 Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu Arg Ala Ala Leu Asn
 790 795 800 805

 gcc ccg att cag gga act gcc gca gac atc atc aag gtg gcc atg atc 2563
 Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile Lys Val Ala Met Ile
 810 815 820

 cgg gtg gac cgt tca ctc aag gaa gct gcc gtg aaa tct cgc gtg ctg 2611
 Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val Lys Ser Arg Val Leu
 825 830 835

 ctt cag gtg cat gat gaa ttg gtc gtg gaa gta gcg gcc ggt gag ttg 2659
 Leu Gln Val His Asp Glu Leu Val Val Glu Val Ala Ala Gly Glu Leu
 840 845 850

 gaa caa gtc cgt gag att ctg gaa cgc gaa atg gat aac gcc atc aag 2707
 Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met Asp Asn Ala Ile Lys
 855 860 865

 ctg tcc gtt cct ttg gaa gtt tca gct ggt gat ggc gtt aac tgg gat 2755
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<210> 148

<211> 889

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

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 35 40 45

 Ser Thr Leu Leu Lys Asp Glu Gln Pro Thr His Val Ala Val Ala Phe
 50 55 60

 Asp Val Gly Arg Lys Thr Phe Arg Thr Asp Met Phe Pro Ala Tyr Lys
 65 70 75 80

 Ala Gln Arg Glu Ala Thr Pro Pro Glu Phe Lys Gly Gln Val Glu Ile
 85 90 95

 Leu Lys Glu Val Leu Ser Thr Leu Gly Ile Thr Thr Ile Glu Lys Ile
 100 105 110

 Asp Phe Glu Ala Asp Asp Val Ile Ala Thr Leu Ser Val Ala Ala Lys
 115 120 125

 Pro Leu Gly Phe Lys Thr Leu Ile Val Thr Gly Asp Arg Asp Ser Phe

130	135	140
Gln Leu Val Asn Asp Thr Thr Thr Val Leu Tyr Pro Met Lys Gly Val 145 150 155 160		
Ser Val Leu His Arg Phe Thr Pro Glu Ala Val Glu Glu Lys Tyr Gly 165 170 175		
Leu Thr Pro Arg Gln Tyr Pro Glu Phe Ala Ala Leu Arg Gly Asp Pro 180 185 190		
Ser Asp Asn Leu Pro Asn Ile Pro Gly Val Gly Glu Lys Thr Ala Thr 195 200 205		
Lys Trp Ile Ala Gln Tyr Glu Thr Leu Asp Asn Leu Leu Asp His Ala 210 215 220		
Asp Glu Ile Lys Gly Lys Val Gly Ala Ser Leu Arg Glu Arg Ile Glu 225 230 235 240		
Gln Val Arg Met Asn Arg Lys Leu Thr Glu Met Val Lys Asp Leu Glu 245 250 255		
Leu Pro Leu Gly Pro Asp Asp Phe Glu Met Lys Pro Val Gln Val Ala 260 265 270		
Glu Val Ala Ala Lys Phe Asp Asp Leu Glu Phe Gly Thr Asn Leu Arg 275 280 285		
Glu Arg Val Leu Ala Val Val Lys Ala Glu Gly Ser Ala Ala Pro Val 290 295 300		
Glu Glu Val Glu Ala Glu Gln Val Val Val Asp Thr Gln Ser Leu Ala 305 310 315 320		
Gln Trp Leu Pro Ala Arg Ala Gly Gln Ala Leu Ala Leu Ala Leu Ala 325 330 335		
Gly Val Ala Lys Pro Ala Ala Gly Asp Thr Tyr Ala Leu Ala Ile Ala 340 345 350		
Asp Thr Lys Arg His Ala Val Leu Val Asp Val Ala Asp Ile Ser Ala 355 360 365		
Glu Asp Glu Lys Ala Leu Ala Thr Trp Leu Ala Ser Glu Asp Pro Lys 370 375 380		
Met Leu His Gly Ala Lys Ala Ala Tyr His Met Leu Ala Gly Arg Gly 385 390 395 400		
Phe Glu Leu His Gly Val Val His Asp Thr Ala Ile Ala Ala Tyr Leu 405 410 415		
Leu Arg Pro Gly Gln Arg Thr Tyr Glu Leu Ala Asp Val Tyr Gln Arg 420 425 430		
His Leu Gln Arg Gln Leu Ser Thr Asn Asp Asn Gly Gly Gln Leu Thr 435 440 445		
Leu Leu Asp Ala Ala Asp Asp Gln Ser Leu Val Asp Asp Val Ile Ala 450 455 460		

Ile Leu Glu Leu Ser Glu Glu Leu Thr Lys Gln Leu Gln Glu Ile Gln
 465 470 475 480
 Ala Phe Glu Leu Tyr His Asp Leu Glu Ile Pro Leu Ser Gly Ile Leu
 485 490 495
 Ala Arg Met Glu Ala Ile Gly Ile Ala Val Asp Val Ala Thr Leu Glu
 500 505 510
 Glu Gln Leu Lys Thr Phe Ile Gly Gln Val Ala Gln Glu Glu Glu Ala
 515 520 525
 Ala Arg Glu Leu Ala Glu Asp Pro Thr Leu Asn Leu Ser Ser Pro Lys
 530 535 540
 Gln Leu Gln Val Val Leu Phe Glu Thr Phe Gly Met Pro Lys Thr Lys
 545 550 555 560
 Lys Thr Lys Thr Gly Tyr Ser Thr Ala Ala Ala Glu Ile Glu Ala Leu
 565 570 575
 Ala Ile Lys Asn Pro His Pro Phe Leu Asp His Leu Leu Ala His Arg
 580 585 590
 Gln Tyr Gln Lys Met Lys Thr Thr Leu Glu Gly Leu Ile Arg Glu Val
 595 600 605
 Ala Pro Asp Gly Arg Ile His Thr Thr Phe Asn Gln Thr Val Ala Ser
 610 615 620
 Thr Gly Arg Leu Ser Ser Thr Asp Pro Asn Leu Gln Asn Ile Pro Val
 625 630 635 640
 Arg Thr Glu Ala Gly Arg Lys Ile Arg Ser Gly Phe Val Val Gly Glu
 645 650 655
 Gly Tyr Glu Thr Leu Leu Thr Ala Asp Tyr Ser Gln Ile Glu Met Arg
 660 665 670
 Val Met Ala His Leu Ser Gln Asp Pro Gly Leu Ile Glu Ala Tyr Arg
 675 680 685
 Glu Gly Glu Asp Leu His Asn Tyr Val Gly Ser Lys Val Phe Asn Val
 690 695 700
 Pro Ile Asp Gly Val Thr Pro Glu Leu Arg Arg Gln Val Lys Ala Met
 705 710 715 720
 Ser Tyr Gly Leu Val Tyr Gly Leu Ser Ala Phe Gly Leu Ser Gln Gln
 725 730 735
 Leu Ser Ile Pro Ala Gly Glu Ala Lys Gln Ile Met Glu Ser Tyr Phe
 740 745 750
 Glu Arg Phe Gly Gly Val Gln Arg Tyr Leu Arg Glu Ile Val Glu Glu
 755 760 765
 Ala Arg Lys Ala Gly Tyr Thr Glu Thr Leu Phe Gly Arg Arg Arg Tyr
 770 775 780

Leu Pro Glu Leu Thr Ser Asp Asn Arg Val Ala Arg Glu Asn Ala Glu
 785 790 795 800
 Arg Ala Ala Leu Asn Ala Pro Ile Gln Gly Thr Ala Ala Asp Ile Ile
 805 810 815
 Lys Val Ala Met Ile Arg Val Asp Arg Ser Leu Lys Glu Ala Ala Val
 820 825 830
 Lys Ser Arg Val Leu Leu Gln Val His Asp Glu Leu Val Val Glu Val
 835 840 845
 Ala Ala Gly Glu Leu Glu Gln Val Arg Glu Ile Leu Glu Arg Glu Met
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 Gly Val Asn Trp Asp Ala Ala Ala His
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<210> 149

<211> 1683

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1660)

<223> RXS00212

<400> 149

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 Met Asn Ile Leu Cys
 1 5
 ctg ctg tgc tgg aaa ttc gcg gtg agg tgt tca tca ctg tgg agg att 163
 Leu Leu Cys Trp Lys Phe Ala Val Arg Cys Ser Ser Leu Trp Arg Ile
 10 15 20
 tcc cag gag gtc aac gcg cag cgc att gct gat ggt ggc aag ccg ttt 211
 Ser Gln Glu Val Asn Ala Gln Arg Ile Ala Asp Gly Gly Lys Pro Phe
 25 30 35
 gcc aac ccg cgt aat gct gcg gct ggt tct ctg cgt cag aaa aat att 259
 Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu Arg Gln Lys Asn Ile
 40 45 50
 gag gac gtg aag aag cgc cgc ctg cgg atg atc agc cat ggc atc ggt 307
 Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile Ser His Gly Ile Gly
 55 60 65
 ttc act gaa ggc ttt agc cct gcg tct cag cat gat gcg tat ctg gca 355
 Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His Asp Ala Tyr Leu Ala
 70 75 80 85
 ttg gct gcc tgg ggt ttg ccc acc tcg ccg tac aca gag gct gtg act 403
 Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr Thr Glu Ala Val Thr

90										95					100					
gat	cca	gaa	gat	gtg	gtg	aaa	aag	gtc	agc	tac	tgg	gct	gat	cac	cgc	451				
Asp	Pro	Glu	Asp	Val	Val	Lys	Lys	Val	Ser	Tyr	Trp	Ala	Asp	His	Arg					
			105					110					115							
cac	gac	gca	ctc	cat	gag	atg	gat	ggc	ctg	gtg	att	aag	gtc	gat	gac	499				
His	Asp	Ala	Leu	His	Glu	Met	Asp	Gly	Leu	Val	Ile	Lys	Val	Asp	Asp					
		120					125					130								
atc	gca	tct	cag	cgt	gct	ttg	ggc	tcc	acc	agc	cgc	gcg	cct	cgc	tgg	547				
Ile	Ala	Ser	Gln	Arg	Ala	Leu	Gly	Ser	Thr	Ser	Arg	Ala	Pro	Arg	Trp					
	135					140					145									
gcc	att	gcg	tac	aag	tac	cct	ccg	gag	gag	gtc	acc	acc	aag	ctg	ctt	595				
Ala	Ile	Ala	Tyr	Lys	Tyr	Pro	Pro	Glu	Glu	Val	Thr	Thr	Lys	Leu	Leu					
150					155					160					165					
gat	att	cag	gtt	ggc	gtt	ggc	cgc	acc	ggc	cgt	gtc	acc	cca	ttc	gcg	643				
Asp	Ile	Gln	Val	Gly	Val	Gly	Arg	Thr	Gly	Arg	Val	Thr	Pro	Phe	Ala					
				170					175					180						
gtc	atg	gag	ccg	gtt	ctt	gtt	gca	gga	tca	acg	gtg	tct	atg	gcg	acg	691				
Val	Met	Glu	Pro	Val	Leu	Val	Ala	Gly	Ser	Thr	Val	Ser	Met	Ala	Thr					
			185					190					195							
ctg	cat	aac	cag	agc	gaa	gtc	aag	cgt	aaa	ggc	gtg	ctc	atc	ggc	gac	739				
Leu	His	Asn	Gln	Ser	Glu	Val	Lys	Arg	Lys	Gly	Val	Leu	Ile	Gly	Asp					
		200					205					210								
acc	gtg	gtt	atc	cgc	aag	gag	ggc	gag	gtt	atc	cca	gag	gtg	ctt	ggc	787				
Thr	Val	Val	Ile	Arg	Lys	Ala	Gly	Glu	Val	Ile	Pro	Glu	Val	Leu	Gly					
	215					220					225									
cct	gtc	gta	gag	ctt	cgt	gac	ggc	aca	gag	cgc	gag	tac	atc	ttc	cca	835				
Pro	Val	Val	Glu	Leu	Arg	Asp	Gly	Thr	Glu	Arg	Glu	Tyr	Ile	Phe	Pro					
230					235					240					245					
acg	ctg	tgc	cct	gaa	tgc	ggc	acc	cgt	ctg	gag	ccc	gag	aag	gcc	gat	883				
Thr	Leu	Cys	Pro	Glu	Cys	Gly	Thr	Arg	Leu	Ala	Pro	Ala	Lys	Ala	Asp					
				250					255					260						
gac	gtg	gat	tgg	cgt	tgc	ccc	aac	atg	caa	agc	tgt	cca	ggc	cag	ctg	931				
Asp	Val	Asp	Trp	Arg	Cys	Pro	Asn	Met	Gln	Ser	Cys	Pro	Gly	Gln	Leu					
			265					270					275							
tcc	acg	cgt	ttg	acc	tac	ctt	gct	ggc	cgt	ggc	gct	ttt	gat	att	gaa	979				
Ser	Thr	Arg	Leu	Thr	Tyr	Leu	Ala	Gly	Arg	Gly	Ala	Phe	Asp	Ile	Glu					
		280					285					290								
gca	ttg	ggc	gaa	aag	ggc	gct	gaa	gac	ctc	att	cgc	acc	ggc	att	ttg	1027				
Ala	Leu	Gly	Glu	Lys	Gly	Ala	Glu	Asp	Leu	Ile	Arg	Thr	Gly	Ile	Leu					
	295					300					305									
ctt	gac	gag	tct	ggc	ctg	ttc	gac	ctc	aca	gag	gac	gat	ctg	ctg	agc	1075				
Leu	Asp	Glu	Ser	Gly	Leu	Phe	Asp	Leu	Thr	Glu	Asp	Asp	Leu	Leu	Ser					
310					315					320					325					
tcc	aat	gtc	tac	acc	acc	aac	gcc	ggc	aaa	gta	aat	gcc	agc	ggc	aag	1123				
Ser	Asn	Val	Tyr	Thr	Thr	Asn	Ala	Gly	Lys	Val	Asn	Ala	Ser	Gly	Lys					
				330					335					340						

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 Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln Thr Asp Leu Trp Arg
 345 350 355

 gtc ctc gtg gca tta tct atc agg cac gta ggc ccc acc gca gcg cgc 1219
 Val Leu Val Ala Leu Ser Ile Arg His Val Gly Pro Thr Ala Ala Arg
 360 365 370

 gcc ctt gca ggt cgc tac cac tcc atc cag gcg ctt atc gac gcc ccc 1267
 Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala Leu Ile Asp Ala Pro
 375 380 385

 ctc gag gaa ctc tcc gaa acc gat gga gta ggt acc atc att gcc caa 1315
 Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly Thr Ile Ile Ala Gln
 390 395 400 405

 tcc ttc aag gac tgg ttc gag gtt gat tgg cac aag gcc atc gtg gac 1363
 Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His Lys Ala Ile Val Asp
 410 415 420

 aag tgg gca gcc gct ggt gtg act atg gag gaa gaa gta ggg gag gtc 1411
 Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu Glu Val Gly Glu Val
 425 430 435

 gct gaa caa acc ctt gaa ggc cta acc atc gtg gtc acc gga ggg ttg 1459
 Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val Val Thr Gly Gly Leu
 440 445 450

 gaa ggc ttc acc aga gat tcg gtg aag gaa gcc atc atc tcc cgt ggc 1507
 Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala Ile Ile Ser Arg Gly
 455 460 465

 gga aaa gcc tct gga tct gtc tcg aag aaa act gac tac gtg gtg att 1555
 Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr Asp Tyr Val Val Ile
 470 475 480 485

 ggt gaa aac gca ggt tcc aag gcc acc aag gca gaa gaa cta ggg ctg 1603
 Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala Glu Glu Leu Gly Leu
 490 495 500

 cgc att ctg gat gag gca gga ttc gtc cgt ttg ctc aat acc ggc tca 1651
 Arg Ile Leu Asp Glu Ala Gly Phe Val Arg Leu Leu Asn Thr Gly Ser
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<211> 520

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

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Gly Gly Lys Pro Phe Ala Asn Pro Arg Asn Ala Ala Ala Gly Ser Leu
 35 40 45
 Arg Gln Lys Asn Ile Glu Asp Val Lys Lys Arg Arg Leu Arg Met Ile
 50 55 60
 Ser His Gly Ile Gly Phe Thr Glu Gly Phe Ser Pro Ala Ser Gln His
 65 70 75 80
 Asp Ala Tyr Leu Ala Leu Ala Ala Trp Gly Leu Pro Thr Ser Pro Tyr
 85 90 95
 Thr Glu Ala Val Thr Asp Pro Glu Asp Val Val Lys Lys Val Ser Tyr
 100 105 110
 Trp Ala Asp His Arg His Asp Ala Leu His Glu Met Asp Gly Leu Val
 115 120 125
 Ile Lys Val Asp Asp Ile Ala Ser Gln Arg Ala Leu Gly Ser Thr Ser
 130 135 140
 Arg Ala Pro Arg Trp Ala Ile Ala Tyr Lys Tyr Pro Pro Glu Glu Val
 145 150 155 160
 Thr Thr Lys Leu Leu Asp Ile Gln Val Gly Val Gly Arg Thr Gly Arg
 165 170 175
 Val Thr Pro Phe Ala Val Met Glu Pro Val Leu Val Ala Gly Ser Thr
 180 185 190
 Val Ser Met Ala Thr Leu His Asn Gln Ser Glu Val Lys Arg Lys Gly
 195 200 205
 Val Leu Ile Gly Asp Thr Val Val Ile Arg Lys Ala Gly Glu Val Ile
 210 215 220
 Pro Glu Val Leu Gly Pro Val Val Glu Leu Arg Asp Gly Thr Glu Arg
 225 230 235 240
 Glu Tyr Ile Phe Pro Thr Leu Cys Pro Glu Cys Gly Thr Arg Leu Ala
 245 250 255
 Pro Ala Lys Ala Asp Asp Val Asp Trp Arg Cys Pro Asn Met Gln Ser
 260 265 270
 Cys Pro Gly Gln Leu Ser Thr Arg Leu Thr Tyr Leu Ala Gly Arg Gly
 275 280 285
 Ala Phe Asp Ile Glu Ala Leu Gly Glu Lys Gly Ala Glu Asp Leu Ile
 290 295 300
 Arg Thr Gly Ile Leu Leu Asp Glu Ser Gly Leu Phe Asp Leu Thr Glu
 305 310 315 320
 Asp Asp Leu Leu Ser Ser Asn Val Tyr Thr Thr Asn Ala Gly Lys Val
 325 330 335
 Asn Ala Ser Gly Lys Lys Leu Leu Asp Asn Leu Gln Lys Ser Lys Gln
 340 345 350

Thr Asp Leu Trp Arg Val Leu Val Ala Leu Ser Ile Arg His Val Gly
 355 360 365
 Pro Thr Ala Ala Arg Ala Leu Ala Gly Arg Tyr His Ser Ile Gln Ala
 370 375 380
 Leu Ile Asp Ala Pro Leu Glu Glu Leu Ser Glu Thr Asp Gly Val Gly
 385 390 395 400
 Thr Ile Ile Ala Gln Ser Phe Lys Asp Trp Phe Glu Val Asp Trp His
 405 410 415
 Lys Ala Ile Val Asp Lys Trp Ala Ala Ala Gly Val Thr Met Glu Glu
 420 425 430
 Glu Val Gly Glu Val Ala Glu Gln Thr Leu Glu Gly Leu Thr Ile Val
 435 440 445
 Val Thr Gly Gly Leu Glu Gly Phe Thr Arg Asp Ser Val Lys Glu Ala
 450 455 460
 Ile Ile Ser Arg Gly Gly Lys Ala Ser Gly Ser Val Ser Lys Lys Thr
 465 470 475 480
 Asp Tyr Val Val Ile Gly Glu Asn Ala Gly Ser Lys Ala Thr Lys Ala
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 <222> (101)..(673)
 <223> RXS00213

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cgaatggccg tgtccaccct tagggttaga atcgggaacc gtg act gaa gat aat 115
 Val Thr Glu Asp Asn
 1 5

gct caa ctg cgt aga acg tgg aac gac tta gcc gag aag gtt cgt tat 163
 Ala Gln Leu Arg Arg Thr Trp Asn Asp Leu Ala Glu Lys Val Arg Tyr
 10 15 20

cac cga gat cgt tat tac aac gaa cag cca gag atc cct gat gct gat 211
 His Arg Asp Arg Tyr Tyr Asn Glu Gln Pro Glu Ile Pro Asp Ala Asp
 25 30 35

ttt gat gcg ctt ttt aag cag ctt cag cag ttg gaa gaa gac cac ccg 259
 Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu Glu Glu Asp His Pro

40	45	50	
gag ctc gcc gtc cct gat agc ccc acc atg gtt gtg ggc gct ccg gtg			307
Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val Val Gly Ala Pro Val			
55	60	65	
gca gag caa tca agc ttt gac aat gtt gag cac ttg gag cga atg ctc			355
Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His Leu Glu Arg Met Leu			
70	75	80	85
agc ttg gac aat gtt ttt gat gag cag gag ttg cgt gat tgg ttg ggc			403
Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu Arg Asp Trp Leu Gly			
90	95	100	
agg acg cca gcc aag cag tat ttg acg gag ttg aaa att gat ggc ttg			451
Arg Thr Pro Ala Lys Gln Tyr Leu Thr Glu Leu Lys Ile Asp Gly Leu			
105	110	115	
tcc atc gac ttg gtg tat cgc aat ggc cag tta gag cgt gcc gct act			499
Ser Ile Asp Leu Val Tyr Arg Asn Gly Gln Leu Glu Arg Ala Ala Thr			
120	125	130	
cgt ggt gat ggt cgc gtg ggc gag gac atc acg gcc aat gct cgc gtg			547
Arg Gly Asp Gly Arg Val Gly Glu Asp Ile Thr Ala Asn Ala Arg Val			
135	140	145	
atc gaa gat atc ccg cac cag ctt cag ggc act gat gaa tat cct gtg			595
Ile Glu Asp Ile Pro His Gln Leu Gln Gly Thr Asp Glu Tyr Pro Val			
150	155	160	165
cct gct gtg ctg gaa att cgc ggt gag gtg ttc atc act gtg gag gat			643
Pro Ala Val Leu Glu Ile Arg Gly Glu Val Phe Ile Thr Val Glu Asp			
170	175	180	
ttc cca gga ggt caa cgc gca gcg cat tgc tgc tgc tgc tgc tgc tgc			696
Phe Pro Gly Gly Gln Arg Ala Ala His Cys			
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<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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Ile Pro Asp Ala Asp Phe Asp Ala Leu Phe Lys Gln Leu Gln Gln Leu	
35	40

Glu Glu Asp His Pro Glu Leu Ala Val Pro Asp Ser Pro Thr Met Val	
50	55

Val Gly Ala Pro Val Ala Glu Gln Ser Ser Phe Asp Asn Val Glu His	
65	70

Leu Glu Arg Met Leu Ser Leu Asp Asn Val Phe Asp Glu Gln Glu Leu	
---	--

85					90					95					
Arg	Asp	Trp	Leu	Gly	Arg	Thr	Pro	Ala	Lys	Gln	Tyr	Leu	Thr	Glu	Leu
			100					105					110		
Lys	Ile	Asp	Gly	Leu	Ser	Ile	Asp	Leu	Val	Tyr	Arg	Asn	Gly	Gln	Leu
		115					120					125			
Glu	Arg	Ala	Ala	Thr	Arg	Gly	Asp	Gly	Arg	Val	Gly	Glu	Asp	Ile	Thr
	130					135					140				
Ala	Asn	Ala	Arg	Val	Ile	Glu	Asp	Ile	Pro	His	Gln	Leu	Gln	Gly	Thr
145						150					155				160
Asp	Glu	Tyr	Pro	Val	Pro	Ala	Val	Leu	Glu	Ile	Arg	Gly	Glu	Val	Phe
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Ile	Thr	Val	Glu	Asp	Phe	Pro	Gly	Gly	Gln	Arg	Ala	Ala	His	Cys	
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<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2077)

<223> RXS00724

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gcc	act	gag	ggc	gat	ctt	ggt	acc	atc	gtg	ggt	cag	gtc	gcc	ttt	gcc	163
Ala	Thr	Glu	Gly	Asp	Leu	Val	Thr	Ile	Val	Gly	Gln	Val	Ala	Phe	Ala	
				10					15					20		

aag	cag	tcc	tat	acc	cag	tcc	ggc	aag	atg	ctg	tac	aag	ggt	aca	gtc	211
Lys	Gln	Ser	Tyr	Thr	Gln	Ser	Gly	Lys	Met	Leu	Tyr	Lys	Val	Thr	Val	
			25					30					35			

ttg	act	gag	acg	gaa	cgc	atc	ggc	att	tcc	ttc	ttc	gga	gcc	aag	cac	259
Leu	Thr	Glu	Thr	Glu	Arg	Ile	Gly	Ile	Ser	Phe	Phe	Gly	Ala	Lys	His	
		40					45					50				

att	ccg	cgt	ctt	ctc	cca	gaa	ggc	act	cgt	gcg	ctt	ttt	acc	ggc	aag	307
Ile	Pro	Arg	Leu	Leu	Pro	Glu	Gly	Thr	Arg	Ala	Leu	Phe	Thr	Gly	Lys	
	55					60					65					

gtg	aag	ttt	ttt	cgc	aac	gaa	cct	cag	cta	tct	cat	cca	gag	ttc	att	355
Val	Lys	Phe	Phe	Arg	Asn	Glu	Pro	Gln	Leu	Ser	His	Pro	Glu	Phe	Ile	
	70				75				80						85	

gtg	atc	cca	gat	cct	gga	tca	ggc	cgc	cga	ctc	acc	gcc	act	ggc	ggt	403
Val	Ile	Pro	Asp	Pro	Gly	Ser	Gly	Arg	Arg	Leu	Thr	Ala	Thr	Gly	Gly	
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atg	aaa	tct	ctg	gct	gcc	tac	ggc	gat	gtg	gaa	gaa	gtg	gca	ctt	cgt	451
Met	Lys	Ser	Leu	Ala	Ala	Tyr	Gly	Asp	Val	Glu	Glu	Val	Ala	Leu	Arg	
			105					110					115			
ttg	gtg	gat	cgc	gaa	tac	atc	ccg	atc	tat	gcc	ggc	acc	gcc	acc	atg	499
Leu	Val	Asp	Arg	Glu	Tyr	Ile	Pro	Ile	Tyr	Ala	Gly	Thr	Ala	Thr	Met	
		120					125					130				
act	acc	tgg	cgg	atc	atg	gct	gca	gtg	caa	cgg	gta	ctg	gaa	acc	atg	547
Thr	Thr	Trp	Arg	Ile	Met	Ala	Ala	Val	Gln	Arg	Val	Leu	Glu	Thr	Met	
		135				140					145					
ccg	gtg	atc	aaa	gaa	cca	ctg	agc	gtg	gtg	ccc	gaa	ggc	atg	ccc	agt	595
Pro	Val	Ile	Lys	Glu	Pro	Leu	Ser	Val	Val	Pro	Glu	Gly	Met	Pro	Ser	
150					155					160					165	
ttc	gac	gag	gcc	atc	cgc	ggc	att	cac	gat	cca	ggc	cat	gaa	tct	ccc	643
Phe	Asp	Glu	Ala	Ile	Arg	Gly	Ile	His	Asp	Pro	Gly	His	Glu	Ser	Pro	
			170						175					180		
agc	acg	ttt	atc	aac	cgt	ctg	aaa	tac	aac	gaa	gca	cta	tcg	ctg	gcc	691
Ser	Thr	Phe	Ile	Asn	Arg	Leu	Lys	Tyr	Asn	Glu	Ala	Leu	Ser	Leu	Ala	
			185					190					195			
acg	gtg	atg	gcg	atc	cgg	cgt	gcc	gat	acc	aag	aac	cgc	aaa	gca	cca	739
Thr	Val	Met	Ala	Ile	Arg	Arg	Ala	Asp	Thr	Lys	Asn	Arg	Lys	Ala	Pro	
		200					205					210				
ccc	atg	ccg	cgc	gca	ctc	aaa	ggg	cat	cag	cac	atg	ctc	atc	gat	gca	787
Pro	Met	Pro	Arg	Ala	Leu	Lys	Gly	His	Gln	His	Met	Leu	Ile	Asp	Ala	
	215					220					225					
ctc	aac	ttt	cag	ctc	aca	gtg	gga	cag	aag	caa	gtg	atc	cgt	gag	atc	835
Leu	Asn	Phe	Gln	Leu	Thr	Val	Gly	Gln	Lys	Gln	Val	Ile	Arg	Glu	Ile	
230					235					240					245	
agc	gcg	gac	att	gaa	caa	cgc	gtt	ccc	atg	tct	cgt	ctg	ctc	caa	ggc	883
Ser	Ala	Asp	Ile	Glu	Gln	Arg	Val	Pro	Met	Ser	Arg	Leu	Leu	Gln	Gly	
				250					255					260		
gag	gtt	ggt	tcg	ggt	aaa	acc	atc	gtg	tcg	ttg	atc	gcg	atg	ctg	cag	931
Glu	Val	Gly	Ser	Gly	Lys	Thr	Ile	Val	Ser	Leu	Ile	Ala	Met	Leu	Gln	
			265					270					275			
gca	att	gat	tcc	ggt	agg	cag	tgc	gcc	atg	ctc	gcc	ccg	acg	gaa	gtg	979
Ala	Ile	Asp	Ser	Gly	Arg	Gln	Cys	Ala	Met	Leu	Ala	Pro	Thr	Glu	Val	
		280					285					290				
ttg	gcc	acc	cag	cat	gcc	cgc	agc	ctg	agc	aaa	act	ctc	gac	gac	gca	1027
Leu	Ala	Thr	Gln	His	Ala	Arg	Ser	Leu	Ser	Lys	Thr	Leu	Asp	Asp	Ala	
	295					300					305					
ggc	ctt	gat	atc	aat	gtt	gtg	ctc	ttg	act	ggc	tcg	atg	ccc	acg	gga	1075
Gly	Leu	Asp	Ile	Asn	Val	Val	Leu	Leu	Thr	Gly	Ser	Met	Pro	Thr	Gly	
310					315					320					325	
gcc	aag	aag	gag	gct	ctg	ctg	gaa	atc	atc	tcc	ggt	gac	gca	gac	att	1123
Ala	Lys	Lys	Glu	Ala	Leu	Leu	Glu	Ile	Ile	Ser	Gly	Asp	Ala	Asp	Ile	
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Val Val Gly Thr His Ala Leu Ile Gln Asp Thr Val Glu Phe Phe Asp	
345 350 355	
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Leu Gly Leu Val Val Val Asp Glu Gln His Arg Phe Gly Val Glu Gln	
360 365 370	
cgc gat caa ctg cgg acc aag ggc agg gaa ggc ctg acc ccg cac cta	1267
Arg Asp Gln Leu Arg Thr Lys Gly Arg Glu Gly Leu Thr Pro His Leu	
375 380 385	
ttg gtt atg act gcg acc cca att ccg cgc acc atc gcc atg acg gtg	1315
Leu Val Met Thr Ala Thr Pro Ile Pro Arg Thr Ile Ala Met Thr Val	
390 395 400 405	
ttc ggc gac ttg gcg gtg tcc acg ttg cgt gaa ctt cca ggc ggg cgc	1363
Phe Gly Asp Leu Ala Val Ser Thr Leu Arg Glu Leu Pro Gly Gly Arg	
410 415 420	
cgg ccg att caa acc tcg gtg ata ccc gat cac aaa cct ggc tgg gtt	1411
Arg Pro Ile Gln Thr Ser Val Ile Pro Asp His Lys Pro Gly Trp Val	
425 430 435	
aaa cgc ggt tgg gaa cgc atc ggt gag gaa gtc ctc gcc gga cgc caa	1459
Lys Arg Gly Trp Glu Arg Ile Gly Glu Glu Val Leu Ala Gly Arg Gln	
440 445 450	
gcc tat gtg gtg tgt ccg cgc att gaa ggc gaa ggc gcc gtg ctg gaa	1507
Ala Tyr Val Val Cys Pro Arg Ile Glu Gly Glu Gly Gly Val Leu Glu	
455 460 465	
atc cac gcc tat ctt tcc gaa cag gta tat cca gga ttg aat gtt gga	1555
Ile His Ala Tyr Leu Ser Glu Gln Val Tyr Pro Gly Leu Asn Val Gly	
470 475 480 485	
atg ctg cac ggt cgc atg gac acg gat ctc aaa gat tcg gtc atg cag	1603
Met Leu His Gly Arg Met Asp Thr Asp Leu Lys Asp Ser Val Met Gln	
490 495 500	
gaa ttc gcc caa ggt gag atc gat att ttg gtc gcc acc acg gtc att	1651
Glu Phe Ala Gln Gly Glu Ile Asp Ile Leu Val Ala Thr Thr Val Ile	
505 510 515	
gag gtc ggt att gac gtt gcc aac gcc acc gtc atg ctc atc cgc gag	1699
Glu Val Gly Ile Asp Val Ala Asn Ala Thr Val Met Leu Ile Arg Glu	
520 525 530	
gcg gaa cgc ttc ggc gtt tcc cag atc cac cag ctg cgc ggc cgt gtt	1747
Ala Glu Arg Phe Gly Val Ser Gln Ile His Gln Leu Arg Gly Arg Val	
535 540 545	
ggc cgt ggg cag cac gat tcc ctc tgc ctg ctg cac acc acc ttc gac	1795
Gly Arg Gly Gln His Asp Ser Leu Cys Leu Leu His Thr Thr Phe Asp	
550 555 560 565	
gag gac tcc cca caa ggc caa cgc ctc gcc gca att tcc acc aca acc	1843
Glu Asp Ser Pro Gln Gly Gln Arg Leu Ala Ala Ile Ser Thr Thr Thr	
570 575 580	
gac ggt ttt caa ctc tct gaa ctt gat ttg cag gta cgc caa gaa ggc	1891

Asp Gly Phe Gln Leu Ser Glu Leu Asp Leu Gln Val Arg Gln Glu Gly
 585 590 595
 gac gtg ttg ggc acc cgc cag tcc ggc agc gac acc aaa ctc cgt cac 1939
 Asp Val Leu Gly Thr Arg Gln Ser Gly Ser Asp Thr Lys Leu Arg His
 600 605 610
 ctc tcg ttt atc agc gac caa aaa atc atc gag cgt gcg ctt atc gac 1987
 Leu Ser Phe Ile Ser Asp Gln Lys Ile Ile Glu Arg Ala Leu Ile Asp
 615 620 625
 gcc acc gag ctg gtt gcc gcc agc cgt tcc agg gcg ctt gag ctg gtc 2035
 Ala Thr Glu Leu Val Ala Ala Ser Arg Ser Arg Ala Leu Glu Leu Val
 630 635 640 645
 agc gac atc gca atg atc aac cag gaa tac ctg gaa aag agc 2077
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 154
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 20 25 30
 Tyr Lys Val Thr Val Leu Thr Glu Thr Glu Arg Ile Gly Ile Ser Phe
 35 40 45
 Phe Gly Ala Lys His Ile Pro Arg Leu Leu Pro Glu Gly Thr Arg Ala
 50 55 60
 Leu Phe Thr Gly Lys Val Lys Phe Phe Arg Asn Glu Pro Gln Leu Ser
 65 70 75 80
 His Pro Glu Phe Ile Val Ile Pro Asp Pro Gly Ser Gly Arg Arg Leu
 85 90 95
 Thr Ala Thr Gly Gly Met Lys Ser Leu Ala Ala Tyr Gly Asp Val Glu
 100 105 110
 Glu Val Ala Leu Arg Leu Val Asp Arg Glu Tyr Ile Pro Ile Tyr Ala
 115 120 125
 Gly Thr Ala Thr Met Thr Thr Trp Arg Ile Met Ala Ala Val Gln Arg
 130 135 140
 Val Leu Glu Thr Met Pro Val Ile Lys Glu Pro Leu Ser Val Val Pro
 145 150 155 160
 Glu Gly Met Pro Ser Phe Asp Glu Ala Ile Arg Gly Ile His Asp Pro
 165 170 175

Gly	His	Glu	Ser	Pro	Ser	Thr	Phe	Ile	Asn	Arg	Leu	Lys	Tyr	Asn	Glu		
			180					185					190				
Ala	Leu	Ser	Leu	Ala	Thr	Val	Met	Ala	Ile	Arg	Arg	Ala	Asp	Thr	Lys		
		195					200					205					
Asn	Arg	Lys	Ala	Pro	Pro	Met	Pro	Arg	Ala	Leu	Lys	Gly	His	Gln	His		
	210					215					220						
Met	Leu	Ile	Asp	Ala	Leu	Asn	Phe	Gln	Leu	Thr	Val	Gly	Gln	Lys	Gln		
225					230					235					240		
Val	Ile	Arg	Glu	Ile	Ser	Ala	Asp	Ile	Glu	Gln	Arg	Val	Pro	Met	Ser		
				245					250					255			
Arg	Leu	Leu	Gln	Gly	Glu	Val	Gly	Ser	Gly	Lys	Thr	Ile	Val	Ser	Leu		
			260					265					270				
Ile	Ala	Met	Leu	Gln	Ala	Ile	Asp	Ser	Gly	Arg	Gln	Cys	Ala	Met	Leu		
		275					280					285					
Ala	Pro	Thr	Glu	Val	Leu	Ala	Thr	Gln	His	Ala	Arg	Ser	Leu	Ser	Lys		
	290					295					300						
Thr	Leu	Asp	Asp	Ala	Gly	Leu	Asp	Ile	Asn	Val	Val	Leu	Leu	Thr	Gly		
305					310					315					320		
Ser	Met	Pro	Thr	Gly	Ala	Lys	Lys	Glu	Ala	Leu	Leu	Glu	Ile	Ile	Ser		
				325					330					335			
Gly	Asp	Ala	Asp	Ile	Val	Val	Gly	Thr	His	Ala	Leu	Ile	Gln	Asp	Thr		
			340					345					350				
Val	Glu	Phe	Phe	Asp	Leu	Gly	Leu	Val	Val	Val	Asp	Glu	Gln	His	Arg		
		355					360					365					
Phe	Gly	Val	Glu	Gln	Arg	Asp	Gln	Leu	Arg	Thr	Lys	Gly	Arg	Glu	Gly		
	370					375					380						
Leu	Thr	Pro	His	Leu	Leu	Val	Met	Thr	Ala	Thr	Pro	Ile	Pro	Arg	Thr		
385					390					395					400		
Ile	Ala	Met	Thr	Val	Phe	Gly	Asp	Leu	Ala	Val	Ser	Thr	Leu	Arg	Glu		
				405					410					415			
Leu	Pro	Gly	Gly	Arg	Arg	Pro	Ile	Gln	Thr	Ser	Val	Ile	Pro	Asp	His		
			420					425					430				
Lys	Pro	Gly	Trp	Val	Lys	Arg	Gly	Trp	Glu	Arg	Ile	Gly	Glu	Glu	Val		
		435					440					445					
Leu	Ala	Gly	Arg	Gln	Ala	Tyr	Val	Val	Cys	Pro	Arg	Ile	Glu	Gly	Glu		
	450					455					460						
Gly	Gly	Val	Leu	Glu	Ile	His	Ala	Tyr	Leu	Ser	Glu	Gln	Val	Tyr	Pro		
465					470					475					480		
Gly	Leu	Asn	Val	Gly	Met	Leu	His	Gly	Arg	Met	Asp	Thr	Asp	Leu	Lys		
				485					490					495			
Asp	Ser	Val	Met	Gln	Glu	Phe	Ala	Gln	Gly	Glu	Ile	Asp	Ile	Leu	Val		

500					505					510					
Ala	Thr	Thr	Val	Ile	Glu	Val	Gly	Ile	Asp	Val	Ala	Asn	Ala	Thr	Val
		515					520					525			
Met	Leu	Ile	Arg	Glu	Ala	Glu	Arg	Phe	Gly	Val	Ser	Gln	Ile	His	Gln
	530					535					540				
Leu	Arg	Gly	Arg	Val	Gly	Arg	Gly	Gln	His	Asp	Ser	Leu	Cys	Leu	Leu
545					550					555					560
His	Thr	Thr	Phe	Asp	Glu	Asp	Ser	Pro	Gln	Gly	Gln	Arg	Leu	Ala	Ala
			565						570					575	
Ile	Ser	Thr	Thr	Thr	Asp	Gly	Phe	Gln	Leu	Ser	Glu	Leu	Asp	Leu	Gln
			580					585					590		
Val	Arg	Gln	Glu	Gly	Asp	Val	Leu	Gly	Thr	Arg	Gln	Ser	Gly	Ser	Asp
		595					600					605			
Thr	Lys	Leu	Arg	His	Leu	Ser	Phe	Ile	Ser	Asp	Gln	Lys	Ile	Ile	Glu
	610					615					620				
Arg	Ala	Leu	Ile	Asp	Ala	Thr	Glu	Leu	Val	Ala	Ala	Ser	Arg	Ser	Arg
625					630					635					640
Ala	Leu	Glu	Leu	Val	Ser	Asp	Ile	Ala	Met	Ile	Asn	Gln	Glu	Tyr	Leu
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Glu Lys Ser															

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<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXS00823

<400> 155

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								Met	Gly	Ser	Ile	Thr		
								1				5		

ccg	cag	aag	cgg	cct	cgc	gtg	ggg	tct	cac	atc	gcg	aac	aag	ggt	caa	163
Pro	Gln	Lys	Arg	Pro	Arg	Val	Gly	Ser	His	Ile	Ala	Asn	Lys	Gly	Gln	
				10					15					20		

gag	act	gat	atc	ggg	cga	aaa	cgc	cga	gct	cga	cgc	atc	aat	cgc	aca	211
Glu	Thr	Asp	Ile	Gly	Arg	Lys	Arg	Arg	Ala	Arg	Arg	Ile	Asn	Arg	Thr	
			25					30					35			

ctc	acc	gtg	gca	tat	ccg	gat	gcg	cac	tgc	gaa	tta	gat	ttc	acc	aat	259
Leu	Thr	Val	Ala	Tyr	Pro	Asp	Ala	His	Cys	Glu	Leu	Asp	Phe	Thr	Asn	
		40					45					50				

ccg cta gaa ctc acg gtc gcc acc att ttg tcc gcc cag tgc acg gac	307
Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser Ala Gln Cys Thr Asp	
55 60 65	
ggt cgc gtg aac cag gtg acg ccc gcg ttg ttc aag cgc tat ccg acg	355
Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe Lys Arg Tyr Pro Thr	
70 75 80 85	
gcc aca gat tac gcc aac gcc gat cgc acg gaa ttg gag gag ttc atc	403
Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu Leu Glu Glu Phe Ile	
90 95 100	
cgt ccg aca ggc ttt tac cgc aac aag gcc act tct tta atc ggc ctg	451
Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr Ser Leu Ile Gly Leu	
105 110 115	
ggt gag gca cta att tcg ctt cac gac ggc cag gtc ccc ggt acc ctt	499
Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln Val Pro Gly Thr Leu	
120 125 130	
gag cag cta gtt gag ctg ccg ggg gtc ggg cgg aaa acc gcc aac gtg	547
Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg Lys Thr Ala Asn Val	
135 140 145	
gtg ctg gga aat gct ttc ggt gtt ccg gga atc acg gtg gat aca cac	595
Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile Thr Val Asp Thr His	
150 155 160 165	
ttt ggc agg ttg gtg cgt cgc ctg aag ctc act gat gaa gaa gat ccc	643
Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr Asp Glu Glu Asp Pro	
170 175 180	
gtc aag gtg gaa aaa gtg atg aac gaa ctc atc gaa aag cct gag tgg	691
Val Lys Val Glu Lys Val Met Asn Glu Leu Ile Glu Lys Pro Glu Trp	
185 190 195	
acc atg ttt tca cat agg ctg atc ttc cac gga cgt agg ata tgt cat	739
Thr Met Phe Ser His Arg Leu Ile Phe His Gly Arg Arg Ile Cys His	
200 205 210	
agt cga cgc gcc gcc tgt gga gcc tgc atg ctg gca gct gat tgc cca	787
Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu Ala Ala Asp Cys Pro	
215 220 225	
tcc ttt ggt ttg gag ggg ccg tca gat cca ttt gag gcg caa aaa ctc	835
Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe Glu Ala Gln Lys Leu	
230 235 240 245	
att aaa agt gat gat agg gag cac ctg ctg aaa atg gca gga atg	880
Ile Lys Ser Asp Arg Glu His Leu Leu Lys Met Ala Gly Met	
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<210> 156

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

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 20 25 30

Arg Ile Asn Arg Thr Leu Thr Val Ala Tyr Pro Asp Ala His Cys Glu
 35 40 45

Leu Asp Phe Thr Asn Pro Leu Glu Leu Thr Val Ala Thr Ile Leu Ser
 50 55 60

Ala Gln Cys Thr Asp Val Arg Val Asn Gln Val Thr Pro Ala Leu Phe
 65 70 75 80

Lys Arg Tyr Pro Thr Ala Thr Asp Tyr Ala Asn Ala Asp Arg Thr Glu
 85 90 95

Leu Glu Glu Phe Ile Arg Pro Thr Gly Phe Tyr Arg Asn Lys Ala Thr
 100 105 110

Ser Leu Ile Gly Leu Gly Glu Ala Leu Ile Ser Leu His Asp Gly Gln
 115 120 125

Val Pro Gly Thr Leu Glu Gln Leu Val Glu Leu Pro Gly Val Gly Arg
 130 135 140

Lys Thr Ala Asn Val Val Leu Gly Asn Ala Phe Gly Val Pro Gly Ile
 145 150 155 160

Thr Val Asp Thr His Phe Gly Arg Leu Val Arg Arg Leu Lys Leu Thr
 165 170 175

Asp Glu Glu Asp Pro Val Lys Val Glu Lys Val Met Asn Glu Leu Ile
 180 185 190

Glu Lys Pro Glu Trp Thr Met Phe Ser His Arg Leu Ile Phe His Gly
 195 200 205

Arg Arg Ile Cys His Ser Arg Arg Ala Ala Cys Gly Ala Cys Met Leu
 210 215 220

Ala Ala Asp Cys Pro Ser Phe Gly Leu Glu Gly Pro Ser Asp Pro Phe
 225 230 235 240

Glu Ala Gln Lys Leu Ile Lys Ser Asp Asp Arg Glu His Leu Leu Lys
 245 250 255

Met Ala Gly Met
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<210> 157

<211> 912

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(889)

<400> 157

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Met Arg Ile Val Asn 5															
tgg aac gtc aac tct gct cgc act cgt gtg gac cgg atg gtc gat ttt 163															
Trp Asn Val Asn Ser Ala Arg Thr Arg Val Asp Arg Met Val Asp Phe 10 15 20															
ttg ctt cgc cat gat gtt gat gta tta gcg gtg cag gaa acc aag tgt 211															
Leu Leu Arg His Asp Val Asp Val Leu Ala Val Gln Glu Thr Lys Cys 25 30 35															
aaa gat gag caa ttt ccc acc gag cgt ttc acc gaa atc ggc tat gag 259															
Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr Glu Ile Gly Tyr Glu 40 45 50															
gta gcc cat ttc ggc ctt aac cag tgg aat ggt gtc gcc att att tcc 307															
Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly Val Ala Ile Ile Ser 55 60 65															
cgc gtt ggc att gaa aat gtg gaa acc cac ttc cct gcc caa ccg gga 355															
Arg Val Gly Ile Glu Asn Val Glu Thr His Phe Pro Ala Gln Pro Gly 70 75 80 85															
ttc aac aaa gac atc acc aag gaa caa tcc atc gaa gcc cgc gcc atc 403															
Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile Glu Ala Arg Ala Ile 90 95 100															
ggc gcc cgc tgc ggt ggt gtc cag gtg tgg agc ctc tat gtt ccc aac 451															
Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser Leu Tyr Val Pro Asn 105 110 115															
ggc cgc gaa atc gca gat cct cac tac gac tac aaa ctg cgc tgg cta 499															
Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr Lys Leu Arg Trp Leu 120 125 130															
ttc tcc ctg cgc aac tac gtg atc gac acc ttg gaa tac cgc ccc gag 547															
Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu Glu Tyr Arg Pro Glu 135 140 145															
gaa aaa ctg gtg ttg ctc ggc gac ttc aac atc gcg ccc aca gac atc 595															
Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile Ala Pro Thr Asp Ile 150 155 160 165															
gac gtc tgg gac atc gca gcc ttc gaa gga aaa acc cac gtc acc gaa 643															
Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys Thr His Val Thr Glu 170 175 180															
cca gaa cgt gca gct ttc gac ggc ctc atc gaa gcc gga ctc aaa gaa 691															
Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu Ala Gly Leu Lys Glu 185 190 195															
acc acc ccc gga cct ggt acc tac acc tac tgg gat tac aaa ggc gca 739															
Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp Asp Tyr Lys Gly Ala 200 205 210															

cgc ttc ctc aaa ggc gaa ggc atg cgc atc gat ttc cag ctc gca tcc 787
 Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp Phe Gln Leu Ala Ser
 215 220 225

 ccg gcc ctt gct gca acc gcg ggt gaa acc ttt gtg gac gtt gaa gaa 835
 Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe Val Asp Val Glu Glu
 230 235 240 245

 cgc agc gga acc ggc gcc tct gac cac gca cca gtc atc gtt gat tac 883
 Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro Val Ile Val Asp Tyr
 250 255 260

 aag gtg taactgcgta tgatctttca gat 912
 Lys Val

<210> 158
 <211> 263
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 158
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 Arg Met Val Asp Phe Leu Leu Arg His Asp Val Asp Val Leu Ala Val
 20 25 30

 Gln Glu Thr Lys Cys Lys Asp Glu Gln Phe Pro Thr Glu Arg Phe Thr
 35 40 45

 Glu Ile Gly Tyr Glu Val Ala His Phe Gly Leu Asn Gln Trp Asn Gly
 50 55 60

 Val Ala Ile Ile Ser Arg Val Gly Ile Glu Asn Val Glu Thr His Phe
 65 70 75 80

 Pro Ala Gln Pro Gly Phe Asn Lys Asp Ile Thr Lys Glu Gln Ser Ile
 85 90 95

 Glu Ala Arg Ala Ile Gly Ala Arg Cys Gly Gly Val Gln Val Trp Ser
 100 105 110

 Leu Tyr Val Pro Asn Gly Arg Glu Ile Ala Asp Pro His Tyr Asp Tyr
 115 120 125

 Lys Leu Arg Trp Leu Phe Ser Leu Arg Asn Tyr Val Ile Asp Thr Leu
 130 135 140

 Glu Tyr Arg Pro Glu Glu Lys Leu Val Leu Leu Gly Asp Phe Asn Ile
 145 150 155 160

 Ala Pro Thr Asp Ile Asp Val Trp Asp Ile Ala Ala Phe Glu Gly Lys
 165 170 175

 Thr His Val Thr Glu Pro Glu Arg Ala Ala Phe Asp Gly Leu Ile Glu
 180 185 190

 Ala Gly Leu Lys Glu Thr Thr Pro Gly Pro Gly Thr Tyr Thr Tyr Trp
 195 200 205

Asp Tyr Lys Gly Ala Arg Phe Leu Lys Gly Glu Gly Met Arg Ile Asp
 210 215 220
 Phe Gln Leu Ala Ser Pro Ala Leu Ala Ala Thr Ala Gly Glu Thr Phe
 225 230 235 240
 Val Asp Val Glu Glu Arg Ser Gly Thr Gly Ala Ser Asp His Ala Pro
 245 250 255
 Val Ile Val Asp Tyr Lys Val
 260

<210> 159
 <211> 849
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(826)
 <223> RXS01066

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 Met Arg Arg Asp Ser
 1 5
 ttt cgg gac cgc gcg cta gta gtc aaa act tat gat ttt ggc gaa gcc 163
 Phe Arg Asp Arg Ala Leu Val Val Lys Thr Tyr Asp Phe Gly Glu Ala
 10 15 20
 gac cgc att att gtg ctg ctc acc cga gac cac ggc atc gtg cgc gga 211
 Asp Arg Ile Ile Val Leu Leu Thr Arg Asp His Gly Ile Val Arg Gly
 25 30 35
 gtt gcc aaa gga gta cgc cga tcc aaa tcc cgg ttt ggg tca agg ctg 259
 Val Ala Lys Gly Val Arg Arg Ser Lys Ser Arg Phe Gly Ser Arg Leu
 40 45 50
 cag ctt ttt gtg gaa ctc gac gtg cag ctc tac cca ggt aga aaa ctg 307
 Gln Leu Phe Val Glu Leu Asp Val Gln Leu Tyr Pro Gly Arg Lys Leu
 55 60 65
 tcc acc atc tct ggc gcg gac acc gtc ggc tac tac gca tca ggc atc 355
 Ser Thr Ile Ser Gly Ala Asp Thr Val Gly Tyr Tyr Ala Ser Gly Ile
 70 75 80 85
 atc gag gac ttc act cgg tat tcc tgt gcg tcc gcc atc ctg gaa atc 403
 Ile Glu Asp Phe Thr Arg Tyr Ser Cys Ala Ser Ala Ile Leu Glu Ile
 90 95 100
 gcc acc cac atc gca gga ctg gaa aac gat ccg cac ctg ttt gaa gaa 451
 Ala Thr His Ile Ala Gly Leu Glu Asn Asp Pro His Leu Phe Glu Glu
 105 110 115
 acc acc cgg gcg ttg aaa aac att cag gac tcc cca gaa ccc atc ctc 499
 Thr Thr Arg Ala Leu Lys Asn Ile Gln Asp Ser Pro Glu Pro Ile Leu

120	125	130	
aac cta gac gag ttc atg ctc cgc gcc atg aac cac gcc ggc tgg gca			547
Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn His Ala Gly Trp Ala			
135	140	145	
cca agc ctt ttc gac tgc gca gcc tgc ggc cga cca gga cct cac aac			595
Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg Pro Gly Pro His Asn			
150	155	160	165
gca ttc cac cca ggc gtc ggc ggg gca gtg tgc ctg tac tgc cga ccg			643
Ala Phe His Pro Gly Val Gly Gly Ala Val Cys Leu Tyr Cys Arg Pro			
	170	175	180
ccg gga agc gcc gaa gtc cca cca gaa gca cta cac atg atg tgg ttg			691
Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu His Met Met Trp Leu			
	185	190	195
gtc gcc aac ggc caa gca gcc cgc att ccc cgg gaa cac cca gag cag			739
Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg Glu His Pro Glu Gln			
	200	205	210
caa acc acc att cac caa ctg aca acc gcg cat ctg cag tgg cat att			787
Gln Thr Thr Ile His Gln Leu Thr Thr Ala His Leu Gln Trp His Ile			
	215	220	225
gaa aga aag ctg ccc acg ctg gcg gtg ctg gat cag gcc tagtgcttag			836
Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp Gln Ala			
230	235	240	
gcttaggcgt ccg			849

<210> 160

<211> 242

<212> PRT

<213> Corynebacterium glutamicum

<400> 160

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Asp	Phe	Gly	Glu	Ala	Asp	Arg	Ile	Ile	Val	Leu	Leu	Thr	Arg	Asp	His
			20					25					30		

Gly	Ile	Val	Arg	Gly	Val	Ala	Lys	Gly	Val	Arg	Arg	Ser	Lys	Ser	Arg
		35					40					45			

Phe	Gly	Ser	Arg	Leu	Gln	Leu	Phe	Val	Glu	Leu	Asp	Val	Gln	Leu	Tyr
	50					55					60				

Pro	Gly	Arg	Lys	Leu	Ser	Thr	Ile	Ser	Gly	Ala	Asp	Thr	Val	Gly	Tyr
65					70					75					80

Tyr	Ala	Ser	Gly	Ile	Ile	Glu	Asp	Phe	Thr	Arg	Tyr	Ser	Cys	Ala	Ser
				85					90					95	

Ala	Ile	Leu	Glu	Ile	Ala	Thr	His	Ile	Ala	Gly	Leu	Glu	Asn	Asp	Pro
		100						105					110		

His	Leu	Phe	Glu	Glu	Thr	Thr	Arg	Ala	Leu	Lys	Asn	Ile	Gln	Asp	Ser
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Pro Glu Pro Ile Leu Asn Leu Asp Glu Phe Met Leu Arg Ala Met Asn 130 135 140		
His Ala Gly Trp Ala Pro Ser Leu Phe Asp Cys Ala Ala Cys Gly Arg 145 150 155 160		
Pro Gly Pro His Asn Ala Phe His Pro Gly Val Gly Gly Ala Val Cys 165 170 175		
Leu Tyr Cys Arg Pro Pro Gly Ser Ala Glu Val Pro Pro Glu Ala Leu 180 185 190		
His Met Met Trp Leu Val Ala Asn Gly Gln Ala Ala Arg Ile Pro Arg 195 200 205		
Glu His Pro Glu Gln Gln Thr Thr Ile His Gln Leu Thr Thr Ala His 210 215 220		
Leu Gln Trp His Ile Glu Arg Lys Leu Pro Thr Leu Ala Val Leu Asp 225 230 235 240		
Gln Ala		

<210> 161
 <211> 1740
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1717)
 <223> RXS02145

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 Met Ser Leu Ala Thr
 1 5
 gtg gga aac aat ctt gat tcc cgt tac acc atg gcg tcg ggt atc cgt 163
 Val Gly Asn Asn Leu Asp Ser Arg Tyr Thr Met Ala Ser Gly Ile Arg
 10 15 20
 cgc cag atc aac aag gtc ttc cca act cac tgg tcc ttc atg ctc ggc 211
 Arg Gln Ile Asn Lys Val Phe Pro Thr His Trp Ser Phe Met Leu Gly
 25 30 35
 gag att gcg ctt tac agc ttc atc gtc ttg ctg ctg act ggt gtc tac 259
 Glu Ile Ala Leu Tyr Ser Phe Ile Val Leu Leu Leu Thr Gly Val Tyr
 40 45 50
 ctg acc ctg ttc ttc gac cca tca atc acc aag gtc att tat gac ggc 307
 Leu Thr Leu Phe Phe Asp Pro Ser Ile Thr Lys Val Ile Tyr Asp Gly
 55 60 65
 ggc tac ctc cca ctg aac ggt gtg gag atg tcc cgt gca tac gca act 355

Gly 70	Tyr	Leu	Pro	Leu	Asn 75	Gly	Val	Glu	Met	Ser 80	Arg	Ala	Tyr	Ala	Thr 85	
gcg	ttg	gat	att	tcc	ttc	gag	gtt	cgc	ggt	ggt	ctg	ttc	atc	cgc	cag	403
Ala	Leu	Asp	Ile	Ser 90	Phe	Glu	Val	Arg	Gly 95	Gly	Leu	Phe	Ile	Arg	Gln 100	
atg	cac	cac	tgg	gca	gcc	ctg	ctg	ttc	gtt	gta	tcc	atg	ctg	gtt	cac	451
Met	His	His	Trp 105	Ala	Ala	Leu	Leu	Phe	Val 110	Val	Ser	Met	Leu	Val	His 115	
atg	ctc	cgt	att	ttc	ttc	acc	ggt	gcg	ttc	cgt	cgc	cca	cgt	gaa	gca	499
Met	Leu	Arg 120	Ile	Phe	Phe	Thr	Gly 125	Ala	Phe	Arg	Arg	Pro 130	Arg	Glu	Ala	
aac	tgg	atc	atc	ggt	gtt	gtt	ctg	atc	atc	ctg	ggt	atg	gct	gaa	ggc	547
Asn	Trp 135	Ile	Ile	Gly	Val	Val	Leu 140	Ile	Ile	Leu	Gly 145	Met	Ala	Glu	Gly	
ttc	atg	ggt	tac	tcc	ctg	cct	gat	gac	ctg	ctc	tct	ggt	gtt	ggt	ctt	595
Phe	Met	Gly	Tyr	Ser	Leu 155	Pro	Asp	Asp	Leu	Leu	Ser	Gly	Val	Gly	Leu 165	
cga	atc	atg	tcc	gcc	atc	atc	gtt	ggt	ctt	ccg	atc	ata	ggt	acc	tgg	643
Arg	Ile	Met	Ser 170	Ala	Ile	Ile	Val	Gly	Leu 175	Pro	Ile	Ile	Gly	Thr	Trp 180	
atg	cac	tgg	ctg	atc	ttc	ggt	gga	gac	ttc	cca	tcc	gat	ctg	atg	ctg	691
Met	His	Trp 185	Leu	Ile	Phe	Gly	Gly	Asp	Phe 190	Pro	Ser	Asp	Leu	Met	Leu 195	
gac	cgc	ttc	tac	atc	gca	cac	gtt	cta	atc	atc	cca	gct	atc	ctg	ctt	739
Asp	Arg	Phe 200	Tyr	Ile	Ala	His	Val 205	Leu	Ile	Ile	Pro	Ala	Ile	Leu	Leu 210	
ggc	ttg	atc	gca	gct	cac	ctg	gca	ctt	gtt	tgg	tac	cag	aag	cac	acc	787
Gly	Leu	Ile 215	Ala	Ala	His	Leu 220	Ala	Leu	Val	Trp	Tyr	Gln	Lys	His	Thr 225	
cag	ttc	cca	ggc	gct	ggc	cgc	act	gag	aac	aac	gtg	atc	ggt	atc	cga	835
Gln	Phe	Pro	Gly	Ala	Gly 235	Arg	Thr	Glu	Asn 240	Asn	Val	Ile	Gly	Ile	Arg 245	
atc	atg	cct	ctg	ttc	gca	gtt	aag	gct	gtt	gct	ttc	ggc	ctc	atc	gtc	883
Ile	Met	Pro	Leu	Phe 250	Ala	Val	Lys	Ala	Val 255	Ala	Phe	Gly	Leu	Ile	Val 260	
ttc	ggt	ttc	ctc	gca	ctg	ctt	gct	ggt	gtc	acc	acc	att	aac	gca	att	931
Phe	Gly	Phe	Leu	Ala	Leu	Leu	Ala	Gly 270	Val	Thr	Thr	Ile	Asn 275	Ala	Ile 275	
tgg	aat	ctt	gga	ccg	tac	aac	cct	tca	cag	gtg	tct	gct	ggt	tcc	cag	979
Trp	Asn	Leu 280	Gly	Pro	Tyr	Asn	Pro 285	Ser	Gln	Val	Ser	Ala	Gly	Ser	Gln 290	
cct	gac	gtt	tac	atg	ctg	tgg	aca	gat	ggt	gct	gct	cgt	gtc	atg	ccg	1027
Pro	Asp	Val	Tyr	Met	Leu	Trp 300	Thr	Asp	Gly	Ala	Ala	Arg	Val	Met	Pro 305	
gca	tgg	gag	ctc	tac	ctc	ggt	aac	tac	act	att	cca	gca	gtc	ttc	tgg	1075
Ala	Trp	Glu	Leu	Tyr	Leu	Gly	Asn	Tyr	Thr	Ile	Pro	Ala	Val	Phe	Trp	

310	315	320	325	
gtt gct gtg atg ctg	ggt atc ctc gtg	gtt ctg ctt gtg	act tac cca	1123
Val Ala Val Met	Leu Gly Ile Leu	Val Leu Leu Val	Thr Tyr Pro	
	330	335	340	
ttc att gag cgt aag	ttc acc ggc gac	gat gca cac cac	aac ttg ctg	1171
Phe Ile Glu Arg	Lys Phe Thr Gly	Asp Asp Ala His	His Asn Leu Leu	
	345	350	355	
cag cgt cct cgc gat	gtt cca gtc cgc	acc tca ctc ggt	gtc atg gcg	1219
Gln Arg Pro Arg	Asp Val Pro Val	Arg Thr Ser Leu	Gly Val Met Ala	
	360	365	370	
ctt gtc ttc tac atc	ctg ctt acc gtt	tct ggt ggt aac	gat gtt tac	1267
Leu Val Phe Tyr	Ile Leu Thr Val	Ser Gly Gly Asn	Asp Val Tyr	
	375	380	385	
gca atg cag ttc cat	gtt tca ctg aac	gcg atg acc tgg	atc ggt cgt	1315
Ala Met Gln Phe	His Val Ser Leu	Asn Ala Met Thr	Trp Ile Gly Arg	
	395	400	405	
atc ggc ctc atc gtt	gga cca gct att	gca tac ttc atc	act tac cga	1363
Ile Gly Leu Ile	Val Gly Pro Ala	Ile Ala Tyr Phe	Ile Thr Tyr Arg	
	410	415	420	
ctg tgc atc ggc ttg	cag cgc tct gac	cgc gag gtc ctg	gag cac ggc	1411
Leu Cys Ile Gly	Leu Gln Arg Ser	Asp Arg Glu Val	Leu Glu His Gly	
	425	430	435	
atc gag acc ggt atc	atc aag cag atg	cca aat ggt gcc	ttc att gaa	1459
Ile Glu Thr Gly	Ile Ile Lys Gln	Met Pro Asn Gly	Ala Phe Ile Glu	
	440	445	450	
gtt cac cag cca ctt	ggc cca gtt gat	gac cat ggt cac	cca atc cca	1507
Val His Gln Pro	Leu Gly Pro Val	Asp Asp His Gly	His Pro Ile Pro	
	455	460	465	
ctg cca tac gct ggc	gct gcg gtt cca	aag cag atg aac	cag ctt ggt	1555
Leu Pro Tyr Ala	Gly Ala Ala Val	Pro Lys Gln Met	Asn Gln Leu Gly	
	475	480	485	
tac gct gag gtt gaa	acc cgc ggt gga	ttc ttc gga cct	gat cca gaa	1603
Tyr Ala Glu Val	Glu Thr Arg Gly	Gly Phe Phe Gly	Pro Asp Pro Glu	
	490	495	500	
gac atc cgt gcg aag	gct aag gaa att	gag cac gca aac	cac att gag	1651
Asp Ile Arg Ala	Lys Ala Lys Glu	Ile Glu His Ala	Asn His Ile Glu	
	505	510	515	
gaa gcg aac act ctt	cggt gca ctc aac	gag gca aac att	gag cgt gac	1699
Glu Ala Asn Thr	Leu Arg Ala Leu	Asn Glu Ala Asn	Ile Glu Arg Asp	
	520	525	530	
aag aat gag ggc aag	aac tagtttctag	gacttcatct ctg		1740
Lys Asn Glu Gly	Lys Asn			
	535			

<210> 162

<211> 539

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

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Ala	Ser	Gly	Ile	Arg	Arg	Gln	Ile	Asn	Lys	Val	Phe	Pro	Thr	His	Trp
			20					25					30		
Ser	Phe	Met	Leu	Gly	Glu	Ile	Ala	Leu	Tyr	Ser	Phe	Ile	Val	Leu	Leu
		35					40					45			
Leu	Thr	Gly	Val	Tyr	Leu	Thr	Leu	Phe	Phe	Asp	Pro	Ser	Ile	Thr	Lys
	50					55					60				
Val	Ile	Tyr	Asp	Gly	Gly	Tyr	Leu	Pro	Leu	Asn	Gly	Val	Glu	Met	Ser
65					70					75					80
Arg	Ala	Tyr	Ala	Thr	Ala	Leu	Asp	Ile	Ser	Phe	Glu	Val	Arg	Gly	Gly
				85					90					95	
Leu	Phe	Ile	Arg	Gln	Met	His	His	Trp	Ala	Ala	Leu	Leu	Phe	Val	Val
			100					105					110		
Ser	Met	Leu	Val	His	Met	Leu	Arg	Ile	Phe	Phe	Thr	Gly	Ala	Phe	Arg
		115					120					125			
Arg	Pro	Arg	Glu	Ala	Asn	Trp	Ile	Ile	Gly	Val	Val	Leu	Ile	Ile	Leu
	130					135					140				
Gly	Met	Ala	Glu	Gly	Phe	Met	Gly	Tyr	Ser	Leu	Pro	Asp	Asp	Leu	Leu
145					150					155					160
Ser	Gly	Val	Gly	Leu	Arg	Ile	Met	Ser	Ala	Ile	Ile	Val	Gly	Leu	Pro
				165					170					175	
Ile	Ile	Gly	Thr	Trp	Met	His	Trp	Leu	Ile	Phe	Gly	Gly	Asp	Phe	Pro
			180					185					190		
Ser	Asp	Leu	Met	Leu	Asp	Arg	Phe	Tyr	Ile	Ala	His	Val	Leu	Ile	Ile
		195					200					205			
Pro	Ala	Ile	Leu	Leu	Gly	Leu	Ile	Ala	Ala	His	Leu	Ala	Leu	Val	Trp
	210					215					220				
Tyr	Gln	Lys	His	Thr	Gln	Phe	Pro	Gly	Ala	Gly	Arg	Thr	Glu	Asn	Asn
225					230					235					240
Val	Ile	Gly	Ile	Arg	Ile	Met	Pro	Leu	Phe	Ala	Val	Lys	Ala	Val	Ala
				245					250					255	
Phe	Gly	Leu	Ile	Val	Phe	Gly	Phe	Leu	Ala	Leu	Leu	Ala	Gly	Val	Thr
			260					265					270		
Thr	Ile	Asn	Ala	Ile	Trp	Asn	Leu	Gly	Pro	Tyr	Asn	Pro	Ser	Gln	Val
		275					280					285			
Ser	Ala	Gly	Ser	Gln	Pro	Asp	Val	Tyr	Met	Leu	Trp	Thr	Asp	Gly	Ala
	290					295					300				

Ala Arg Val Met Pro Ala Trp Glu Leu Tyr Leu Gly Asn Tyr Thr Ile
 305 310 315 320
 Pro Ala Val Phe Trp Val Ala Val Met Leu Gly Ile Leu Val Val Leu
 325 330 335
 Leu Val Thr Tyr Pro Phe Ile Glu Arg Lys Phe Thr Gly Asp Asp Ala
 340 345 350
 His His Asn Leu Leu Gln Arg Pro Arg Asp Val Pro Val Arg Thr Ser
 355 360 365
 Leu Gly Val Met Ala Leu Val Phe Tyr Ile Leu Leu Thr Val Ser Gly
 370 375 380
 Gly Asn Asp Val Tyr Ala Met Gln Phe His Val Ser Leu Asn Ala Met
 385 390 395 400
 Thr Trp Ile Gly Arg Ile Gly Leu Ile Val Gly Pro Ala Ile Ala Tyr
 405 410 415
 Phe Ile Thr Tyr Arg Leu Cys Ile Gly Leu Gln Arg Ser Asp Arg Glu
 420 425 430
 Val Leu Glu His Gly Ile Glu Thr Gly Ile Ile Lys Gln Met Pro Asn
 435 440 445
 Gly Ala Phe Ile Glu Val His Gln Pro Leu Gly Pro Val Asp Asp His
 450 455 460
 Gly His Pro Ile Pro Leu Pro Tyr Ala Gly Ala Ala Val Pro Lys Gln
 465 470 475 480
 Met Asn Gln Leu Gly Tyr Ala Glu Val Glu Thr Arg Gly Gly Phe Phe
 485 490 495
 Gly Pro Asp Pro Glu Asp Ile Arg Ala Lys Ala Lys Glu Ile Glu His
 500 505 510
 Ala Asn His Ile Glu Glu Ala Asn Thr Leu Arg Ala Leu Asn Glu Ala
 515 520 525
 Asn Ile Glu Arg Asp Lys Asn Glu Gly Lys Asn
 530 535

<210> 163

<211> 1002

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(979)

<223> RXS02476

<400> 163

cgggcggagt tctatcaaca ttacgcaaag gcataagctt tattattcca ctcggtgtga 60

 catatgacct aaagtgcag tcagtacaat catttaggtc atg tca ttt aca gct 115
 Met Ser Phe Thr Ala

															1	5	
ttt	caa	aca	gcc	ctg	ctc	gtg	tgg	ttt	aga	gca	aat	gcc	cgc	gat	ctt	163	
Phe	Gln	Thr	Ala	Leu	Leu	Val	Trp	Phe	Arg	Ala	Asn	Ala	Arg	Asp	Leu		
				10					15					20			
gcg	tgg	cgt	gat	ccc	aat	act	tca	gca	tgg	gga	att	ctc	ctt	tca	gag	211	
Ala	Trp	Arg	Asp	Pro	Asn	Thr	Ser	Ala	Trp	Gly	Ile	Leu	Leu	Ser	Glu		
				25					30					35			
gtg	atg	agc	caa	caa	act	ccc	gtc	gcg	cga	gtc	gag	ccg	att	tgg	cgt	259	
Val	Met	Ser	Gln	Gln	Thr	Pro	Val	Ala	Arg	Val	Glu	Pro	Ile	Trp	Arg		
				40					45					50			
gag	tgg	atg	gaa	aaa	tgg	ccc	act	ccg	gaa	gat	ttc	gcg	aat	gcg	agc	307	
Glu	Trp	Met	Glu	Lys	Trp	Pro	Thr	Pro	Glu	Asp	Phe	Ala	Asn	Ala	Ser		
				55					60					65			
acc	gat	gag	att	ttg	cgg	tcg	tgg	ggc	aag	ttg	ggc	tat	cca	cgt	agg	355	
Thr	Asp	Glu	Ile	Leu	Arg	Ser	Trp	Gly	Lys	Leu	Gly	Tyr	Pro	Arg	Arg		
				70					75					80			
gcg	ctg	agg	ttg	aag	gaa	tgt	gcg	gag	gtg	atc	gtc	gaa	aag	cat	gcc	403	
Ala	Leu	Arg	Leu	Lys	Glu	Cys	Ala	Glu	Val	Ile	Val	Glu	Lys	His	Ala		
				90					95					100			
ggc	gag	gtg	ccg	gat	acg	gtg	gag	gcg	ctg	ctc	gcg	ttg	ccg	ggg	atc	451	
Gly	Glu	Val	Pro	Asp	Thr	Val	Glu	Ala	Leu	Leu	Ala	Leu	Pro	Gly	Ile		
				105					110					115			
ggt	gat	tac	acg	gcg	cgc	gcg	gtc	gcg	gcg	ttt	cat	ttt	ggg	cag	cgc	499	
Gly	Asp	Tyr	Thr	Ala	Arg	Ala	Val	Ala	Ala	Phe	His	Phe	Gly	Gln	Arg		
				120					125					130			
gtg	ccg	gtg	gtc	gat	acg	aac	gtg	cgt	cgc	gtg	tac	cag	cgc	gcg	gta	547	
Val	Pro	Val	Val	Asp	Thr	Asn	Val	Arg	Arg	Val	Tyr	Gln	Arg	Ala	Val		
				135					140					145			
gcc	gga	cgt	tac	ctt	gcg	ggg	cct	gcg	aaa	aag	caa	gag	ctt	atc	gac	595	
Ala	Gly	Arg	Tyr	Leu	Ala	Gly	Pro	Ala	Lys	Lys	Gln	Glu	Leu	Ile	Asp		
				150					155					160			
gtc	tcc	ctt	ctc	ctt	ccc	aac	act	cac	gcc	cca	gaa	ttc	tct	gcc	gca	643	
Val	Ser	Leu	Leu	Leu	Pro	Asn	Thr	His	Ala	Pro	Glu	Phe	Ser	Ala	Ala		
				170					175					180			
ata	atg	gag	ttg	ggt	gct	ctt	atc	tgc	acg	gcc	act	tcc	cca	aag	tgt	691	
Ile	Met	Glu	Leu	Gly	Ala	Leu	Ile	Cys	Thr	Ala	Thr	Ser	Pro	Lys	Cys		
				185					190					195			
gac	acc	tgc	cca	ctg	ctt	gac	cag	tgt	caa	tgg	caa	aaa	ctt	ggc	tgt	739	
Asp	Thr	Cys	Pro	Leu	Leu	Asp	Gln	Cys	Gln	Trp	Gln	Lys	Leu	Gly	Cys		
				200					205					210			
ccc	tcc	ccg	agt	gaa	gag	gag	ctg	gct	tca	gcg	aaa	aag	cgt	gtg	cag	787	
Pro	Ser	Pro	Ser	Glu	Glu	Glu	Leu	Ala	Ser	Ala	Lys	Lys	Arg	Val	Gln		
				215					220					225			
aaa	ttt	gtg	gga	acc	gac	cga	caa	gtc	cgt	ggc	cta	atc	atg	gac	gta	835	
Lys	Phe	Val	Gly	Thr	Asp	Arg	Gln	Val	Arg	Gly	Leu	Ile	Met	Asp	Val		
				230					235					240			
														245			

ctg cgc aat gcc acc gca cct gtg cca cta tcc gcg att gat gtc gtg 883
 Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser Ala Ile Asp Val Val
 250 255 260

tgg cct gac gat gcc caa cgc tcc cgg gcg ctg ttt tcg ctc att gag 931
 Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu Phe Ser Leu Ile Glu
 265 270 275

gac gga ctc gcg gaa caa aat gag gcg ggt tat ttc cac ctg cca cgg 979
 Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr Phe His Leu Pro Arg
 280 285 290

taaaccactg cgcgcctgca aaa 1002

<210> 164

<211> 293

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Ser Phe Thr Ala Phe Gln Thr Ala Leu Leu Val Trp Phe Arg Ala
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Asn Ala Arg Asp Leu Ala Trp Arg Asp Pro Asn Thr Ser Ala Trp Gly
 20 25 30

Ile Leu Leu Ser Glu Val Met Ser Gln Gln Thr Pro Val Ala Arg Val
 35 40 45

Glu Pro Ile Trp Arg Glu Trp Met Glu Lys Trp Pro Thr Pro Glu Asp
 50 55 60

Phe Ala Asn Ala Ser Thr Asp Glu Ile Leu Arg Ser Trp Gly Lys Leu
 65 70 75 80

Gly Tyr Pro Arg Arg Ala Leu Arg Leu Lys Glu Cys Ala Glu Val Ile
 85 90 95

Val Glu Lys His Ala Gly Glu Val Pro Asp Thr Val Glu Ala Leu Leu
 100 105 110

Ala Leu Pro Gly Ile Gly Asp Tyr Thr Ala Arg Ala Val Ala Ala Phe
 115 120 125

His Phe Gly Gln Arg Val Pro Val Val Asp Thr Asn Val Arg Arg Val
 130 135 140

Tyr Gln Arg Ala Val Ala Gly Arg Tyr Leu Ala Gly Pro Ala Lys Lys
 145 150 155 160

Gln Glu Leu Ile Asp Val Ser Leu Leu Leu Pro Asn Thr His Ala Pro
 165 170 175

Glu Phe Ser Ala Ala Ile Met Glu Leu Gly Ala Leu Ile Cys Thr Ala
 180 185 190

Thr Ser Pro Lys Cys Asp Thr Cys Pro Leu Leu Asp Gln Cys Gln Trp
 195 200 205

Gln Lys Leu Gly Cys Pro Ser Pro Ser Glu Glu Glu Leu Ala Ser Ala
 210 215 220

Lys Lys Arg Val Gln Lys Phe Val Gly Thr Asp Arg Gln Val Arg Gly
 225 230 235 240

Leu Ile Met Asp Val Leu Arg Asn Ala Thr Ala Pro Val Pro Leu Ser
 245 250 255

Ala Ile Asp Val Val Trp Pro Asp Asp Ala Gln Arg Ser Arg Ala Leu
 260 265 270

Phe Ser Leu Ile Glu Asp Gly Leu Ala Glu Gln Asn Glu Ala Gly Tyr
 275 280 285

Phe His Leu Pro Arg
 290

<210> 165
 <211> 720
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(697)
 <223> RXS02990

<400> 165
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gcttgttcct gctttttcgt caacgaaggg caacaacgcg atg gat atc caa gcc 115
 Met Asp Ile Gln Ala
 1 5

gaa aag att gaa aag ctc aga aaa gca ctc gac aac ttt gaa cgc gct 163
 Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp Asn Phe Glu Arg Ala
 10 15 20

cat gcg cga ggc gaa tca gac ttc ttt gac cat gaa aaa gaa gaa aag 211
 His Ala Arg Gly Glu Ser Asp Phe Phe Asp His Glu Lys Glu Glu Lys
 25 30 35

aaa gcc aac gta cgc aga cgt gcc ctg ctg ctg ctt aac caa cgc gca 259
 Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu Leu Asn Gln Arg Ala
 40 45 50

cga tca gtc aac gaa cta agc acc aga ctt aaa gca ctg gag ttt gag 307
 Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys Ala Leu Glu Phe Glu
 55 60 65

gaa gac atc atc aat gag gtc att ggc gat ctc acc aga tcc aaa ctg 355
 Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu Thr Arg Ser Lys Leu
 70 75 80 85

ctt gat gat gaa gtt ttt gcc act gag tgg gtt cgg caa cgt gct gcc 403
 Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val Arg Gln Arg Ala Ala
 90 95 100

agg cga gga aaa tct tcg cgt gcg ctg gac cgc gaa ctg cag gaa aaa 451

Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg Glu Leu Gln Glu Lys
 105 110 115

 ggc gtc gac aag caa acg cgt gct gcg gcg ctt gag caa atc gac cag 499
 Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu Glu Gln Ile Asp Gln
 120 125 130

 gcc gat gag cgg gac acg gcg cgg gcg gtg gcc gtg aaa aag gcg cgc 547
 Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala Val Lys Lys Ala Arg
 135 140 145

 tca gag acc aag att ccg cag gac cgc gcc gac tac gac aaa gcg ctt 595
 Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp Tyr Asp Lys Ala Leu
 150 155 160 165

 cgg cgc gtg gtt ggt gcg ctg gca cgg cgg gga ttt ccg gct gga atg 643
 Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly Phe Pro Ala Gly Met
 170 175 180

 tcc atg gac ctt gcg cgg gaa gcg cta gac gcg cga atc gag gat ttg 691
 Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala Arg Ile Glu Asp Leu
 185 190 195

 aaa aac taaaccccg atgggaatca tcc 720
 Lys Asn

<210> 166

<211> 199

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Asp Ile Gln Ala Glu Lys Ile Glu Lys Leu Arg Lys Ala Leu Asp
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 Asn Phe Glu Arg Ala His Ala Arg Gly Glu Ser Asp Phe Phe Asp His
 20 25 30

 Glu Lys Glu Glu Lys Lys Ala Asn Val Arg Arg Arg Ala Leu Leu Leu
 35 40 45

 Leu Asn Gln Arg Ala Arg Ser Val Asn Glu Leu Ser Thr Arg Leu Lys
 50 55 60

 Ala Leu Glu Phe Glu Glu Asp Ile Ile Asn Glu Val Ile Gly Asp Leu
 65 70 75 80

 Thr Arg Ser Lys Leu Leu Asp Asp Glu Val Phe Ala Thr Glu Trp Val
 85 90 95

 Arg Gln Arg Ala Ala Arg Arg Gly Lys Ser Ser Arg Ala Leu Asp Arg
 100 105 110

 Glu Leu Gln Glu Lys Gly Val Asp Lys Gln Thr Arg Ala Ala Ala Leu
 115 120 125

 Glu Gln Ile Asp Gln Ala Asp Glu Arg Asp Thr Ala Arg Ala Val Ala
 130 135 140

Val Lys Lys Ala Arg Ser Glu Thr Lys Ile Pro Gln Asp Arg Ala Asp
 145 150 155 160

Tyr Asp Lys Ala Leu Arg Arg Val Val Gly Ala Leu Ala Arg Arg Gly
 165 170 175

Phe Pro Ala Gly Met Ser Met Asp Leu Ala Arg Glu Ala Leu Asp Ala
 180 185 190

Arg Ile Glu Asp Leu Lys Asn
 195

<210> 167
 <211> 747
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(724)
 <223> RXS03098

<400> 167
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ttccgtcacc accctcttcg agggcgaggc ctaaaccacc atg ccc acc acg gac 115
 Met Pro Thr Thr Asp
 1 5

gtc ttc aac cgc gtc cgg ttg gca ttg gaa cct cta gct gat ccc gca 163
 Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro Leu Ala Asp Pro Ala
 10 15 20

cgt gcc acc gga atg gca agc tac atg cgg gat cag ttt tct ttt ctc 211
 Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp Gln Phe Ser Phe Leu
 25 30 35

ggc atc cca tcc acc ccc aga aaa gaa gcc tgc aaa ccc gtg ctg tcc 259
 Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys Lys Pro Val Leu Ser
 40 45 50

gcg cta aaa gag ttg gac act gac ttt gtc tca gac tgc ttt ggc gca 307
 Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser Asp Cys Phe Gly Ala
 55 60 65

gct gaa cgg gaa tac cag tat gtc gcc tgc gat cac atc aat cgc gtc 355
 Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp His Ile Asn Arg Val
 70 75 80 85

ggc atc acc gat tta ggt ttt gcc aaa gca tta gtg cag acc aaa tcc 403
 Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu Val Gln Thr Lys Ser
 90 95 100

tgg tgg gac acc gtc gat tcc cta gca aaa ccg atc ggc gcc aaa cac 451
 Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro Ile Gly Ala Lys His
 105 110 115

gat gat gat ctg atg aaa acg tgg gcg ctt gat gag gac ttc tgg gtg 499
 Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp Glu Asp Phe Trp Val
 120 125 130

cgc cgc atc gcg atc atc cac caa ctg ggc cgc aag aaa aac acc gac 547
 Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg Lys Lys Asn Thr Asp
 135 140 145

 gct gcc ctg ctg gcc tgg atc atc gag cag aac ctc ggc tcc agc gag 595
 Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn Leu Gly Ser Ser Glu
 150 155 160 165

 ttc ttc atc aac aaa gcg atc ggc tgg gca ctg cgg gat ttc gcc cgc 643
 Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu Arg Asp Phe Ala Arg
 170 175 180

 cac gac ccc agc tgg gtc cgg gct ttt gtc gac gcc acg gac ctt tcc 691
 His Asp Pro Ser Trp Val Arg Ala Phe Val Asp Ala Thr Asp Leu Ser
 185 190 195

 cca ctg agc cgg cga gaa gcc ctg aag aat att tagccctcag gcatcatctg 744
 Pro Leu Ser Arg Arg Glu Ala Leu Lys Asn Ile
 200 205

 agc 747

<210> 168
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 168
 Met Pro Thr Thr Asp Val Phe Asn Arg Val Arg Leu Ala Leu Glu Pro
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 Leu Ala Asp Pro Ala Arg Ala Thr Gly Met Ala Ser Tyr Met Arg Asp
 20 25 30

 Gln Phe Ser Phe Leu Gly Ile Pro Ser Thr Pro Arg Lys Glu Ala Cys
 35 40 45

 Lys Pro Val Leu Ser Ala Leu Lys Glu Leu Asp Thr Asp Phe Val Ser
 50 55 60

 Asp Cys Phe Gly Ala Ala Glu Arg Glu Tyr Gln Tyr Val Ala Cys Asp
 65 70 75 80

 His Ile Asn Arg Val Gly Ile Thr Asp Leu Gly Phe Ala Lys Ala Leu
 85 90 95

 Val Gln Thr Lys Ser Trp Trp Asp Thr Val Asp Ser Leu Ala Lys Pro
 100 105 110

 Ile Gly Ala Lys His Asp Asp Asp Leu Met Lys Thr Trp Ala Leu Asp
 115 120 125

 Glu Asp Phe Trp Val Arg Arg Ile Ala Ile Ile His Gln Leu Gly Arg
 130 135 140

 Lys Lys Asn Thr Asp Ala Ala Leu Leu Ala Trp Ile Ile Glu Gln Asn
 145 150 155 160

 Leu Gly Ser Ser Glu Phe Phe Ile Asn Lys Ala Ile Gly Trp Ala Leu

			165						170						175
Arg	Asp	Phe	Ala	Arg	His	Asp	Pro	Ser	Trp	Val	Arg	Ala	Phe	Val	Asp
			180					185					190		
Ala	Thr	Asp	Leu	Ser	Pro	Leu	Ser	Arg	Arg	Glu	Ala	Leu	Lys	Asn	Ile
		195					200					205			

<210> 169

<211> 806

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(783)

<223> RXS03175

<400> 169

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Val	Arg	Ala	Ser	Glu	Lys	Asp	Thr	Ala	Thr	Ala	Leu	Gln	Pro	Ala	Leu	
1				5				10						15		
gat	aac	gga	tgg	cac	tac	att	ggg	gcc	cca	gca	gct	gcc	aag	gga	cgt	96
Asp	Asn	Gly	Trp	His	Tyr	Ile	Gly	Ala	Pro	Ala	Ala	Ala	Lys	Gly	Arg	
			20					25					30			
gcc	ggg	gtc	ggc	att	ttg	tct	agg	cat	gaa	ctt	gaa	gat	gtg	aac	atc	144
Ala	Gly	Val	Gly	Ile	Leu	Ser	Arg	His	Glu	Leu	Glu	Asp	Val	Asn	Ile	
		35					40					45				
ggg	ttt	gga	tct	ttc	ctt	gac	tcc	ggc	cgc	tac	att	gaa	gca	acc	atc	192
Gly	Phe	Gly	Ser	Phe	Leu	Asp	Ser	Gly	Arg	Tyr	Ile	Glu	Ala	Thr	Ile	
	50					55					60					
aaa	gac	acc	acc	ctg	gat	gtg	cca	gta	acc	gtg	gca	tct	ctt	tac	ctc	240
Lys	Asp	Thr	Thr	Leu	Asp	Val	Pro	Val	Thr	Val	Ala	Ser	Leu	Tyr	Leu	
	65				70				75						80	
ccc	tca	ggg	tca	gcg	ggc	acc	gac	aag	cag	gat	gaa	aag	tac	cgc	ttc	288
Pro	Ser	Gly	Ser	Ala	Gly	Thr	Asp	Lys	Gln	Asp	Glu	Lys	Tyr	Arg	Phe	
			85					90						95		
ctc	gat	gaa	ttc	gaa	ggg	ttc	ctg	gac	cag	cgc	gct	aaa	gaa	cgc	tcc	336
Leu	Asp	Glu	Phe	Glu	Gly	Phe	Leu	Asp	Gln	Arg	Ala	Lys	Glu	Arg	Ser	
			100				105						110			
cac	atg	gtc	atc	ggg	ggc	gac	tgg	aac	atc	tgc	cac	cgc	cgc	gaa	gac	384
His	Met	Val	Ile	Gly	Gly	Asp	Trp	Asn	Ile	Cys	His	Arg	Arg	Glu	Asp	
		115					120					125				
ctg	aaa	aac	tgg	aaa	acc	aac	caa	aag	aaa	tcc	ggg	ttc	ctt	ccc	gac	432
Leu	Lys	Asn	Trp	Lys	Thr	Asn	Gln	Lys	Lys	Ser	Gly	Phe	Leu	Pro	Asp	
	130					135					140					
gaa	cgc	gca	ttc	atg	gat	tca	gtc	ttt	ggc	acc	ttc	cca	gat	gag	gca	480
Glu	Arg	Ala	Phe	Met	Asp	Ser	Val	Phe	Gly	Thr	Phe	Pro	Asp	Glu	Ala	
	145				150				155					160		
acc	cag	gtt	gca	ggg	ggc	ggc	gac	ttc	ttc	ggg	gcc	gtg	gac	tat	gaa	528

Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu
 165 170 175
 gga acg agg cgt cga gaa gca act acg gac cct gcg tgg ttc gac gtt 576
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val
 180 185 190
 gca cgt cgc ctg caa cct gaa ggc gac ggc ccc tac act tgg tgg acc 624
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr
 195 200 205
 tac cgc gga aaa gcc ttc gac acc ggc gcc gga tgg cgc atc gac tac 672
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr
 210 215 220
 caa gca gca acc gca gcg atg ctc gaa cgc gca gaa cgc tcc tgg gta 720
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val
 225 230 235 240
 gac aaa gcc gct gca tac gat ttg cgc tgg tca gat cac tca cca ctg 768
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu
 245 250 255
 aac gtg atc tac tcc taaaatgctg ctgacaattc tat 806
 Asn Val Ile Tyr Ser
 260

<210> 170

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

Val Arg Ala Ser Glu Lys Asp Thr Ala Thr Ala Leu Gln Pro Ala Leu
 1 5 10 15
 Asp Asn Gly Trp His Tyr Ile Gly Ala Pro Ala Ala Ala Lys Gly Arg
 20 25 30
 Ala Gly Val Gly Ile Leu Ser Arg His Glu Leu Glu Asp Val Asn Ile
 35 40 45
 Gly Phe Gly Ser Phe Leu Asp Ser Gly Arg Tyr Ile Glu Ala Thr Ile
 50 55 60
 Lys Asp Thr Thr Leu Asp Val Pro Val Thr Val Ala Ser Leu Tyr Leu
 65 70 75 80
 Pro Ser Gly Ser Ala Gly Thr Asp Lys Gln Asp Glu Lys Tyr Arg Phe
 85 90 95
 Leu Asp Glu Phe Glu Gly Phe Leu Asp Gln Arg Ala Lys Glu Arg Ser
 100 105 110
 His Met Val Ile Gly Gly Asp Trp Asn Ile Cys His Arg Arg Glu Asp
 115 120 125
 Leu Lys Asn Trp Lys Thr Asn Gln Lys Lys Ser Gly Phe Leu Pro Asp
 130 135 140

Glu Arg Ala Phe Met Asp Ser Val Phe Gly Thr Phe Pro Asp Glu Ala
 145 150 155 160
 Thr Gln Val Ala Gly Ala Gly Asp Phe Phe Gly Ala Val Asp Tyr Glu
 165 170 175
 Gly Thr Arg Arg Arg Glu Ala Thr Thr Asp Pro Ala Trp Phe Asp Val
 180 185 190
 Ala Arg Arg Leu Gln Pro Glu Gly Asp Gly Pro Tyr Thr Trp Trp Thr
 195 200 205
 Tyr Arg Gly Lys Ala Phe Asp Thr Gly Ala Gly Trp Arg Ile Asp Tyr
 210 215 220
 Gln Ala Ala Thr Ala Ala Met Leu Glu Arg Ala Glu Arg Ser Trp Val
 225 230 235 240
 Asp Lys Ala Ala Ala Tyr Asp Leu Arg Trp Ser Asp His Ser Pro Leu
 245 250 255
 Asn Val Ile Tyr Ser
 260

<210> 171
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1183)
 <223> RXN03069

<400> 171
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 gatcgagaag ttgcgctcgg ggaggtacag ggcacgcttc atg cac gag ggt agg 115
 Met His Glu Gly Arg
 1 5
 cga tac tct gcc ccg tat acc ttc ggt acc aag ggt gag gcg cag gag 163
 Arg Tyr Ser Ala Pro Tyr Thr Phe Gly Thr Lys Gly Glu Ala Gln Glu
 10 15 20
 ttc ttg gcc tct gaa cgc acg gcc atc atc aat ggc aca tgg atg gat 211
 Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn Gly Thr Trp Met Asp
 25 30 35
 ttt gag atg cgg gag agg ttc gag cag gca cag cgc gaa gcc gaa gaa 259
 Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln Arg Glu Ala Glu Glu
 40 45 50
 cgc atg atg gag acc ttc ttc agt tat gca tcg agg tgg ata gaa acc 307
 Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser Arg Trp Ile Glu Thr
 55 60 65
 cgg aca aat gcc caa gga aag aaa ctc agc caa ggg gtg aaa gat gat 355
 Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln Gly Val Lys Asp Asp
 70 75 80 85

tac ttt cgt tat ata aaa tca gat cga cta agt tat tgg gct gat tat	403
Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser Tyr Trp Ala Asp Tyr	
90 95 100	
gcg ctc tgt gaa atc act gtc gct gat gtc cgt gag tgg tat agc gat	451
Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg Glu Trp Tyr Ser Asp	
105 110 115	
act att cag gac ggt aaa ttg acc tca atg gcg cgg agt tac agc atg	499
Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala Arg Ser Tyr Ser Met	
120 125 130	
atg aag tct gtc atg gag act gca gtg gag gat ggc att atc ccg atg	547
Met Lys Ser Val Met Glu Thr Ala Val Glu Asp Gly Ile Ile Pro Met	
135 140 145	
aat ccg tgc aaa gtc cgt ggc ggg ggt aat acg aaa aca ggc aaa aag	595
Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr Lys Thr Gly Lys Lys	
150 155 160 165	
gtt gat gtc cca acc gat gcc gag ctt gag gcg atc att ggt gca ctg	643
Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala Ile Ile Gly Ala Leu	
170 175 180	
ccg agt aag tac ttt tgt ttg gct att gtt gct gcc gct ggt gca ctt	691
Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala Ala Ala Gly Ala Leu	
185 190 195	
cga ttc ggt gaa atc gtt gcg ctg cgt acc act gat gtg gat gtt tat	739
Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr Asp Val Asp Val Tyr	
200 205 210	
ttt gat cgc agc gga ttt gta gat tgt gtt cga ata agg att tct cgg	787
Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg Ile Arg Ile Ser Arg	
215 220 225	
agc att agg cac acg aga tac cat ggc cga gtt gaa ggt ccg cct aaa	835
Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys	
230 235 240 245	
act gaa gct ggt gtt cgt agc ctc tat atc tat ggc aaa gat gca gca	883
Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr Gly Lys Asp Ala Ala	
250 255 260	
gaa att gcc aag cat gtg gac acg att gat gtg ggt ttg cga cta tgg	931
Glu Ile Ala Lys His Val Asp Thr Ile Asp Val Gly Leu Arg Leu Trp	
265 270 275	
agc tcg atg aga gat cct gat gaa ccc atg ccg tat cac acc ttt aag	979
Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro Tyr His Thr Phe Lys	
280 285 290	
cac aac tgg gat agg gcg cgg gaa agt gtc cac agt aaa gcg acc gtt	1027
His Asn Trp Asp Arg Ala Arg Glu Ser Val His Ser Lys Ala Thr Val	
295 300 305	
cac tcg atg agg cat tat tcg ggt acg aag tat gca cag gtt ggg gcg	1075
His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr Ala Gln Val Gly Ala	
310 315 320 325	

aca ctc aag gag gtg atg gcg cgg ctg ggg cac tca aca cct agt gca 1123
 Thr Leu Lys Glu Val Met Ala Arg Leu Gly His Ser Thr Pro Ser Ala
 330 335 340

gca ctg cgt tat cag cac tca ggc gag cgt gat gaa gag cta gca aag 1171
 Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp Glu Glu Leu Ala Lys
 345 350 355

cgc atg gcg cgc taaacactcg gcagtgagtt tca 1206
 Arg Met Ala Arg
 360

<210> 172

<211> 361

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

Met His Glu Gly Arg Arg Tyr Ser Ala Pro Tyr Thr Phe Gly Thr Lys
 1 5 10 15

Gly Glu Ala Gln Glu Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn
 20 25 30

Gly Thr Trp Met Asp Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln
 35 40 45

Arg Glu Ala Glu Glu Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser
 50 55 60

Arg Trp Ile Glu Thr Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln
 65 70 75 80

Gly Val Lys Asp Asp Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser
 85 90 95

Tyr Trp Ala Asp Tyr Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg
 100 105 110

Glu Trp Tyr Ser Asp Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala
 115 120 125

Arg Ser Tyr Ser Met Met Lys Ser Val Met Glu Thr Ala Val Glu Asp
 130 135 140

Gly Ile Ile Pro Met Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr
 145 150 155 160

Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala
 165 170 175

Ile Ile Gly Ala Leu Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala
 180 185 190

Ala Ala Gly Ala Leu Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr
 195 200 205

Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg
 210 215 220

Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val
 225 230 235 240
 Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr
 245 250 255
 Gly Lys Asp Ala Ala Glu Ile Ala Lys His Val Asp Thr Ile Asp Val
 260 265 270
 Gly Leu Arg Leu Trp Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro
 275 280 285
 Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His
 290 295 300
 Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr
 305 310 315 320
 Ala Gln Val Gly Ala Thr Leu Lys Glu Val Met Ala Arg Leu Gly His
 325 330 335
 Ser Thr Pro Ser Ala Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp
 340 345 350
 Glu Glu Leu Ala Lys Arg Met Ala Arg
 355 360

<210> 173
 <211> 1206
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1183)
 <223> FRXA02890

<400> 173
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 Met His Glu Gly Arg
 1 5
 cga tac tct gcc ccg cat acc ttc ggt acc aag ggt gag gcg cag gag 163
 Arg Tyr Ser Ala Pro His Thr Phe Gly Thr Lys Gly Glu Ala Gln Glu
 10 15 20
 ttc ttg gcc tct gaa cgc acg gcc atc atc aat ggc aca tgg atg gat 211
 Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn Gly Thr Trp Met Asp
 25 30 35
 ttt gag atg cgg gag agg ttc gag cag gca cag cgc gaa gcc gaa gaa 259
 Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln Arg Glu Ala Glu Glu
 40 45 50
 cgc atg atg gag acc ttc ttc agt tat gca tcg agg tgg ata gaa acc 307
 Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser Arg Trp Ile Glu Thr
 55 60 65

cgg aca aat gcc caa gga aag aaa ctc agc caa ggg gtg aaa gat gat	355
Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln Gly Val Lys Asp Asp	
70 75 80 85	
tac ttt cgt tat ata aaa tca gat cga cta agt tat tgg gct gat tat	403
Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser Tyr Trp Ala Asp Tyr	
90 95 100	
gcg ctc tgt gaa atc act gtc gct gat gtc cgt gag tgg tat agc gat	451
Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg Glu Trp Tyr Ser Asp	
105 110 115	
act att cag gac ggt aaa ttg acc tca atg gcg cgg agt tac agc atg	499
Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala Arg Ser Tyr Ser Met	
120 125 130	
atg aag tct gtc atg gag act gca gtg gag gat ggc att atc ccg atg	547
Met Lys Ser Val Met Glu Thr Ala Val Glu Asp Gly Ile Ile Pro Met	
135 140 145	
aat ccg tgc aaa gtc cgt ggc ggg ggt aat acg aaa aca ggc aaa aag	595
Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr Lys Thr Gly Lys Lys	
150 155 160 165	
gtt gat gtc cca acc gat gcc gag ctt gag gcg atc att ggt gca ctg	643
Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala Ile Ile Gly Ala Leu	
170 175 180	
ccg agt aag tac ttt tgt ttg gct att gtt gct gcc gct ggt gca ctt	691
Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala Ala Ala Gly Ala Leu	
185 190 195	
cga ttc ggt gaa atc gtt gcg ctg cgt acc act gat gtg gat gtt tat	739
Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr Asp Val Asp Val Tyr	
200 205 210	
ttt gat cgc agc gga ttt gta gat tgt gtt cga ata agg att tct cgg	787
Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg Ile Arg Ile Ser Arg	
215 220 225	
agc att agg cac acg aga tac cat ggc cga gtt gaa ggt ccg cct aaa	835
Ser Ile Arg His Thr Arg Tyr His Gly Arg Val Glu Gly Pro Pro Lys	
230 235 240 245	
act gaa gct ggt gtt cgt agc ctc tat atc tat ggc aaa gat gca gca	883
Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr Gly Lys Asp Ala Ala	
250 255 260	
gaa att gcc aag cat gtg gac acg att gat gtg ggt ttg cga cta tgg	931
Glu Ile Ala Lys His Val Asp Thr Ile Asp Val Gly Leu Arg Leu Trp	
265 270 275	
agc tcg atg aga gat cct gat gaa ccc atg ccg tat cac acc ttt aag	979
Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro Tyr His Thr Phe Lys	
280 285 290	
cac aac tgg gat agg gcg cgg gaa agt gtc cac agt aaa gcg acc gtt	1027
His Asn Trp Asp Arg Ala Arg Glu Ser Val His Ser Lys Ala Thr Val	
295 300 305	
cac tcg atg agg cat tat tcg ggt acg aag tat gca cag gtt ggg gcg	1075

His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr Ala Gln Val Gly Ala
 310 315 320 325
 aca ctc aag gag gtg atg gcg cgg ctg ggg cac tca aca cct agt gca 1123
 Thr Leu Lys Glu Val Met Ala Arg Leu Gly His Ser Thr Pro Ser Ala
 330 335 340
 gca ctg cgt tat cag cac tca ggc gag cgt gat gaa gag cta gca aag 1171
 Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp Glu Glu Leu Ala Lys
 345 350 355
 cgc atg gcg cgc taaacactcg gcagtgagtt tca 1206
 Arg Met Ala Arg
 360

<210> 174
 <211> 361
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 174
 Met His Glu Gly Arg Arg Tyr Ser Ala Pro His Thr Phe Gly Thr Lys
 1 5 10 15
 Gly Glu Ala Gln Glu Phe Leu Ala Ser Glu Arg Thr Ala Ile Ile Asn
 20 25 30
 Gly Thr Trp Met Asp Phe Glu Met Arg Glu Arg Phe Glu Gln Ala Gln
 35 40 45
 Arg Glu Ala Glu Glu Arg Met Met Glu Thr Phe Phe Ser Tyr Ala Ser
 50 55 60
 Arg Trp Ile Glu Thr Arg Thr Asn Ala Gln Gly Lys Lys Leu Ser Gln
 65 70 75 80
 Gly Val Lys Asp Asp Tyr Phe Arg Tyr Ile Lys Ser Asp Arg Leu Ser
 85 90 95
 Tyr Trp Ala Asp Tyr Ala Leu Cys Glu Ile Thr Val Ala Asp Val Arg
 100 105 110
 Glu Trp Tyr Ser Asp Thr Ile Gln Asp Gly Lys Leu Thr Ser Met Ala
 115 120 125
 Arg Ser Tyr Ser Met Met Lys Ser Val Met Glu Thr Ala Val Glu Asp
 130 135 140
 Gly Ile Ile Pro Met Asn Pro Cys Lys Val Arg Gly Gly Gly Asn Thr
 145 150 155 160
 Lys Thr Gly Lys Lys Val Asp Val Pro Thr Asp Ala Glu Leu Glu Ala
 165 170 175
 Ile Ile Gly Ala Leu Pro Ser Lys Tyr Phe Cys Leu Ala Ile Val Ala
 180 185 190
 Ala Ala Gly Ala Leu Arg Phe Gly Glu Ile Val Ala Leu Arg Thr Thr
 195 200 205

Asp Val Asp Val Tyr Phe Asp Arg Ser Gly Phe Val Asp Cys Val Arg
 210 215 220
 Ile Arg Ile Ser Arg Ser Ile Arg His Thr Arg Tyr His Gly Arg Val
 225 230 235 240
 Glu Gly Pro Pro Lys Thr Glu Ala Gly Val Arg Ser Leu Tyr Ile Tyr
 245 250 255
 Gly Lys Asp Ala Ala Glu Ile Ala Lys His Val Asp Thr Ile Asp Val
 260 265 270
 Gly Leu Arg Leu Trp Ser Ser Met Arg Asp Pro Asp Glu Pro Met Pro
 275 280 285
 Tyr His Thr Phe Lys His Asn Trp Asp Arg Ala Arg Glu Ser Val His
 290 295 300
 Ser Lys Ala Thr Val His Ser Met Arg His Tyr Ser Gly Thr Lys Tyr
 305 310 315 320
 Ala Gln Val Gly Ala Thr Leu Lys Glu Val Met Ala Arg Leu Gly His
 325 330 335
 Ser Thr Pro Ser Ala Ala Leu Arg Tyr Gln His Ser Gly Glu Arg Asp
 340 345 350
 Glu Glu Leu Ala Lys Arg Met Ala Arg
 355 360

<210> 175
 <211> 1035
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1012)
 <223> RXA01601

<400> 175
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 gtcgaaaagc gcacggcatt gttcctgaca tgaaaaaact atg aag gct cgc gtt 115
 Met Lys Ala Arg Val
 1 5
 tta gcg aaa aca tgg ctg aca cat ttg gcc gtg gag cgt ggc ttg tcg 163
 Leu Ala Lys Thr Trp Leu Thr His Leu Ala Val Glu Arg Gly Leu Ser
 10 15 20
 gca aat acg ctg agt aat tat cgg cgc gat gtg gaa cgc tat tgc gac 211
 Ala Asn Thr Leu Ser Asn Tyr Arg Arg Asp Val Glu Arg Tyr Cys Asp
 25 30 35
 tgg ctc gag gca gct ggg ctg gat gat att cgt gat atc acc acc gcg 259
 Trp Leu Glu Ala Ala Gly Leu Asp Asp Ile Arg Asp Ile Thr Thr Ala
 40 45 50
 cat gtg gaa agt tat gtc aaa gac ctg cgc cgc ggg att gat gga caa 307

His	Val	Glu	Ser	Tyr	Val	Lys	Asp	Leu	Arg	Arg	Gly	Ile	Asp	Gly	Gln		
	55					60					65						
caa	gcg	ttg	tct	gcg	tcc	tcg	gca	ggt	cgc	gcg	ctc	atc	gtc	gcg	cgc	355	
Gln	Ala	Leu	Ser	Ala	Ser	Ser	Ala	Gly	Arg	Ala	Leu	Ile	Val	Ala	Arg	85	
70					75				80								
ggg	ttg	cac	aag	ttt	gca	ttg	atg	gag	ggc	gag	gtg	gct	gcg	gac	gtt	403	
Gly	Leu	His	Lys	Phe	Ala	Leu	Met	Glu	Gly	Glu	Val	Ala	Ala	Asp	Val		
				90					95					100			
gcg	gct	gat	gtg	tcg	cca	cog	gcc	atg	ggc	cgg	cat	tta	cct	gac	acg	451	
Ala	Ala	Asp	Val	Ser	Pro	Pro	Ala	Met	Gly	Arg	His	Leu	Pro	Asp	Thr		
			105					110					115				
ctc	agc	atc	aac	gag	gta	gcc	ctg	ctt	atc	gac	gcg	atc	cca	cat	tca	499	
Leu	Ser	Ile	Asn	Glu	Val	Ala	Leu	Leu	Ile	Asp	Ala	Ile	Pro	His	Ser		
		120					125					130					
gat	atc	gcc	act	ccc	gtt	gat	ctc	cgt	gac	cga	gcg	ctg	gtg	gaa	tta	547	
Asp	Ile	Ala	Thr	Pro	Val	Asp	Leu	Arg	Asp	Arg	Ala	Leu	Val	Glu	Leu		
	135					140					145						
ctt	tat	gga	act	ggc	gcg	cgt	atc	tct	gag	gcg	att	ggg	ctg	gca	gtt	595	
Leu	Tyr	Gly	Thr	Gly	Ala	Arg	Ile	Ser	Glu	Ala	Ile	Gly	Leu	Ala	Val		
150					155					160					165		
gat	gat	gtg	tcg	gaa	atg	cct	gaa	gtt	ctt	cgc	atc	acg	ggc	aaa	ggt	643	
Asp	Asp	Val	Ser	Glu	Met	Pro	Glu	Val	Leu	Arg	Ile	Thr	Gly	Lys	Gly		
				170				175						180			
tcc	aaa	caa	cgg	atc	gtg	cct	ttt	ggt	tcg	atg	gca	caa	caa	gcg	gtc	691	
Ser	Lys	Gln	Arg	Ile	Val	Pro	Phe	Gly	Ser	Met	Ala	Gln	Gln	Ala	Val		
			185					190					195				
cgg	gaa	tat	ttg	gtc	aga	gcc	aga	ccc	gcg	ttg	agt	aag	ggg	aaa	agc	739	
Arg	Glu	Tyr	Leu	Val	Arg	Ala	Arg	Pro	Ala	Leu	Ser	Lys	Gly	Lys	Ser		
		200					205					210					
cat	gcg	ctt	ttt	ctc	aac	caa	cgc	ggc	ggt	cgg	cta	tct	cgg	caa	tct	787	
His	Ala	Leu	Phe	Leu	Asn	Gln	Arg	Gly	Gly	Pro	Leu	Ser	Arg	Gln	Ser		
	215					220					225						
gcg	tgg	gca	gtg	ctg	aag	aaa	acg	gtt	gag	cgc	gca	ggt	tta	gat	aaa	835	
Ala	Trp	Ala	Val	Leu	Lys	Lys	Thr	Val	Glu	Arg	Ala	Gly	Leu	Asp	Lys		
230					235					240					245		
gat	att	tct	ccc	cac	acc	ctg	cgg	cac	agc	ttt	gcc	acc	cat	ctc	ctc	883	
Asp	Ile	Ser	Pro	His	Thr	Leu	Arg	His	Ser	Phe	Ala	Thr	His	Leu	Leu		
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gaa	ggt	ggc	gcc	gat	gtc	cgt	gtg	gtg	cag	gaa	ctc	ctg	ggt	cat	tct	931	
Glu	Gly	Gly	Ala	Asp	Val	Arg	Val	Val	Gln	Glu	Leu	Leu	Gly	His	Ser		
			265				270						275				
tct	gtg	acg	acc	act	cag	att	tac	acg	cac	atc	aca	gcc	gat	agc	ttg	979	
Ser	Val	Thr	Thr	Thr	Gln	Ile	Tyr	Thr	His	Ile	Thr	Ala	Asp	Ser	Leu		
		280				285						290					
cgg	gaa	gtg	tgg	cgc	ggg	gct	cat	cct	cgt	gcg	tgaaagccct	tgcgatttct	1032				
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taa

1035

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<213> Corynebacterium glutamicum

<400> 176

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Glu Arg Tyr Cys Asp Trp Leu Glu Ala Ala Gly Leu Asp Asp Ile Arg
 35 40 45

Asp Ile Thr Thr Ala His Val Glu Ser Tyr Val Lys Asp Leu Arg Arg
 50 55 60

Gly Ile Asp Gly Gln Gln Ala Leu Ser Ala Ser Ser Ala Gly Arg Ala
 65 70 75 80

Leu Ile Val Ala Arg Gly Leu His Lys Phe Ala Leu Met Glu Gly Glu
 85 90 95

Val Ala Ala Asp Val Ala Ala Asp Val Ser Pro Pro Ala Met Gly Arg
 100 105 110

His Leu Pro Asp Thr Leu Ser Ile Asn Glu Val Ala Leu Leu Ile Asp
 115 120 125

Ala Ile Pro His Ser Asp Ile Ala Thr Pro Val Asp Leu Arg Asp Arg
 130 135 140

Ala Leu Val Glu Leu Leu Tyr Gly Thr Gly Ala Arg Ile Ser Glu Ala
 145 150 155 160

Ile Gly Leu Ala Val Asp Asp Val Ser Glu Met Pro Glu Val Leu Arg
 165 170 175

Ile Thr Gly Lys Gly Ser Lys Gln Arg Ile Val Pro Phe Gly Ser Met
 180 185 190

Ala Gln Gln Ala Val Arg Glu Tyr Leu Val Arg Ala Arg Pro Ala Leu
 195 200 205

Ser Lys Gly Lys Ser His Ala Leu Phe Leu Asn Gln Arg Gly Gly Pro
 210 215 220

Leu Ser Arg Gln Ser Ala Trp Ala Val Leu Lys Lys Thr Val Glu Arg
 225 230 235 240

Ala Gly Leu Asp Lys Asp Ile Ser Pro His Thr Leu Arg His Ser Phe
 245 250 255

Ala Thr His Leu Leu Glu Gly Gly Ala Asp Val Arg Val Val Gln Glu
 260 265 270

Leu Leu Gly His Ser Ser Val Thr Thr Thr Gln Ile Tyr Thr His Ile
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Thr Ala Asp Ser Leu Arg Glu Val Trp Arg Gly Ala His Pro Arg Ala
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<223> RXA01228

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Val His Phe Ile Lys
1 5

gaa aac ctg atc ttc tcg gcg gaa tcc aat gct ttg cgg gcc cag ctc 163
Glu Asn Leu Ile Phe Ser Ala Glu Ser Asn Ala Leu Arg Ala Gln Leu
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atg ctg agc att ctc ggc tcc ttc gct gag ttc gaa cgc tcc atc atc 211
Met Leu Ser Ile Leu Gly Ser Phe Ala Glu Phe Glu Arg Ser Ile Ile
25 30 35

cgg gag cgc caa gcc gag ggg atc gcc tgg cga aaa agg ccg gca agt 259
Arg Glu Arg Gln Ala Glu Gly Ile Ala Trp Arg Lys Arg Pro Ala Ser
40 45 50

aca agg gcc gca aac gcg ccc tca ccc cgg acg acg tcg aga aag ccc 307
Thr Arg Ala Ala Asn Ala Pro Ser Pro Arg Thr Thr Ser Arg Lys Pro
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Gly Asn Gly
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Met Lys Ser Thr Gly 5															
aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc 163															
Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr 20															
atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211															
Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp 35															
gca ctc gac tac acc tcc acc tgc cca gaa tgc tcc caa cct ggg gtg 259															
Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val 40															
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Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly 55															
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Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg Tyr Arg Cys Thr Asn 70															
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Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp 90															
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His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg 105															
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Leu Ala Ile Asp Arg Met Ser Val His Ala Thr Ala Lys Ala Leu Gly 120															
cta ggg tgg gat tta acc tgc caa cta gcc ctc gat atg tgc cgt gag 547															
Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu Asp Met Cys Arg Glu 135															
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Val	Asp	Glu	His	Lys 170	Trp	Ser	His	Asn	Arg 175	Ala	Lys	His	Gly	Asp	Gly 180	
ttt	gtc	acc	gtg	att	gtc	gat	atg	acc	ggg	cat	cgg	tat	gac	tca	cgg	691
Phe	Val	Thr	Val	Ile 185	Val	Asp	Met	Thr 190	Gly	His	Arg	Tyr	Asp	Ser	Arg 195	
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Cys	Pro	Ala 200	Arg	Leu	Leu	Asp	Val 205	Val	Pro	Gly	Arg	Ser 210	Ala	Asp	Ala	
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Leu	Arg	Ser	Trp	Leu	Gly 215	Ser	Arg 220	Gly	Glu	Gln	Phe	Arg	Asn	Gln	Ile 225	
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Glu	Leu	Ile	Pro	Ser 250	Ala	Arg	Arg	Val 255	Met	Asp	Pro	Phe	His	Val 260	Val	
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Arg	Leu	Ala	Gly	Asp 265	Lys	Leu	Thr 270	Ala	Cys	Arg	Gln	Arg	Leu	Gln 275	Arg	
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Glu	Lys	Tyr 280	Gln	Arg	Arg	Gly	Leu 285	Ser	Gln	Asp	Pro	Leu	Tyr	Lys	Asn 290	
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Arg	Lys	Thr	Leu	Leu	Thr 295	Thr	His 300	Lys	Trp	Leu	Ser 305	Pro	Arg	Gln	Gln	
gaa	agc	ttg	gag	cag	ttg	tgg	gcg	tat	gac	aaa	gac	tac	ggg	gcg	tta	1075
Glu	Ser	Leu	Glu	Gln	Leu 310	Trp	Ala 315	Tyr	Asp	Lys 320	Asp	Tyr	Gly	Ala	Leu 325	
aag	ctt	gcg	tgg	ctt	gcg	tat	cag	gcg	att	att	gat	tgt	tat	cag	atg	1123
Lys	Leu	Ala	Trp	Leu 330	Ala	Tyr	Gln	Ala	Ile 335	Ile	Asp	Cys	Tyr	Gln 340	Met	
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Gly	Asn	Lys	Arg 345	Glu	Ala	Lys	Lys 350	Lys	Met	Arg	Thr	Ile 355	Ile	Asp	Gln	
ctt	cgg	gtg	ttg	aag	ggg	ccg	aat	aag	gaa	ctc	gcg	cag	ttg	ggt	cgt	1219
Leu	Arg	Val 360	Leu	Lys	Gly	Pro	Asn 365	Lys	Glu	Leu	Ala	Gln 370	Leu	Gly	Arg	
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Ser	Leu	Phe 375	Lys	Arg	Leu	Gly	Asp 380	Val	Leu	Ala	Tyr 385	Phe	Asp	Val	Gly	
gtc	tcc	aac	ggt	ccg	gtc	gaa	gcg	atc	aac	gga	cgg	ttg	gag	cat	ttg	1315
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Leu	Ile	Glu 35	Ala	Asp	Ala	Leu	Asp 40	Tyr	Thr	Ser	Thr	Cys 45	Pro	Glu	Cys
Ser 50	Gln	Pro	Gly	Val	Phe	Arg 55	His	His	Thr	His	Arg 60	Met	Leu	Ile	Asp
Leu 65	Pro	Ile	Val	Gly	Phe 70	Pro	Thr	Lys	Leu	Phe 75	Ile	Arg	Leu	Pro	Arg 80
Tyr	Arg	Cys	Thr	Asn 85	Pro	Thr	Cys	Lys	Gln 90	Lys	Tyr	Phe	Gln	Ala 95	Glu
Leu	Ser	Cys	Ala 100	Asp	His	Gly	Lys	Lys 105	Val	Thr	His	Arg	Val 110	Thr	Arg
Trp	Ile	Leu 115	Gln	Arg	Leu	Ala	Ile 120	Asp	Arg	Met	Ser	Val 125	His	Ala	Thr
Ala	Lys 130	Ala	Leu	Gly	Leu	Gly 135	Trp	Asp	Leu	Thr	Cys 140	Gln	Leu	Ala	Leu
Asp 145	Met	Cys	Arg	Glu	Leu 150	Val	Tyr	Asn	Asp	Pro 155	His	His	Leu	Asp	Gly 160
Val	Tyr	Val	Ile	Gly 165	Val	Asp	Glu	His	Lys 170	Trp	Ser	His	Asn 175	Arg	Ala
Lys	His	Gly	Asp 180	Gly	Phe	Val	Thr	Val 185	Ile	Val	Asp	Met	Thr 190	Gly	His
Arg	Tyr	Asp 195	Ser	Arg	Cys	Pro	Ala 200	Arg	Leu	Leu	Asp	Val 205	Val	Pro	Gly
Arg 210	Ser	Ala	Asp	Ala	Leu	Arg 215	Ser	Trp	Leu	Gly	Ser 220	Arg	Gly	Glu	Gln

Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr
 225 230 235 240
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp
 245 250 255
 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg
 260 265 270
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp
 275 280 285
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu
 290 295 300
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys
 305 310 315 320
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile
 325 330 335
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg
 340 345 350
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu
 355 360 365
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala
 370 375 380
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly
 385 390 395 400
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn
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 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys
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 Ile Asn Ala Leu
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 <222> (101)..(466)
 <223> RXN01969

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 Leu Trp Ala Tyr Asp
 1 5
 aaa gcc tac ggg gcg tta aag ctt gcg tgg ctt gcg tat cag gcg att 163

Lys Ala Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile
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 att gat tgt tat cag atg ggt aat aag cgt gaa gcg aag aag aaa atg 211
 Ile Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met
 25 30 35
 cgg acc att att gat cag ctt cgg gtg ttg aag ggg ccg aat aag gaa 259
 Arg Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu
 40 45 50
 ctc gcg cag ttg ggt cgt agt ttg ttt aaa cga ctt ggt gat gtg ttg 307
 Leu Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu
 55 60 65
 gcg tat ttc gat gtt ggt gtc tcc aac ggt ccg gtc gaa gcg atc aac 355
 Ala Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn
 70 75 80 85
 gga cgg ttg gag cat ttg cgt ggg att gct cta ggt ttc cgt aat ttg 403
 Gly Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu
 90 95 100
 aac cac tac att ctg cgg tgc ctt atc cat tca ggg cag ttg gtc cat 451
 Asn His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His
 105 110 115
 aag atc aat gca ctc taaaacagga agagccactt aag 489
 Lys Ile Asn Ala Leu
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<211> 122

<212> PRT

<213> *Corynebacterium glutamicum*

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 35 40 45
 Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg
 50 55 60
 Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly Val Ser Asn Gly Pro
 65 70 75 80
 Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Ala Leu
 85 90 95
 Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg Cys Leu Ile His Ser
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 Gly Gln Leu Val His Lys Ile Asn Ala Leu
 115 120

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Met Lys Ser Thr Gly 1 5															
aac atc atc gct gac acc atc tgc cgc act gcg gaa cta gga ctc acc 163															
Asn Ile Ile Ala Asp Thr Ile Cys Arg Thr Ala Glu Leu Gly Leu Thr 10 15 20															
atc acc ggc gct tcc gat gca ggt gat tac acc ctg atc gaa gca gac 211															
Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr Leu Ile Glu Ala Asp 25 30 35															
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Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys Ser Gln Pro Gly Val 40 45 50															
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Phe Arg His His Thr His Arg Met Leu Ile Asp Leu Pro Ile Val Gly 55 60 65															
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Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu Leu Ser Cys Ala Asp 90 95 100															
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His Gly Lys Lys Val Thr His Arg Val Thr Arg Trp Ile Leu Gln Arg 105 110 115															
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Leu Val Tyr Asn Asp Pro His His Leu Asp Gly Val Tyr Val Ile Gly 150 155 160 165															
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Val Asp Glu His Lys Trp Ser His Asn Arg Ala Lys His Gly Asp Gly															

170										175					180					
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Cys	Pro	Ala	Arg	Leu	Leu	Asp	Val	Val	Pro	Gly	Arg	Ser	Ala	Asp	Ala					
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cgg	atc	gtg	tcc	atg	gat	gga	ttc	caa	ggc	tac	gcc	aca	gca	agt	aaa	835				
Arg	Ile	Val	Ser	Met	Asp	Gly	Phe	Gln	Gly	Tyr	Ala	Thr	Ala	Ser	Lys					
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cgg	ctt	gct	ggg	gac	aag	ctc	acc	gcc	tgc	cgg	caa	cgc	ctc	cag	cgg	931				
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			265					270					275							
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cgg	aag	acc	ttg	ttg	acc	acg	cac	aag	tgg	ttg	agt	cct	cgt	cag	caa	1027				
Arg	Lys	Thr	Leu	Leu	Thr	Thr	His	Lys	Trp	Leu	Ser	Pro	Arg	Gln	Gln					
	295					300					305									
gaa	agc	ttg	gag	cag	ttg	tgg	gcg	tat	gac	aaa	gac	tac	ggg	gcg	tta	1075				
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Lys	Leu	Ala	Trp	Leu	Ala	Tyr	Gln	Ala	Ile	Ile	Asp	Cys	Tyr	Gln	Met					
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Gly	Asn	Lys	Arg	Glu	Ala	Lys	Lys	Lys	Met	Arg	Thr	Ile	Ile	Asp	Gln					
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agt	ttg	ttt	aaa	cga	ctt	ggg	gat	gtg	ttg	gcg	tat	ttc	gat	gtt	ggg	1267				
Ser	Leu	Phe	Lys	Arg	Leu	Gly	Asp	Val	Leu	Ala	Tyr	Phe	Asp	Val	Gly					
	375					380					385									
gtc	tcc	aac	ggg	ccg	gtc	gaa	gcg	atc	aac	gga	cgg	ttg	gag	cat	ttg	1315				
Val	Ser	Asn	Gly	Pro	Val	Glu	Ala	Ile	Asn	Gly	Arg	Leu	Glu	His	Leu					
390					395					400					405					
cgt	ggg	att	gct	cta	ggg	ttc	cgt	aat	ttg	aac	cac	tac	att	ctg	cgg	1363				
Arg	Gly	Ile	Ala	Leu	Gly	Phe	Arg	Asn	Leu	Asn	His	Tyr	Ile	Leu	Arg					
				410					415					420						

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taaaacagga agagcccgt aac 1431

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<211> 436

<212> PRT

<213> Corynebacterium glutamicum

<400> 184

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Glu Leu Gly Leu Thr Ile Thr Gly Ala Ser Asp Ala Gly Asp Tyr Thr
 20 25 30

Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys
 35 40 45

Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp
 50 55 60

Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg
 65 70 75 80

Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu
 85 90 95

Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg
 100 105 110

Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr
 115 120 125

Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu
 130 135 140

Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly
 145 150 155 160

Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala
 165 170 175

Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His
 180 185 190

Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly
 195 200 205

Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln
 210 215 220

Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr
 225 230 235 240

Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp
 245 250 255

Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg
 260 265 270
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp
 275 280 285
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu
 290 295 300
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys
 305 310 315 320
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile
 325 330 335
 Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg
 340 345 350
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu
 355 360 365
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala
 370 375 380
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly
 385 390 395 400
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn
 405 410 415
 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys
 420 425 430
 Ile Asn Ala Leu
 435

<210> 185
 <211> 900
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(877)
 <223> RXN01541

<400> 185
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 Met Thr Thr Pro His
 1 5
 tcc cac cgc gca cca cgt ctg gca tcc acg gtc att att gcc cgc gag 163
 Ser His Arg Ala Pro Arg Leu Ala Ser Thr Val Ile Ile Ala Arg Glu
 10 15 20
 tct gct gac tca ggt acc tta gaa ttc ttt atc cag cag cga caa tcc 211
 Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln Arg Gln Ser

25					30					35						
act	atg	gct	tat	gca	gca	aac	gct	gtt	gtt	ttc	cca	ggc	ggc	ggt	gtt	259
Thr	Met	Ala	Tyr	Ala	Ala	Asn	Ala	Val	Val	Phe	Pro	Gly	Gly	Gly	Val	
		40					45					50				
gag	gac	agc	gat	tat	ccc	ttt	atg	ctc	ccc	cac	cgc	gat	cag	cac	atg	307
Glu	Asp	Ser	Asp	Tyr	Pro	Phe	Met	Leu	Pro	His	Arg	Asp	Gln	His	Met	
		55					60					65				
tcg	cct	gaa	cac	atc	aag	cat	cat	gcc	agc	cga	ctc	cac	atg	gac	tca	355
Ser	Pro	Glu	His	Ile	Lys	His	His	Ala	Ser	Arg	Leu	His	Met	Asp	Ser	
		70					75					80			85	
gaa	act	atg	gca	gct	cat	att	tcc	gct	gca	cgc	cgg	gaa	gta	tgg	gaa	403
Glu	Thr	Met	Ala	Ala	His	Ile	Ser	Ala	Ala	Arg	Arg	Glu	Val	Trp	Glu	
				90					95					100		
gaa	aca	ggc	gtt	gat	ctc	ggt	aat	tac	aac	cat	gaa	ctc	atc	ccg	atc	451
Glu	Thr	Gly	Val	Asp	Leu	Gly	Asn	Tyr	Asn	His	Glu	Leu	Ile	Pro	Ile	
			105					110					115			
gac	cgc	tgg	atc	aca	cct	gat	att	cct	gct	ttt	agg	cgc	cgt	tac	gac	499
Asp	Arg	Trp	Ile	Thr	Pro	Asp	Ile	Pro	Ala	Phe	Arg	Arg	Arg	Tyr	Asp	
			120				125					130				
acc	gcc	acc	ttt	gta	ctt	att	cta	agc	aaa	gac	agc	act	aac	gca	gct	547
Thr	Ala	Thr	Phe	Val	Leu	Ile	Leu	Ser	Lys	Asp	Ser	Thr	Asn	Ala	Ala	
			135				140					145				
ctg	cag	cac	cag	cat	caa	acc	acc	gag	gcc	acc	cat	tct	tat	tgg	gca	595
Leu	Gln	His	Gln	His	Gln	Thr	Thr	Glu	Ala	Thr	His	Ser	Tyr	Trp	Ala	
									160						165	
act	gca	gaa	gaa	ctg	ctc	act	caa	tgg	tca	aca	ggt	cat	ctc	aac	ctg	643
Thr	Ala	Glu	Glu	Leu	Leu	Thr	Gln	Trp	Ser	Thr	Gly	His	Leu	Asn	Leu	
				170					175					180		
ttg	tta	cca	acg	tgg	tgg	cat	atc	aac	cag	ctc	aat	cac	ctc	cac	acg	691
Leu	Leu	Pro	Thr	Trp	Trp	His	Ile	Asn	Gln	Leu	Asn	His	Leu	His	Thr	
			185					190					195			
cta	aac	cag	ctg	tat	agc	ttt	gcc	cag	cgt	acc	cat	aat	ccg	cag	cac	739
Leu	Asn	Gln	Leu	Tyr	Ser	Phe	Ala	Gln	Arg	Thr	His	Asn	Pro	Gln	His	
			200				205					210				
act	cca	ccc	aca	gtg	ttt	gct	aac	tgg	act	gca	ccg	gct	gat	gag	gcc	787
Thr	Pro	Pro	Thr	Val	Phe	Ala	Asn	Trp	Thr	Ala	Pro	Ala	Asp	Glu	Ala	
			215				220					225				
gcc	atg	cag	cac	tat	ggg	ttc	cct	gat	ccc	gat	gcg	tac	ttt	gac	cat	835
Ala	Met	Gln	His	Tyr	Gly	Phe	Pro	Asp	Pro	Asp	Ala	Tyr	Phe	Asp	His	
							235					240			245	
gcc	act	atc	gca	gga	aaa	cac	cac	aca	ctc	atc	aca	aga	aag			877
Ala	Thr	Ile	Ala	Gly	Lys	His	His	Thr	Leu	Ile	Thr	Arg	Lys			
				250					255							
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<210> 186
 <211> 259
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 186

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Ile	Ile	Ala	Arg	Glu	Ser	Ala	Asp	Ser	Gly	Thr	Leu	Glu	Phe	Phe	Ile
			20					25					30		
Gln	Gln	Arg	Gln	Ser	Thr	Met	Ala	Tyr	Ala	Ala	Asn	Ala	Val	Val	Phe
		35					40					45			
Pro	Gly	Gly	Gly	Val	Glu	Asp	Ser	Asp	Tyr	Pro	Phe	Met	Leu	Pro	His
	50					55					60				
Arg	Asp	Gln	His	Met	Ser	Pro	Glu	His	Ile	Lys	His	His	Ala	Ser	Arg
65					70					75					80
Leu	His	Met	Asp	Ser	Glu	Thr	Met	Ala	Ala	His	Ile	Ser	Ala	Ala	Arg
				85					90						95
Arg	Glu	Val	Trp	Glu	Glu	Thr	Gly	Val	Asp	Leu	Gly	Asn	Tyr	Asn	His
			100					105					110		
Glu	Leu	Ile	Pro	Ile	Asp	Arg	Trp	Ile	Thr	Pro	Asp	Ile	Pro	Ala	Phe
		115					120					125			
Arg	Arg	Arg	Tyr	Asp	Thr	Ala	Thr	Phe	Val	Leu	Ile	Leu	Ser	Lys	Asp
		130				135					140				
Ser	Thr	Asn	Ala	Ala	Leu	Gln	His	Gln	His	Gln	Thr	Thr	Glu	Ala	Thr
145					150					155					160
His	Ser	Tyr	Trp	Ala	Thr	Ala	Glu	Glu	Leu	Leu	Thr	Gln	Trp	Ser	Thr
				165					170					175	
Gly	His	Leu	Asn	Leu	Leu	Leu	Pro	Thr	Trp	Trp	His	Ile	Asn	Gln	Leu
			180					185					190		
Asn	His	Leu	His	Thr	Leu	Asn	Gln	Leu	Tyr	Ser	Phe	Ala	Gln	Arg	Thr
		195					200					205			
His	Asn	Pro	Gln	His	Thr	Pro	Pro	Thr	Val	Phe	Ala	Asn	Trp	Thr	Ala
		210				215					220				
Pro	Ala	Asp	Glu	Ala	Ala	Met	Gln	His	Tyr	Gly	Phe	Pro	Asp	Pro	Asp
225					230					235					240
Ala	Tyr	Phe	Asp	His	Ala	Thr	Ile	Ala	Gly	Lys	His	His	Thr	Leu	Ile
				245					250					255	

Thr Arg Lys

<210> 187
 <211> 794
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(771)

<223> FRXA01541

<400> 187

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gcc cgc gag tct gct gac tca ggt acc tta gaa ttc ttt atc cag cag	96
Ala Arg Glu Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln	
20 25 30	
cga caa tcc act atg gct tat gca gca aac gct gtt gtt ttc cca ggc	144
Arg Gln Ser Thr Met Ala Tyr Ala Ala Asn Ala Val Val Phe Pro Gly	
35 40 45	
ggc ggt gtt gag gac agc gat tat ccc ttt atg ctc ccc cac cgc gat	192
Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp	
50 55 60	
cag cac atg tcg cct gaa cac atc aag cat cat gcc agc cga ctc cac	240
Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His	
65 70 75 80	
atg gac tca gaa act atg gca gct cat att tcc gct gca cgc cgg gaa	288
Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu	
85 90 95	
gta tgg gaa gaa aca ggc gtt gat ctc ggt aat tac aac cat gaa ctc	336
Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His Glu Leu	
100 105 110	
atc ccg atc gac cgc tgg atc aca cct gat att cct gct ttt agg cgc	384
Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg	
115 120 125	
cgt tac gac acc gcc acc ttt gta ctt att cta agc aaa gac agc act	432
Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp Ser Thr	
130 135 140	
aac gca gct ctg cag cac cag cat caa acc acc gag gcc acc cat tct	480
Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr His Ser	
145 150 155 160	
tat tgg gca act gca gaa gaa ctg ctc act caa tgg tca aca ggt cat	528
Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His	
165 170 175	
ctc aac ctg ttg tta cca acg tgg tgg cat atc aac cag ctc aat cac	576
Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu Asn His	
180 185 190	
ctc cac acg cta aac cag ctg tat agc ttt gcc cag cgt acc cat aat	624
Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr His Asn	
195 200 205	
ccg cag cac act cca ccc aca gtg ttt gct aac tgg act gca ccg gct	672

Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala
 210 215 220

gat gag gcc gcc atg cag cac tat ggg ttc cct gat ccc gat gcg tac 720
 Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr
 225 230 235 240

ttt gac cat gcc act atc gca gga aaa cac cac aca ctc atc aca aga 768
 Phe Asp His Ala Thr Ile Ala Gly Lys His His Thr Leu Ile Thr Arg
 245 250 255

aag taggtctcac catgactttt gca 794
 Lys

<210> 188
 <211> 257
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 188
 Ile Phe Asn Ser His Arg Ala Pro Arg Leu Ala Ser Thr Val Ile Ile
 1 5 10 15

Ala Arg Glu Ser Ala Asp Ser Gly Thr Leu Glu Phe Phe Ile Gln Gln
 20 25 30

Arg Gln Ser Thr Met Ala Tyr Ala Ala Asn Ala Val Val Phe Pro Gly
 35 40 45

Gly Gly Val Glu Asp Ser Asp Tyr Pro Phe Met Leu Pro His Arg Asp
 50 55 60

Gln His Met Ser Pro Glu His Ile Lys His His Ala Ser Arg Leu His
 65 70 75 80

Met Asp Ser Glu Thr Met Ala Ala His Ile Ser Ala Ala Arg Arg Glu
 85 90 95

Val Trp Glu Glu Thr Gly Val Asp Leu Gly Asn Tyr Asn His Glu Leu
 100 105 110

Ile Pro Ile Asp Arg Trp Ile Thr Pro Asp Ile Pro Ala Phe Arg Arg
 115 120 125

Arg Tyr Asp Thr Ala Thr Phe Val Leu Ile Leu Ser Lys Asp Ser Thr
 130 135 140

Asn Ala Ala Leu Gln His Gln His Gln Thr Thr Glu Ala Thr His Ser
 145 150 155 160

Tyr Trp Ala Thr Ala Glu Glu Leu Leu Thr Gln Trp Ser Thr Gly His
 165 170 175

Leu Asn Leu Leu Leu Pro Thr Trp Trp His Ile Asn Gln Leu Asn His
 180 185 190

Leu His Thr Leu Asn Gln Leu Tyr Ser Phe Ala Gln Arg Thr His Asn
 195 200 205

Pro Gln His Thr Pro Pro Thr Val Phe Ala Asn Trp Thr Ala Pro Ala
210 215 220

Asp Glu Ala Ala Met Gln His Tyr Gly Phe Pro Asp Pro Asp Ala Tyr
225 230 235 240

Phe Asp His Ala Thr Ile Ala Gly Lys His His Thr Leu Ile Thr Arg
245 250 255

Lys

<210> 189

<211> 1059

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1036)

<223> RXA02590

<400> 189

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ggtcttacct ccacctggcc cctcgtgggc tggttccctc atg ggc atc tca ttg 115
Met Gly Ile Ser Leu
1 5

ttg tca tca ctg ttg aaa atc cat ggt ttt cca gtc gtc gca gat ttc 163
Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro Val Val Ala Asp Phe
10 15 20

ttc ttc gcg tta gct gtt gtg gtg gca att gtc att att ggc ggt tgg 211
Phe Phe Ala Leu Ala Val Val Val Ala Ile Val Ile Ile Gly Gly Trp
25 30 35

cta atc tac cgc tct cct tca ttc aaa act gaa gtc atg ccg gca tgg 259
Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu Val Met Pro Ala Trp
40 45 50

gca atg ctg tcc atg ggt ttg atc gca ttg gga act gca agc ccc gta 307
Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly Thr Ala Ser Pro Val
55 60 65

gtt ttg ggt gat gat ctg tgg gga ttt atg ttt gtg tgc tgg tct att 355
Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe Val Cys Trp Ser Ile
70 75 80 85

ggc aca gcc gtg gga ctt gtt gcc tat tcc tta tat ata acg gcc att 403
Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu Tyr Ile Thr Ala Ile
90 95 100

ttg cga tct aag gcg ggc aca cca act ttt gcg tgg ggt ctt cct ctt 451
Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala Trp Gly Leu Pro Leu
105 110 115

gtc acg ccg atg gtt gct tcc acc tcg gca gca caa ctc cat gag cac 499
Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala Gln Leu His Glu His
120 125 130

ttt gaa ctt ccg gcg atg ctg tgg gtt tct ttc ggg ctc ttc ctt tta 547
 Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe Gly Leu Phe Leu Leu
 135 140 145

act ttg gcg tct gca cca gca gtt ttt acc cga gtg tat ttc tac tat 595
 Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg Val Tyr Phe Tyr Tyr
 150 155 160 165

ttc ggc ccc aag gcg cag ggc atc cca ctg atg gca aca cca aca tca 643
 Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met Ala Thr Pro Thr Ser
 170 175 180

tgg att cct ttg ggt atg gtg ggc caa tcc act gca gca gct cag ctc 691
 Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr Ala Ala Ala Gln Leu
 185 190 195

atc ggt gcg tcc ttt gga tcc aag aca gca atc aca atg ggc att att 739
 Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile Thr Met Gly Ile Ile
 200 205 210

tac ggc atc atc atg gga att ttt acg att cct ctg gga gcc atc gct 787
 Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro Leu Gly Ala Ile Ala
 215 220 225

cac ttt gtg ttc tac aga gct gtt ttc aaa ggg gcg aca tac agc ccc 835
 His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly Ala Thr Tyr Ser Pro
 230 235 240 245

aca tgg tgg gcc agt acc ttc cca gtt ggc act ttg agt ttg ggt gcg 883
 Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr Leu Ser Leu Gly Ala
 250 255 260

cat ttt tta tca cag agc acc gga gtg gag tgg ttt aac tac ttc agc 931
 His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp Phe Asn Tyr Phe Ser
 265 270 275

ctg tac ttg att gct tta atg ctc ttt cat gtc atc gtg tcc acc atc 979
 Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val Ile Val Ser Thr Ile
 280 285 290

gcc ggt acg att gca gta atg aga aga atc gtc gga aag ctt aaa tct 1027
 Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val Gly Lys Leu Lys Ser
 295 300 305

caa ctg gcc taaattgcag cgagaggtct aaa 1059
 Gln Leu Ala
 310

<210> 190

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 190

Met Gly Ile Ser Leu Leu Ser Ser Leu Leu Lys Ile His Gly Phe Pro
 1 5 10 15

Val Val Ala Asp Phe Phe Phe Ala Leu Ala Val Val Val Ala Ile Val
 20 25 30

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Ile Ile Gly Gly Trp Leu Ile Tyr Arg Ser Pro Ser Phe Lys Thr Glu
      35                      40                      45

Val Met Pro Ala Trp Ala Met Leu Ser Met Gly Leu Ile Ala Leu Gly
      50                      55                      60

Thr Ala Ser Pro Val Val Leu Gly Asp Asp Leu Trp Gly Phe Met Phe
      65                      70                      75                      80

Val Cys Trp Ser Ile Gly Thr Ala Val Gly Leu Val Ala Tyr Ser Leu
      85                      90                      95

Tyr Ile Thr Ala Ile Leu Arg Ser Lys Ala Gly Thr Pro Thr Phe Ala
      100                     105                     110

Trp Gly Leu Pro Leu Val Thr Pro Met Val Ala Ser Thr Ser Ala Ala
      115                     120                     125

Gln Leu His Glu His Phe Glu Leu Pro Ala Met Leu Trp Val Ser Phe
      130                     135                     140

Gly Leu Phe Leu Leu Thr Leu Ala Ser Ala Pro Ala Val Phe Thr Arg
      145                     150                     155                     160

Val Tyr Phe Tyr Tyr Phe Gly Pro Lys Ala Gln Gly Ile Pro Leu Met
      165                     170                     175

Ala Thr Pro Thr Ser Trp Ile Pro Leu Gly Met Val Gly Gln Ser Thr
      180                     185                     190

Ala Ala Ala Gln Leu Ile Gly Ala Ser Phe Gly Ser Lys Thr Ala Ile
      195                     200                     205

Thr Met Gly Ile Ile Tyr Gly Ile Ile Met Gly Ile Phe Thr Ile Pro
      210                     215                     220

Leu Gly Ala Ile Ala His Phe Val Phe Tyr Arg Ala Val Phe Lys Gly
      225                     230                     235                     240

Ala Thr Tyr Ser Pro Thr Trp Trp Ala Ser Thr Phe Pro Val Gly Thr
      245                     250                     255

Leu Ser Leu Gly Ala His Phe Leu Ser Gln Ser Thr Gly Val Glu Trp
      260                     265                     270

Phe Asn Tyr Phe Ser Leu Tyr Leu Ile Ala Leu Met Leu Phe His Val
      275                     280                     285

Ile Val Ser Thr Ile Ala Gly Thr Ile Ala Val Met Arg Arg Ile Val
      290                     295                     300

Gly Lys Leu Lys Ser Gln Leu Ala
      305                     310

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<210> 191

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXA00016

<400> 191

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                               Val Ile Arg Phe Arg
                               1           5

ttc gtt gat gac gct cga aag acc tac tcg gtt aag cgg ata tgt gac 163
Phe Val Asp Asp Ala Arg Lys Thr Tyr Ser Val Lys Arg Ile Cys Asp
                        10                15                20

gtg ttg aag ctc aat cgt tcc tca tat tac aaa tgg aaa agc acc gcc 211
Val Leu Lys Leu Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Ser Thr Ala
                        25                30                35

ttc acg cgt gaa aaa cgc ctg ctc agc gac gct att ctt ggg gtc cag 259
Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala Ile Leu Gly Val Gln
                        40                45                50

gtc aag act gta ttc acc act cac agt ggc tgt tat ggg gcc aaa cga 307
Val Lys Thr Val Phe Thr Thr His Ser Gly Cys Tyr Gly Ala Lys Arg
                        55                60                65

atc gcg gct gaa ctc aaa gac cag atc ggc cat gac ctt gcg aac cac 355
Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His Asp Leu Ala Asn His
                        70                75                80                85

aag cgg gtt gcc cgg atc atg cga tcg ttg aag ctg ttc gga tac aca 403
Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys Leu Phe Gly Tyr Thr
                        90                95                100

aag aaa cgc aag gtc acc acc acc gtg ccg gac aaa acc aag aca gtg 451
Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp Lys Thr Lys Thr Val
                        105                110                115

ttc cct gac ctt gtc ggc cgg aag ttc acc gct gac aag ccg aac cag 499
Phe Pro Asp Leu Val Gly Arg Lys Phe Thr Ala Asp Lys Pro Asn Gln
                        120                125                130

ctc tat gtc ggg gat atc acc tat ctg cca att cag gat ggg tcg aat 547
Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Gln Asp Gly Ser Asn
                        135                140                145

atg tac ctg gcc acg gtc att gac tgt tac tcc cgc agg ttg gtg ggc 595
Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly
                        150                155                160                165

ttt tct atc gca gat cac atg cgc acg agc ttg gtc cag gac gcg ctg 643
Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Asp Ala Leu
                        170                175                180

ctc atg gct aaa gac cag cgt gga aac ctc aaa ggt gcg att ttt cac 691
Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys Gly Ala Ile Phe His
                        185                190                195

tcc gac cac ggc agc gtt tac acg tct cat gcg ttt cag gag acg tgt 739

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Ser Asp His Gly Ser Val Tyr Thr Ser His Ala Phe Gln Glu Thr Cys
 200 205 210
 aag aaa cta ggg atc agg cag tcg atg gga tca att ggc acc agt gct 787
 Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser Ile Gly Thr Ser Ala
 215 220 225
 gac aac gct ttg gcg gag tct ttc aat gcc gcg atg aag cgg gaa gtc 835
 Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala Met Lys Arg Glu Val
 230 235 240 245
 ctg cag gat tcc aag acc ttt gaa aat caa ttg tgc tgt cgc cgg gac 883
 Leu Gln Asp Ser Lys Thr Phe Glu Asn Gln Leu Cys Cys Arg Arg Asp
 250 255 260
 gtc ttc cgc tgg tgt acc cgt tac aac acg gtt cgc cgg cat tcc tgg 931
 Val Phe Arg Trp Cys Thr Arg Tyr Asn Thr Val Arg Arg His Ser Trp
 265 270 275
 tgt aga tat ctg gct ccg gtc gtg ttt gag gag cgc ggt cct gct atc 979
 Cys Arg Tyr Leu Ala Pro Val Val Phe Glu Glu Arg Gly Pro Ala Ile
 280 285 290
 ctg aga tct gct tcc tgatcaaatc ctccgtgtcc acc 1017
 Leu Arg Ser Ala Ser
 295

<210> 192

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Val Ile Arg Phe Arg Phe Val Asp Asp Ala Arg Lys Thr Tyr Ser Val
 1 5 10 15
 Lys Arg Ile Cys Asp Val Leu Lys Leu Asn Arg Ser Ser Tyr Tyr Lys
 20 25 30
 Trp Lys Ser Thr Ala Phe Thr Arg Glu Lys Arg Leu Leu Ser Asp Ala
 35 40 45
 Ile Leu Gly Val Gln Val Lys Thr Val Phe Thr Thr His Ser Gly Cys
 50 55 60
 Tyr Gly Ala Lys Arg Ile Ala Ala Glu Leu Lys Asp Gln Ile Gly His
 65 70 75 80
 Asp Leu Ala Asn His Lys Arg Val Ala Arg Ile Met Arg Ser Leu Lys
 85 90 95
 Leu Phe Gly Tyr Thr Lys Lys Arg Lys Val Thr Thr Thr Val Pro Asp
 100 105 110
 Lys Thr Lys Thr Val Phe Pro Asp Leu Val Gly Arg Lys Phe Thr Ala
 115 120 125
 Asp Lys Pro Asn Gln Leu Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile
 130 135 140

Gln Asp Gly Ser Asn Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser
 145 150 155 160
 Arg Arg Leu Val Gly Phe Ser Ile Ala Asp His Met Arg Thr Ser Leu
 165 170 175
 Val Gln Asp Ala Leu Leu Met Ala Lys Asp Gln Arg Gly Asn Leu Lys
 180 185 190
 Gly Ala Ile Phe His Ser Asp His Gly Ser Val Tyr Thr Ser His Ala
 195 200 205
 Phe Gln Glu Thr Cys Lys Lys Leu Gly Ile Arg Gln Ser Met Gly Ser
 210 215 220
 Ile Gly Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala
 225 230 235 240
 Met Lys Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Glu Asn Gln Leu
 245 250 255
 Cys Cys Arg Arg Asp Val Phe Arg Trp Cys Thr Arg Tyr Asn Thr Val
 260 265 270
 Arg Arg His Ser Trp Cys Arg Tyr Leu Ala Pro Val Val Phe Glu Glu
 275 280 285
 Arg Gly Pro Ala Ile Leu Arg Ser Ala Ser
 290 295

<210> 193

<211> 573

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(550)

<223> RXA00265

<400> 193

tgggctcacc aggcttccag caccgcgagct tcccaacgct gctatcaagg cacgtaaaaa 60

cccagcacca actgcacgac cagaaacgag aattgattaa atg cgc tcc gct cac 115
 Met Arg Ser Ala His
 1 5

ggc cca tac att gat aag ttc ttc ccc gag cca tac aag aac atg ctc 163
 Gly Pro Tyr Ile Asp Lys Phe Phe Pro Glu Pro Tyr Lys Asn Met Leu
 10 15 20

gag ctc acc aag act ctg cga aag atc tac ccg gac gtt gat ctg cct 211
 Glu Leu Thr Lys Thr Leu Arg Lys Ile Tyr Pro Asp Val Asp Leu Pro
 25 30 35

acc tca ttg att gag ctg gtc aat gtc cgc gtt tct caa atc aac gga 259
 Thr Ser Leu Ile Glu Leu Val Asn Val Arg Val Ser Gln Ile Asn Gly
 40 45 50

tgt ggc acc tgc tta agt tta cat gtt ccc gct gct cgc cgt gcc ggc 307

Cys Gly Thr Cys Leu Ser Leu His Val Pro Ala Ala Arg Arg Ala Gly
 55 60 65
 gtt cca gag aag aaa ctc gat gct ctg gca gcg tgg caa atg gtg gat 355
 Val Pro Glu Lys Lys Leu Asp Ala Leu Ala Ala Trp Gln Met Val Asp
 70 75 80 85
 gaa ttc acc gtg gag gaa aag gca gca cta cag cta gca gaa tcc tta 403
 Glu Phe Thr Val Glu Glu Lys Ala Ala Leu Gln Leu Ala Glu Ser Leu
 90 95 100
 acc ttg ctg gaa tcc cgc gaa ggt cac ctg gct gca cgc aca gcc tgc 451
 Thr Leu Leu Glu Ser Arg Glu Gly His Leu Ala Ala Arg Thr Ala Cys
 105 110 115
 agt gtg ttt gcc gaa gag cag gta gct gcc ctg gaa tgg gct atc att 499
 Ser Val Phe Ala Glu Glu Gln Val Ala Ala Leu Glu Trp Ala Ile Ile
 120 125 130
 gcg atc aat gct ttc aac cgc att tct att gcc agt ggg cac cca ctg 547
 Ala Ile Asn Ala Phe Asn Arg Ile Ser Ile Ala Ser Gly His Pro Leu
 135 140 145
 ctc tagtaatcag gcagcaaaaa act 573
 Leu
 150

<210> 194
 <211> 150
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 194
 Met Arg Ser Ala His Gly Pro Tyr Ile Asp Lys Phe Phe Pro Glu Pro
 1 5 10 15
 Tyr Lys Asn Met Leu Glu Leu Thr Lys Thr Leu Arg Lys Ile Tyr Pro
 20 25 30
 Asp Val Asp Leu Pro Thr Ser Leu Ile Glu Leu Val Asn Val Arg Val
 35 40 45
 Ser Gln Ile Asn Gly Cys Gly Thr Cys Leu Ser Leu His Val Pro Ala
 50 55 60
 Ala Arg Arg Ala Gly Val Pro Glu Lys Lys Leu Asp Ala Leu Ala Ala
 65 70 75 80
 Trp Gln Met Val Asp Glu Phe Thr Val Glu Glu Lys Ala Ala Leu Gln
 85 90 95
 Leu Ala Glu Ser Leu Thr Leu Leu Glu Ser Arg Glu Gly His Leu Ala
 100 105 110
 Ala Arg Thr Ala Cys Ser Val Phe Ala Glu Glu Gln Val Ala Ala Leu
 115 120 125
 Glu Trp Ala Ile Ile Ala Ile Asn Ala Phe Asn Arg Ile Ser Ile Ala
 130 135 140

Ser Gly His Pro Leu Leu
145 150

<210> 195
<211> 381
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(358)
<223> RXA00938

<400> 195
atgatctacc gctgggtcca gaaatacgcc cctgagctgg acaagcaaac acggtggtac 60

cggcaggtgc ctgactggca ggccagttcc tggcgggtgg atg aga cct ata tcc 115
Met Arg Pro Ile Ser
1 5

ggg tcg gcg gca ggt ggt gct acc tct gat ctg gcg atc acc gcc ggt 163
Gly Ser Ala Ala Gly Gly Ala Thr Ser Asp Leu Ala Ile Thr Ala Gly
10 15 20

ggc cag acc ctg gac ttt tac ctc tct ccg aag cgg aac gtg gcc gca 211
Gly Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala
25 30 35

gcg aag cgt ttc ctg gcc aag gcc ctc aga tcc aat gcg tca gcc ggg 259
Ala Lys Arg Phe Leu Ala Lys Ala Leu Arg Ser Asn Ala Ser Ala Gly
40 45 50

tat ccc aga gtg atc aac acc gat aaa gca ccc tcc cta gcc agg gca 307
Tyr Pro Arg Val Ile Asn Thr Asp Lys Ala Pro Ser Leu Ala Arg Ala
55 60 65

atc acc gag ttg aag tca gag gga atc tgc ccg cca aca gtg gaa cac 355
Ile Thr Glu Leu Lys Ser Glu Gly Ile Cys Pro Pro Thr Val Glu His
70 75 80 85

cgg tagtgaaat acctcaacaa cat 381
Arg

<210> 196
<211> 86
<212> PRT
<213> Corynebacterium glutamicum

<400> 196
Met Arg Pro Ile Ser Gly Ser Ala Ala Gly Gly Ala Thr Ser Asp Leu
1 5 10 15

Ala Ile Thr Ala Gly Gly Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys
20 25 30

Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Ala Leu Arg Ser
35 40 45

Asn Ala Ser Ala Gly Tyr Pro Arg Val Ile Asn Thr Asp Lys Ala Pro
 50 55 60

Ser Leu Ala Arg Ala Ile Thr Glu Leu Lys Ser Glu Gly Ile Cys Pro
 65 70 75 80

Pro Thr Val Glu His Arg
 85

<210> 197
 <211> 339
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(316)
 <223> RXA01264

<400> 197
 atcaagacat gattgcggcg tatgggaatc cgtagaaatc agaggaaaag aagctgatga 60

gaaggggatc aacagcctgc gcaaaggcct accagcgaga atg gac gag ctt gcc 115
 Met Asp Glu Leu Ala
 1 5

caa ctg ggg cac acc ttg tgg cgt cgg cgt aag aac gtg ttg gcg tcc 163
 Gln Leu Gly His Thr Leu Trp Arg Arg Arg Lys Asn Val Leu Ala Ser
 10 15 20

ttc aat atc ggt gca tcc aac gga cct gtc gag gcc atc aac ggc aga 211
 Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg
 25 30 35

ctt gag cac ctg cgc ggg atc acc ttg ggg ttc agg aac ctc aac cac 259
 Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe Arg Asn Leu Asn His
 40 45 50

tac atc ttg cgg tgc ttg atc caa gcc gga caa ctg cag agg aag atc 307
 Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln Leu Gln Arg Lys Ile
 55 60 65

aat gta ctc taaatccgaa gagttggcaa aga 339
 Asn Val Leu
 70

<210> 198
 <211> 72
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 198
 Met Asp Glu Leu Ala Gln Leu Gly His Thr Leu Trp Arg Arg Arg Lys
 1 5 10 15

Asn Val Leu Ala Ser Phe Asn Ile Gly Ala Ser Asn Gly Pro Val Glu
 20 25 30

Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile Thr Leu Gly Phe

35 40 45
 Arg Asn Leu Asn His Tyr Ile Leu Arg Cys Leu Ile Gln Ala Gly Gln
 50 55 60
 Leu Gln Arg Lys Ile Asn Val Leu
 65 70

<210> 199
 <211> 273
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(250)
 <223> RXA01265

<400> 199
 tacgaggaag atcttcacaa aatcctgtac tgcgcggatg actgatccaa gttcaaccac 60
 cggggcactg ctagatcttg cagcgccttg tgattgacgg atg agt gtg tct gcc 115
 Met Ser Val Ser Ala
 1 5
 acg gct aaa gca ctg aag atc ggc tgg gaa cta gtc aac cag gtt gca 163
 Thr Ala Lys Ala Leu Lys Ile Gly Trp Glu Leu Val Asn Gln Val Ala
 10 15 20
 ctc gat gct tgc cga cag ctc att tac aac gac ccg cgc cac ctt gaa 211
 Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp Pro Arg His Leu Glu
 25 30 35
 gtc gat gaa cat gta tgg aag tat act cga aag cca ggt tagccgtcga 260
 Val Asp Glu His Val Trp Lys Tyr Thr Arg Lys Pro Gly
 40 45 50
 acctggtgac cat 273

<210> 200
 <211> 50
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 200
 Met Ser Val Ser Ala Thr Ala Lys Ala Leu Lys Ile Gly Trp Glu Leu
 1 5 10 15
 Val Asn Gln Val Ala Leu Asp Ala Cys Arg Gln Leu Ile Tyr Asn Asp
 20 25 30
 Pro Arg His Leu Glu Val Asp Glu His Val Trp Lys Tyr Thr Arg Lys
 35 40 45
 Pro Gly
 50

<210> 201

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<211> 267
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(244)  
<223> RXA01327
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<400> 201
gaaatccaaa tatcctctac gaacgcaatg gtcacacagt tttcaaactc gaaatcgcct 60

tattcgacaa catcgattgt aacgcctcga catcgaccgt atg agt atc gca gca 115
                                         Met Ser Ile Ala Ala
                                         1                               5

acc gcg aaa gcc ctc ggt cta ggc tgg gat ctc acc tgc caa cta gcc 163
Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala
                        10                               15                               20

cta gat atg tgc cac gaa ctc atc tac tac gac ccc acc cac cta gaa 211
Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp Pro Thr His Leu Glu
                        25                               30                               35

att gtg cac gtt att ggc gtc gat gag cac aaa tgatctcata accgattaaa 264
Ile Val His Val Ile Gly Val Asp Glu His Lys
                        40                               45

aca 267

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<210> 202
<211> 48
<212> PRT
<213> Corynebacterium glutamicum
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<400> 202
Met Ser Ile Ala Ala Thr Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu
  1             5             10             15

Thr Cys Gln Leu Ala Leu Asp Met Cys His Glu Leu Ile Tyr Tyr Asp
      20             25             30

Pro Thr His Leu Glu Ile Val His Val Ile Gly Val Asp Glu His Lys
      35             40             45

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<210> 203
<211> 498
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(475)  
<223> RXA01328
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<400> 203
cacaaatgat ctcataaccg attaaaacat ggtgatggct atgtcaccgt cattgttaat 60
atgaccagcc ttccaccgcg atgccacgtc cccagcgagg ttg ctt gat gta gtc 115
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Leu Leu Asp Val Val
1 5

gaa ggc cgc agt gct gat gcg ttg cgg gcg tgg ctt gca cgc cga agc 163
Glu Gly Arg Ser Ala Asp Ala Leu Arg Ala Trp Leu Ala Arg Arg Ser
10 15 20

cca gca ttt cga cac caa gta cgc att gta act atg gat gga ttc caa 211
Pro Ala Phe Arg His Gln Val Arg Ile Val Thr Met Asp Gly Phe Gln
25 30 35

ggc tat gcc aca acc agc aaa caa ctt ctg ccc gcc gca cgc cga gtc 259
Gly Tyr Ala Thr Thr Ser Lys Gln Leu Leu Pro Ala Ala Arg Arg Val
40 45 50

atg gat cct ttc cac gtg gta ctc ctc gcc ggc gat aaa ctc acc cga 307
Met Asp Pro Phe His Val Val Leu Leu Ala Gly Asp Lys Leu Thr Arg
55 60 65

tgc cga caa cgt ttg cag cag gaa aaa tac cac cgg cgg ggt ttg cat 355
Cys Arg Gln Arg Leu Gln Gln Glu Lys Tyr His Arg Arg Gly Leu His
70 75 80 85

gat gac ccg ttg tat aag aac cgg aaa acc ttg ctg acc acg caa aaa 403
Asp Asp Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr Gln Lys
90 95 100

tgg ttg agt aag aaa aag caa agc gtc ttg atg agt tgt tta gct ttg 451
Trp Leu Ser Lys Lys Lys Gln Ser Val Leu Met Ser Cys Leu Ala Leu
105 110 115

ata aag act acg cgg cac tgc aac tgatgtggca ggcgtatcaa ggc 498
Ile Lys Thr Thr Arg His Cys Asn
120 125

<210> 204

<211> 125

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 204

Leu Leu Asp Val Val Glu Gly Arg Ser Ala Asp Ala Leu Arg Ala Trp
1 5 10 15

Leu Ala Arg Arg Ser Pro Ala Phe Arg His Gln Val Arg Ile Val Thr
20 25 30

Met Asp Gly Phe Gln Gly Tyr Ala Thr Thr Ser Lys Gln Leu Leu Pro
35 40 45

Ala Ala Arg Arg Val Met Asp Pro Phe His Val Val Leu Leu Ala Gly
50 55 60

Asp Lys Leu Thr Arg Cys Arg Gln Arg Leu Gln Gln Glu Lys Tyr His
65 70 75 80

Arg Arg Gly Leu His Asp Asp Pro Leu Tyr Lys Asn Arg Lys Thr Leu
85 90 95

Leu Thr Thr Gln Lys Trp Leu Ser Lys Lys Lys Gln Ser Val Leu Met

100 105 110

Ser Cys Leu Ala Leu Ile Lys Thr Thr Arg His Cys Asn
115 120 125

<210> 205
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA01329

<400> 205
aaaagcaaag cgtcttgatg agttgttttag ctttgataaa gactacgcgg cactgcaact 60
gatgtggcag gcgtatcaag gcattattga ctgatacaac atg gcc gat aaa cgc 115
Met Ala Asp Lys Arg
1 5
cgc gca aag acc atg atg cgc gag att gtt gac cag atg cgg cta ctg 163
Arg Ala Lys Thr Met Met Arg Glu Ile Val Asp Gln Met Arg Leu Leu
10 15 20
aaa gga caa gcg aat cga gaa ctt gca caa cta ggc cgc agc cta cac 211
Lys Gly Gln Ala Asn Arg Glu Leu Ala Gln Leu Gly Arg Ser Leu His
25 30 35
aaa cgc ctc ggt gac atc ctg gcg tat ttc gat gtc gga atc tct aac 259
Lys Arg Leu Gly Asp Ile Leu Ala Tyr Phe Asp Val Gly Ile Ser Asn
40 45 50
gga ccc gta gaa gca atc aac gga cga ctc gaa cac ctc cgc gga atc 307
Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ile
55 60 65
gcc cta gga ttt cgc aac ctc aac cac tac atc ctg cac tgt ctc atc 355
Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu His Cys Leu Ile
70 75 80 85
cac tcc gga caa ctc acc cac aaa atc aac gca ctc taaaaccgga 401
His Ser Gly Gln Leu Thr His Lys Ile Asn Ala Leu
90 95
agagcccgat tgc 414

<210> 206
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 206
Met Ala Asp Lys Arg Arg Ala Lys Thr Met Met Arg Glu Ile Val Asp
1 5 10 15
Gln Met Arg Leu Leu Lys Gly Gln Ala Asn Arg Glu Leu Ala Gln Leu
20 25 30

Gly Arg Ser Leu His Lys Arg Leu Gly Asp Ile Leu Ala Tyr Phe Asp
 35 40 45
 Val Gly Ile Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu
 50 55 60
 His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile
 65 70 75 80
 Leu His Cys Leu Ile His Ser Gly Gln Leu Thr His Lys Ile Asn Ala
 85 90 95
 Leu

<210> 207
 <211> 954
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(931)
 <223> RXA01443

<400> 207
 gaaagctgct aaatattttcc cggcaagaga caaactggtg agctgcttcc ggtttggtga 60

 cgacgtgcga aaaacctatc cgggtaagcg gttatgcgaa gtg ttg aaa atc aac 115
 Val Leu Lys Ile Asn
 1 5

 cgc tcc tcg tac tac aaa tgg aaa aag act gcc ccg acc agg agc aac 163
 Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala Pro Thr Arg Ser Asn
 10 15 20

 cgc ctg ctc agc gac gca gtc tta gga gcg aag atc aag tcc atc ttc 211
 Arg Leu Leu Ser Asp Ala Val Leu Gly Ala Lys Ile Lys Ser Ile Phe
 25 30 35

 acg aaa gaa cgc ggc tgc tac ggc tca aaa cgc atc acg gct gag ctc 259
 Thr Lys Glu Arg Gly Cys Tyr Gly Ser Lys Arg Ile Thr Ala Glu Leu
 40 45 50

 aac gat gat cct ggc agc act ccg gtt aac cat aaa cga gtc gcc cgg 307
 Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His Lys Arg Val Ala Arg
 55 60 65

 atc atg gca tca tta aag ctg ttt ggt ttc acg aag aaa cgc agg gtc 355
 Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr Lys Lys Arg Arg Val
 70 75 80 85

 atc acg acc gtg tct gat aaa aag aag cct gtc ttc cct gac ctg gtc 403
 Ile Thr Thr Val Ser Asp Lys Lys Lys Pro Val Phe Pro Asp Leu Val
 90 95 100

 aaa cgt cat ttt aac gca cta gca gca aat gaa gtt tac gtc ggg gat 451
 Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu Val Tyr Val Gly Asp
 105 110 115

att act tac cta ccg atc gca gat ggc acg aac atg tat ctg gct acg 499
 Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn Met Tyr Leu Ala Thr
 120 125 130

gtc att gat tgc tat tcc cgt agg ctg gtg ggt ttt gcg att gcg gat 547
 Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly Phe Ala Ile Ala Asp
 135 140 145

cat atg cgc acg tca ttg gtg cag gag gca ttg ctg atg gcg aag agt 595
 His Met Arg Thr Ser Leu Val Gln Glu Ala Leu Leu Met Ala Lys Ser
 150 155 160 165

cag cga ggc agc ctg aag ggt gcg gtg ttt cat tcg gat cac ggc agt 643
 Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His Ser Asp His Gly Ser
 170 175 180

gtg tac acc tcg cag gcg ttt cag gac act tgt aaa aag ttg ggt gtt 691
 Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys Lys Lys Leu Gly Val
 185 190 195

cgt cag tcg atg ggt gct gtt ggt acc agt gcg gat aat tcg ctg gcg 739
 Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala Asp Asn Ser Leu Ala
 200 205 210

gag tcg ttt aat gcc gcc ctc aag cga gag gtg ctg cag gat tcc aag 787
 Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val Leu Gln Asp Ser Lys
 215 220 225

acg ttt gcc aat cag ttg gtg tgc cgc cgg gag gta ttt cgc tgg tgt 835
 Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu Val Phe Arg Trp Cys
 230 235 240 245

acc agg tac agc aca aat cgc agg cat tct tgg tgt ggc tat gtg gtg 883
 Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp Cys Gly Tyr Val Val
 250 255 260

cct gcg gtg ttc gag agt aga aat tta gct att ctg aaa tct gtt tcc 931
 Pro Ala Val Phe Glu Ser Arg Asn Leu Ala Ile Leu Lys Ser Val Ser
 265 270 275

tgattaaatc gcctgtgttt cca 954

<210> 208

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 208

Val Leu Lys Ile Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala
 1 5 10 15

Pro Thr Arg Ser Asn Arg Leu Leu Ser Asp Ala Val Leu Gly Ala Lys
 20 25 30

Ile Lys Ser Ile Phe Thr Lys Glu Arg Gly Cys Tyr Gly Ser Lys Arg
 35 40 45

Ile Thr Ala Glu Leu Asn Asp Asp Pro Gly Ser Thr Pro Val Asn His
 50 55 60

Lys Arg Val Ala Arg Ile Met Ala Ser Leu Lys Leu Phe Gly Phe Thr
 65 70 75 80
 Lys Lys Arg Arg Val Ile Thr Thr Val Ser Asp Lys Lys Lys Pro Val
 85 90 95
 Phe Pro Asp Leu Val Lys Arg His Phe Asn Ala Leu Ala Ala Asn Glu
 100 105 110
 Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Thr Asn
 115 120 125
 Met Tyr Leu Ala Thr Val Ile Asp Cys Tyr Ser Arg Arg Leu Val Gly
 130 135 140
 Phe Ala Ile Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu
 145 150 155 160
 Leu Met Ala Lys Ser Gln Arg Gly Ser Leu Lys Gly Ala Val Phe His
 165 170 175
 Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys
 180 185 190
 Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala
 195 200 205
 Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val
 210 215 220
 Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu
 225 230 235 240
 Val Phe Arg Trp Cys Thr Arg Tyr Ser Thr Asn Arg Arg His Ser Trp
 245 250 255
 Cys Gly Tyr Val Val Pro Ala Val Phe Glu Ser Arg Asn Leu Ala Ile
 260 265 270
 Leu Lys Ser Val Ser
 275

<210> 209
 <211> 390
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(367)
 <223> RXA01444

<400> 209
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 acatcccaac attctgggat agaaaggtaa cctaccgatc atg cca acc aag acc 115
 Met Pro Thr Lys Thr
 1 5

tat tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc 163
 Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
 10 15 20

 gac ggg gcc tca ctc caa cag atc gcc aac gat ctc ggc atc aac cga 211
 Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg
 25 30 35

 gta acc ctg aaa aac tgg atc atc aaa tac gga tcc aac cac aac gta 259
 Val Thr Leu Lys Asn Trp Ile Ile Lys Tyr Gly Ser Asn His Asn Val
 40 45 50

 caa ggg aca acc cca tct gcg gca gtc tct gaa gct gaa caa atc cgg 307
 Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu Ala Glu Gln Ile Arg
 55 60 65

 cag ctg aag aag gaa aac gcg cta caa cgc gca aga acg cga cat cct 355
 Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala Arg Thr Arg His Pro
 70 75 80 85

 gcg gaa agc tgc taaatatttc ccggcaagag aca 390
 Ala Glu Ser Cys

<210> 210
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 210
 Met Pro Thr Lys Thr Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala
 1 5 10 15

 Leu Tyr Glu Asn Ser Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp
 20 25 30

 Leu Gly Ile Asn Arg Val Thr Leu Lys Asn Trp Ile Ile Lys Tyr Gly
 35 40 45

 Ser Asn His Asn Val Gln Gly Thr Thr Pro Ser Ala Ala Val Ser Glu
 50 55 60

 Ala Glu Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu Gln Arg Ala
 65 70 75 80

 Arg Thr Arg His Pro Ala Glu Ser Cys
 85

<210> 211
 <211> 492
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(469)
 <223> RXA01648

<400> 211


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ccaatgaagt ttacgtcggg gatattactt atctgccgat tgctgatggg tcgaatatgt 60
atttgacgac ggtcattgat tgctattctt agcacggttg gtg ggt ttt gcc ttt 115
                                   Val Gly Phe Ala Phe
                                   1 5
gcg gat cat atg cgc acg tca ttg gtg cag gag gcg ttg atg atg gcg 163
Ala Asp His Met Arg Thr Ser Leu Val Gln Glu Ala Leu Met Met Ala
                                   10 15 20
aag agt cag cga ggc agt cta cag ggt gct gtt ttt cat tcg gat cac 211
Lys Ser Gln Arg Gly Ser Leu Gln Gly Ala Val Phe His Ser Asp His
                                   25 30 35
ggc agt gtg tac acc tcg cag gcg ttt cag gac act tgt aaa aag ttg 259
Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp Thr Cys Lys Lys Leu
                                   40 45 50
ggt gtt cgt cag tcg atg ggt gct gtt ggt acc agt gcg gat aat tcg 307
Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr Ser Ala Asp Asn Ser
                                   55 60 65
cta gcg gag tcg ttt aat gcc gcg ctc aag cgg gaa gtg ctg cag gat 355
Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg Glu Val Leu Gln Asp
                                   70 75 80 85
tcc aag acg ttt gct aat cag ttg gtg tgc cgt cgg gag gta ttt cgg 403
Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg Arg Glu Val Phe Arg
                                   90 95 100
tgg tgt gac cta gta caa cac ggt gcg cag aca ttc ttg gtg tgg cta 451
Trp Cys Asp Leu Val Gln His Gly Ala Gln Thr Phe Leu Val Trp Leu
                                   105 110 115
tgt ggc gcc tgc ggt gtt tgaggtccag gggtctgcta ttc 492
Cys Gly Ala Cys Gly Val
                                   120

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<210> 212

<211> 123

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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Val Gly Phe Ala Phe Ala Asp His Met Arg Thr Ser Leu Val Gln Glu
  1 5 10 15
Ala Leu Met Met Ala Lys Ser Gln Arg Gly Ser Leu Gln Gly Ala Val
  20 25 30
Phe His Ser Asp His Gly Ser Val Tyr Thr Ser Gln Ala Phe Gln Asp
  35 40 45
Thr Cys Lys Lys Leu Gly Val Arg Gln Ser Met Gly Ala Val Gly Thr
  50 55 60
Ser Ala Asp Asn Ser Leu Ala Glu Ser Phe Asn Ala Ala Leu Lys Arg
  65 70 75 80
Glu Val Leu Gln Asp Ser Lys Thr Phe Ala Asn Gln Leu Val Cys Arg

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      85                      90                      95
Arg Glu Val Phe Arg Trp Cys Asp Leu Val Gln His Gly Ala Gln Thr
      100                      105                      110

Phe Leu Val Trp Leu Cys Gly Ala Cys Gly Val
      115                      120

<210> 213
<211> 543
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(520)
<223> RXA01649

<400> 213
ggctgctaaa tattttcccg gcaagaggca agacttatga cccgcttctg gtttgttgac 60

gacgtgcgaa aaacctactg aagttaagcg gttatgcgaa gtg ttg aaa att aac 115
                               Val Leu Lys Ile Asn
                               1           5

cgt tcc tcg tat tac aaa tgg aaa aag act gct ctg acg agg aag aaa 163
Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala Leu Thr Arg Lys Lys
      10                      15                      20

ctc ctg ctc agc gac gca gtc ctg gga gcg aag atc aag tcc atc ttc 211
Leu Leu Leu Ser Asp Ala Val Leu Gly Ala Lys Ile Lys Ser Ile Phe
      25                      30                      35

act aaa gaa cgc ggc tgt tat ggt gcg aaa cgt att acg gcc gag ctt 259
Thr Lys Glu Arg Gly Cys Tyr Gly Ala Lys Arg Ile Thr Ala Glu Leu
      40                      45                      50

aat gac ggg cca ggt aca aca act ccg gtt aac cac aag cga gtc gct 307
Asn Asp Gly Pro Gly Thr Thr Thr Pro Val Asn His Lys Arg Val Ala
      55                      60                      65

cga gtg atg tct tcg atg aag ctt gtt ggt ttt acg aag aaa cgc aag 355
Arg Val Met Ser Ser Met Lys Leu Val Gly Phe Thr Lys Lys Arg Lys
      70                      75                      80                      85

gtc atc acc aca atc cca gca gct gtc aag ccg gtg ttc ccg gac ttg 403
Val Ile Thr Thr Ile Pro Ala Ala Val Lys Pro Val Phe Pro Asp Leu
      90                      95                      100

gtg aag cgt caa ttc aac gct ttg gct gcc aat gaa gtt tac gtc ggg 451
Val Lys Arg Gln Phe Asn Ala Leu Ala Ala Asn Glu Val Tyr Val Gly
      105                      110                      115

gat att act tat ctg ccg att gct gat ggg tcg aat atg tat ttg acg 499
Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Ser Asn Met Tyr Leu Thr
      120                      125                      130

acg gtc att gat tgc tat tct tagcacgggt ggtgggtttt gcc 543
Thr Val Ile Asp Cys Tyr Ser
      135                      140

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<210> 214
 <211> 140
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 214
 Val Leu Lys Ile Asn Arg Ser Ser Tyr Tyr Lys Trp Lys Lys Thr Ala
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 Leu Thr Arg Lys Lys Leu Leu Leu Ser Asp Ala Val Leu Gly Ala Lys
 20 25 30
 Ile Lys Ser Ile Phe Thr Lys Glu Arg Gly Cys Tyr Gly Ala Lys Arg
 35 40 45
 Ile Thr Ala Glu Leu Asn Asp Gly Pro Gly Thr Thr Thr Pro Val Asn
 50 55 60
 His Lys Arg Val Ala Arg Val Met Ser Ser Met Lys Leu Val Gly Phe
 65 70 75 80
 Thr Lys Lys Arg Lys Val Ile Thr Thr Ile Pro Ala Ala Val Lys Pro
 85 90 95
 Val Phe Pro Asp Leu Val Lys Arg Gln Phe Asn Ala Leu Ala Ala Asn
 100 105 110
 Glu Val Tyr Val Gly Asp Ile Thr Tyr Leu Pro Ile Ala Asp Gly Ser
 115 120 125
 Asn Met Tyr Leu Thr Thr Val Ile Asp Cys Tyr Ser
 130 135 140

<210> 215
 <211> 237
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(214)
 <223> RXA01650

<400> 215
 cagatcgcca acgatctcgg catcaaccga gtaaccctga aaaacttcga tcaataaata 60
 cggtgcgcat gcctcaacca acaccaaaga agcaacagca atg tcg gaa gct gaa 115
 Met Ser Glu Ala Glu
 1 5
 caa atc aga cag cta aag aag gaa aac gca cta ctg cgt gaa gaa cgc 163
 Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu Leu Arg Glu Glu Arg
 10 15 20
 gac att ttg cgc aag gct gct aaa tat ttt ccc ggc aag agg caa gac 211
 Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Pro Gly Lys Arg Gln Asp
 25 30 35

tta tgacccgctt ctggtttgtt gac
Leu

237

<210> 216
<211> 38
<212> PRT
<213> Corynebacterium glutamicum

<400> 216
Met Ser Glu Ala Glu Gln Ile Arg Gln Leu Lys Lys Glu Asn Ala Leu
1 5 10 15
Leu Arg Glu Glu Arg Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Pro
20 25 30
Gly Lys Arg Gln Asp Leu
35

<210> 217
<211> 258
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(235)
<223> RXA01651

<400> 217
caatctctaa ggagaaagtt tatgacaaat aggacctgac ccctgtttgg tagacaccta 60
acatcccaac attctgggac agaaaggtaa cctacctatc atg cca acc aag acc 115
Met Pro Thr Lys Thr
1 5
tac tcc gag gag ttc aaa cgc gac gcc gtt gct ttg tac gag aac tcc 163
Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
10 15 20
gat ggg gcc tca ctc caa cag atc gcc aac gat ctc ggc atc aac cga 211
Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp Leu Gly Ile Asn Arg
25 30 35
gta acc ctg aaa aac ttc gat caa taaatacggg gcgcatgcct caa 258
Val Thr Leu Lys Asn Phe Asp Gln
40 45

<210> 218
<211> 45
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Pro Thr Lys Thr Tyr Ser Glu Glu Phe Lys Arg Asp Ala Val Ala
1 5 10 15
Leu Tyr Glu Asn Ser Asp Gly Ala Ser Leu Gln Gln Ile Ala Asn Asp

20	25	30	
Leu Gly Ile Asn Arg Val Thr Leu Lys Asn Phe Asp Gln			
35	40	45	
 <210> 219			
<211> 534			
<212> DNA			
<213> Corynebacterium glutamicum			
 <220>			
<221> CDS			
<222> (101)..(511)			
<223> RXN01680			
 <400> 219			
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cagcacatgc catcccgaaa catatccgcc ccaatcagaa atg gca ggt cac acc 115			
		Met Ala Gly His Thr	
		1 5	
cac aaa acc cac cgg act gct tat aag cag ttg gaa gcc ttg gcc cgc 163			
His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu Glu Ala Leu Ala Arg			
10 15 20			
aat ggg cat ttg ttt acc tat att gat cca cca gca gag gtt gac ggg 211			
Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro Ala Glu Val Asp Gly			
25 30 35			
gtg gtg aaa tca aca acg aac tgt ttg gaa ggt ggt atc aac gct cag 259			
Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly Gly Ile Asn Ala Gln			
40 45 50			
att aaa gcg ttg gcg aga aac cat cgg ggg atg ttt gat gaa cat caa 307			
Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met Phe Asp Glu His Gln			
55 60 65			
cgt atc gcg gtg gat tgg tgg tta ttg atg cat acg cag ttg cct ggc 355			
Arg Ile Ala Val Asp Trp Trp Leu Leu Met His Thr Gln Leu Pro Gly			
70 75 80 85			
gat ccg gtt gag atc gcc agg caa caa aac tgg ggt caa gac gga ctc 403			
Asp Pro Val Glu Ile Ala Arg Gln Gln Asn Trp Gly Gln Asp Gly Leu			
90 95 100			
gcc aac gtc ccc gac ttg atc caa caa gaa caa cca cac gac cac tac 451			
Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln Pro His Asp His Tyr			
105 110 115			
ggg cgc ccg gtt acc tat gac acc gga atc gat gcc aca acg aca cgc 499			
Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp Ala Thr Thr Thr Arg			
120 125 130			
cgt aaa agc aag taaaaatccc ggcccaccaa caa 534			
Arg Lys Ser Lys			
135			

<210> 220

<211> 137
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 220

Met	Ala	Gly	His	Thr	His	Lys	Thr	His	Arg	Thr	Ala	Tyr	Lys	Gln	Leu
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Glu	Ala	Leu	Ala	Arg	Asn	Gly	His	Leu	Phe	Thr	Tyr	Ile	Asp	Pro	Pro
			20					25					30		
Ala	Glu	Val	Asp	Gly	Val	Val	Lys	Ser	Thr	Thr	Asn	Cys	Leu	Glu	Gly
		35					40					45			
Gly	Ile	Asn	Ala	Gln	Ile	Lys	Ala	Leu	Ala	Arg	Asn	His	Arg	Gly	Met
	50					55					60				
Phe	Asp	Glu	His	Gln	Arg	Ile	Ala	Val	Asp	Trp	Trp	Leu	Leu	Met	His
	65				70					75					80
Thr	Gln	Leu	Pro	Gly	Asp	Pro	Val	Glu	Ile	Ala	Arg	Gln	Gln	Asn	Trp
				85					90					95	
Gly	Gln	Asp	Gly	Leu	Ala	Asn	Val	Pro	Asp	Leu	Ile	Gln	Gln	Glu	Gln
			100					105					110		
Pro	His	Asp	His	Tyr	Gly	Arg	Pro	Val	Thr	Tyr	Asp	Thr	Gly	Ile	Asp
		115					120					125			
Ala	Thr	Thr	Thr	Arg	Arg	Lys	Ser	Lys							
	130					135									

<210> 221
 <211> 534
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(511)

<223> FRXA01680

<400> 221

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cagcacatgc	catcccgaaa	catatccgcc	ccaatcagaa	atg gca ggt cac acc		115
				Met Ala Gly His Thr		
				1	5	
cac aaa acc	cac cgg act	gct tat aag	cag ttg gaa	gcc ttg gcc cgc		163
His Lys Thr	His Arg Thr	Ala Tyr Lys	Gln Leu Glu	Ala Leu Ala Arg		
	10		15	20		
aat ggg cat	ttg ttt acc	tat att gat	cca cca gca	gag gtt gac ggg		211
Asn Gly His	Leu Phe Thr	Tyr Ile Asp	Pro Pro Ala	Glu Val Asp Gly		
	25		30	35		
gtg gtg aaa	tca aca acg	aac tgt ttg	gaa ggt ggt	atc aac gct cag		259
Val Val Lys	Ser Thr Thr	Asn Cys Leu	Glu Gly Gly	Ile Asn Ala Gln		
	40		45	50		

att aaa gcg ttg gcg aga aac cat cgg ggg atg ttt gat gaa cat caa 307
 Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met Phe Asp Glu His Gln
 55 60 65

cgt atc gcg gtg gat tgg tgg tta ttg atg cat acg cag ttg cct ggc 355
 Arg Ile Ala Val Asp Trp Trp Leu Leu Met His Thr Gln Leu Pro Gly
 70 75 80 85

gat ccg gat gag atc gcc agg caa caa aac tgg ggt caa gac gga ctc 403
 Asp Pro Asp Glu Ile Ala Arg Gln Gln Asn Trp Gly Gln Asp Gly Leu
 90 95 100

gcc aac gtc ccc gac ttg atc caa caa gaa caa cca cac gac cac tac 451
 Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln Pro His Asp His Tyr
 105 110 115

ggg cgc ccg gtt acc tat gac acc gga atc gat gcc aca acg aca cgc 499
 Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp Ala Thr Thr Thr Arg
 120 125 130

cgt aaa agc aag taaaaatccc ggccccaccaa caa 534
 Arg Lys Ser Lys
 135

<210> 222

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Met Ala Gly His Thr His Lys Thr His Arg Thr Ala Tyr Lys Gln Leu
 1 5 10 15

Glu Ala Leu Ala Arg Asn Gly His Leu Phe Thr Tyr Ile Asp Pro Pro
 20 25 30

Ala Glu Val Asp Gly Val Val Lys Ser Thr Thr Asn Cys Leu Glu Gly
 35 40 45

Gly Ile Asn Ala Gln Ile Lys Ala Leu Ala Arg Asn His Arg Gly Met
 50 55 60

Phe Asp Glu His Gln Arg Ile Ala Val Asp Trp Trp Leu Leu Met His
 65 70 75 80

Thr Gln Leu Pro Gly Asp Pro Asp Glu Ile Ala Arg Gln Gln Asn Trp
 85 90 95

Gly Gln Asp Gly Leu Ala Asn Val Pro Asp Leu Ile Gln Gln Glu Gln
 100 105 110

Pro His Asp His Tyr Gly Arg Pro Val Thr Tyr Asp Thr Gly Ile Asp
 115 120 125

Ala Thr Thr Thr Arg Arg Lys Ser Lys
 130 135

<210> 223

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<220>
<221> CDS
<222> (101)..(682)
<223> RXN01784
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acg atg ttt gac ctc acg ggc acc cga acc cag acg cgg tgatcgtcag 692

Thr Met Phe Asp Leu Thr Gly Thr Arg Thr Gln Thr Arg
 185 190

ccggatattc gag

705

<210> 224
 <211> 194
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 224
 Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg
 1 5 10 15
 Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys Gln Thr Arg Trp Tyr
 20 25 30
 Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp Arg Val Asp Glu Thr
 35 40 45
 Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu Tyr Arg Ala Ile Thr
 50 55 60
 Ala Gly Gly Gln Thr Leu Glu Phe Tyr Leu Ser Pro Lys Arg Asn Val
 65 70 75 80
 Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr
 85 90 95
 Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala
 100 105 110
 Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile Cys Pro Gln Thr Val
 115 120 125
 Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His
 130 135 140
 Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg
 145 150 155 160
 Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser Leu
 165 170 175
 Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr Gly Thr Arg Thr Gln
 180 185 190

Thr Arg

<210> 225
 <211> 572
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (1)..(549)
 <223> FRXA01784

<400> 225

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acc acc atc tac cgc tgg gtc cag aaa tac gcc ctt gag ctg gat aag      48
Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys
  1              5              10              15

cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg      96
Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
              20              25              30

cgg gtg gat gag acc tat atc cgg gtc ggc ggc acg tgg tgc tat ctc     144
Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
              35              40              45

tac cgg gct att acc gcg ggt ggg cag acc ctg gag ttt tat ctc tca     192
Tyr Arg Ala Ile Thr Ala Gly Gln Thr Leu Glu Phe Tyr Leu Ser
              50              55              60

cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg     240
Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
              65              70              75              80

cga tcg aat acg aca gcc ggg tcc ccg cgg gtc atc aac acc gac aag     288
Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
              85              90              95

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc     336
Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
              100              105              110

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt     384
Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
              115              120              125

atc gag gga gat cat ggc cga ctt aaa aga atc ctg ggg ccg aag gga     432
Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly
              130              135              140

gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gaa     480
Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
              145              150              155              160

gcg atg cat tca tta cgg aaa ggc cag ggc acg atg ttt gac ctc acg     528
Ala Met His Ser Leu Arg Lys Gly Gln Gly Thr Met Phe Asp Leu Thr
              165              170              175

ggc acc cga acc cag acg cgg tgatcgtcag ccggatattc gag              572
Gly Thr Arg Thr Gln Thr Arg
              180

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<210> 226

<211> 183

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

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Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Leu Glu Leu Asp Lys
  1              5              10              15

Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp

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20					25					30						
Arg	Val	Asp	Glu	Thr	Tyr	Ile	Arg	Val	Gly	Gly	Thr	Trp	Cys	Tyr	Leu	
35					40					45						
Tyr	Arg	Ala	Ile	Thr	Ala	Gly	Gln	Thr	Leu	Glu	Phe	Tyr	Leu	Ser		
50					55					60						
Pro	Lys	Arg	Asn	Val	Ala	Ala	Ala	Lys	Arg	Phe	Leu	Ala	Lys	Thr	Leu	
65					70					75					80	
Arg	Ser	Asn	Thr	Thr	Ala	Gly	Ser	Pro	Arg	Val	Ile	Asn	Thr	Asp	Lys	
85					90					95						
Ala	Pro	Ala	Leu	Ala	Lys	Ala	Ile	Ser	Glu	Leu	Lys	Ala	Glu	Gly	Ile	
100					105					110						
Cys	Pro	Gln	Thr	Val	Glu	His	Arg	Gln	Val	Lys	Tyr	Leu	Asn	Asn	Val	
115					120					125						
Ile	Glu	Gly	Asp	His	Gly	Arg	Leu	Lys	Arg	Ile	Leu	Gly	Pro	Lys	Gly	
130					135					140						
Ala	Phe	Lys	Asn	Arg	Ile	Ser	Ala	Tyr	Arg	Thr	Leu	Lys	Gly	Met	Glu	
145					150					155					160	
Ala	Met	His	Ser	Leu	Arg	Lys	Gly	Gln	Gly	Thr	Met	Phe	Asp	Leu	Thr	
165					170					175						
Gly	Thr	Arg	Thr	Gln	Thr	Arg										
180																

<210> 227

<211> 1329

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1306)

<223> RXA01862

<400> 227

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ataatccaac	tcctactca	tcgctaggag	gcacagactc	atg gcc tat gac ttc	115
				Met Ala Tyr Asp Phe	
				1 5	

gtc att gga atg gac gtc ggc aaa tac ttc cac cac gcc tgc gtc ctc	163
Val Ile Gly Met Asp Val Gly Lys Tyr Phe His His Ala Cys Val Leu	
10 15 20	

gat ccc cag ggc aga caa gtc cta tcc aaa cgc atc aac caa cac gaa	211
Asp Pro Gln Gly Arg Gln Val Leu Ser Lys Arg Ile Asn Gln His Glu	
25 30 35	

ggc tcg cta cgc aag ctc ttc gac aaa ttc ctg gcc aat gac gcc gag	259
Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu Ala Asn Asp Ala Glu	
40 45 50	

gtc ctt gtc gtc gtc gat cag ccc aac aac atc ggc agg cta acc gtc	307
Val Leu Val Val Val Asp Gln Pro Asn Asn Ile Gly Arg Leu Thr Val	
55 60 65	
gca gtc gcc caa gca atg gga gcc gac gtt cgc tac ctc ccc ggg ctt	355
Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg Tyr Leu Pro Gly Leu	
70 75 80 85	
gcc atg cga caa ctt tca cgt atc cac gtc ggc aac tcc aag acc gat	403
Ala Met Arg Gln Leu Ser Arg Ile His Val Gly Asn Ser Lys Thr Asp	
90 95 100	
gta cgg gac gct tat gtc atc gcc cat gcc ggc ctc aac ctt ccg gat	451
Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly Leu Asn Leu Pro Asp	
105 110 115	
gcc ctg cgt agc gtc gac cgc gtt gag gaa gtc ttc ctc cag ctg aaa	499
Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val Phe Leu Gln Leu Lys	
120 125 130	
gtc ctc aac ggt atc gac gaa gac ctc gcc cgc gcc tac aca cgc ctg	547
Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg Ala Tyr Thr Arg Leu	
135 140 145	
atc aac cag atg caa tcc gcg ctc gtg ggc acc tac ccc gca ttc gaa	595
Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr Tyr Pro Ala Phe Glu	
150 155 160 165	
cat gtc ctg cgt ggg cag atg att cac cgc aag tgg att ctc cac ctt	643
His Val Leu Arg Gly Gln Met Ile His Arg Lys Trp Ile Leu His Leu	
170 175 180	
ctg gcg aaa tac ggt ggc ccc acc aag att cga cgc gtc ggc aaa gca	691
Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg Arg Val Gly Lys Ala	
185 190 195	
cgg ctg gca gct ttc gca cgt ggt cac agg gca cgt aat cct gag cca	739
Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala Arg Asn Pro Glu Pro	
200 205 210	
gtt atc gat gcc atg ctt gct gcg atc cac ggc cag acg gta tcc atc	787
Val Ile Asp Ala Met Leu Ala Ala Ile His Gly Gln Thr Val Ser Ile	
215 220 225	
gcc ggc gca gaa tac gcg gaa ctt ggc gta gca atg tcc gcc aaa gat	835
Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala Met Ser Ala Lys Asp	
230 235 240 245	
gca cta gcc aag ctg gag cac cgc aaa gag att gaa ggc cag gta ctc	883
Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile Glu Gly Gln Val Leu	
250 255 260	
gag ctg atc cag gac att cct cag acc gag att ctc ttg tcc atg ccc	931
Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile Leu Leu Ser Met Pro	
265 270 275	
ggc atc ggc cca cgt agc gcc gcg caa atc ctt atg acc gtc ggc gat	979
Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu Met Thr Val Gly Asp	
280 285 290	

atg tcc gac ttt ccc gat gca gcg cac ctg gcg tcc tat gca ggc ctg 1027
 Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala Ser Tyr Ala Gly Leu
 295 300 305
 tcg ccg cag aca aat cag tcg gga acg tcg atc atg tcg aat tcg ccc 1075
 Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile Met Ser Asn Ser Pro
 310 315 320 325
 aac cgg gcc ggc aac aag aaa ttg aag aac gcc cta tgg cag tcg tct 1123
 Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala Leu Trp Gln Ser Ser
 330 335 340
 ttt gca tcg atc aga ttc cac gag cgt tcc cgg caa ttc tat gaa cga 1171
 Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg Gln Phe Tyr Glu Arg
 345 350 355
 aaa cgc aac gaa ggc aaa aga cac aac gcc gca gtc gtc gcg ctc gca 1219
 Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala Val Val Ala Leu Ala
 360 365 370
 cgc cga cgc ctc aac gtc ctc ttc gcc atg atg cgc agc gga gag ctc 1267
 Arg Arg Arg Leu Asn Val Leu Phe Ala Met Met Arg Ser Gly Glu Leu
 375 380 385
 tac aga gac atc ccc aca gcc cag gag gcc gca gcg gcc tagccccctac 1316
 Tyr Arg Asp Ile Pro Thr Ala Gln Glu Ala Ala Ala Ala
 390 395 400
 aagccccgaa gcc 1329

<210> 228

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Ala Tyr Asp Phe Val Ile Gly Met Asp Val Gly Lys Tyr Phe His
 1 5 10 15
 His Ala Cys Val Leu Asp Pro Gln Gly Arg Gln Val Leu Ser Lys Arg
 20 25 30
 Ile Asn Gln His Glu Gly Ser Leu Arg Lys Leu Phe Asp Lys Phe Leu
 35 40 45
 Ala Asn Asp Ala Glu Val Leu Val Val Val Asp Gln Pro Asn Asn Ile
 50 55 60
 Gly Arg Leu Thr Val Ala Val Ala Gln Ala Met Gly Ala Asp Val Arg
 65 70 75 80
 Tyr Leu Pro Gly Leu Ala Met Arg Gln Leu Ser Arg Ile His Val Gly
 85 90 95
 Asn Ser Lys Thr Asp Val Arg Asp Ala Tyr Val Ile Ala His Ala Gly
 100 105 110
 Leu Asn Leu Pro Asp Ala Leu Arg Ser Val Asp Arg Val Glu Glu Val
 115 120 125

Phe Leu Gln Leu Lys Val Leu Asn Gly Ile Asp Glu Asp Leu Ala Arg
 130 135 140
 Ala Tyr Thr Arg Leu Ile Asn Gln Met Gln Ser Ala Leu Val Gly Thr
 145 150 155 160
 Tyr Pro Ala Phe Glu His Val Leu Arg Gly Gln Met Ile His Arg Lys
 165 170 175
 Trp Ile Leu His Leu Leu Ala Lys Tyr Gly Gly Pro Thr Lys Ile Arg
 180 185 190
 Arg Val Gly Lys Ala Arg Leu Ala Ala Phe Ala Arg Gly His Arg Ala
 195 200 205
 Arg Asn Pro Glu Pro Val Ile Asp Ala Met Leu Ala Ala Ile His Gly
 210 215 220
 Gln Thr Val Ser Ile Ala Gly Ala Glu Tyr Ala Glu Leu Gly Val Ala
 225 230 235 240
 Met Ser Ala Lys Asp Ala Leu Ala Lys Leu Glu His Arg Lys Glu Ile
 245 250 255
 Glu Gly Gln Val Leu Glu Leu Ile Gln Asp Ile Pro Gln Thr Glu Ile
 260 265 270
 Leu Leu Ser Met Pro Gly Ile Gly Pro Arg Ser Ala Ala Gln Ile Leu
 275 280 285
 Met Thr Val Gly Asp Met Ser Asp Phe Pro Asp Ala Ala His Leu Ala
 290 295 300
 Ser Tyr Ala Gly Leu Ser Pro Gln Thr Asn Gln Ser Gly Thr Ser Ile
 305 310 315 320
 Met Ser Asn Ser Pro Asn Arg Ala Gly Asn Lys Lys Leu Lys Asn Ala
 325 330 335
 Leu Trp Gln Ser Ser Phe Ala Ser Ile Arg Phe His Glu Arg Ser Arg
 340 345 350
 Gln Phe Tyr Glu Arg Lys Arg Asn Glu Gly Lys Arg His Asn Ala Ala
 355 360 365
 Val Val Ala Leu Ala Arg Arg Arg Leu Asn Val Leu Phe Ala Met Met
 370 375 380
 Arg Ser Gly Glu Leu Tyr Arg Asp Ile Pro Thr Ala Gln Glu Ala Ala
 385 390 395 400
 Ala Ala

<210> 229

<211> 504

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(481)
 <223> RXA01953

<400> 229

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caaaaacttg acgagcgcaa cctgggggat ctaccagcgg atg atc gcg gcc tac 115
                                   Met Ile Ala Ala Tyr
                                   1 5

cgc gag aag gac cga tcc ctc ggc cgc gcg gcg atg gag gcg ctc atc 163
Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala Met Glu Ala Leu Ile
                10                15                20

gac gcc gtc agc caa gac gtc ccc gcc ggg ctg gac gag ttg cgc aag 211
Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu Asp Glu Leu Arg Lys
                25                30                35

ctc ggt cgg acc ctg aag gct cgc gcc acc gac gtg ctg gcc tac ttc 259
Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp Val Leu Ala Tyr Phe
                40                45                50

gag cgg cct ggc acc agc aat ggc ccc aca gag gcg atc aac gga cgc 307
Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu Ala Ile Asn Gly Arg
                55                60                65

ctg gag cac ctg cgc ggc tcg gcc ctg ggc ttc cgc aac ctg acc aac 355
Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe Arg Asn Leu Thr Asn
                70                75                80                85

tac atc gcc aga tcc ctg ctc gag ttc cgg cgg att cag acc tca act 403
Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg Ile Gln Thr Ser Thr
                90                95                100

aca ccc tca tct gtg aag agc cgc ttt aga cat ccc tca tcg tca cgg 451
Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His Pro Ser Ser Ser Arg
                105                110                115

acc act atg aac gat gtc ccg act cac cta tgaacgatgt cctgaacctta cac 504
Thr Thr Met Asn Asp Val Pro Thr His Leu
                120                125

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<210> 230
 <211> 127
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 230

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Met Ile Ala Ala Tyr Arg Glu Lys Asp Arg Ser Leu Gly Arg Ala Ala
  1 5 10 15

Met Glu Ala Leu Ile Asp Ala Val Ser Gln Asp Val Pro Ala Gly Leu
  20 25 30

Asp Glu Leu Arg Lys Leu Gly Arg Thr Leu Lys Ala Arg Ala Thr Asp
  35 40 45

Val Leu Ala Tyr Phe Glu Arg Pro Gly Thr Ser Asn Gly Pro Thr Glu
  50 55 60

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Ala Ile Asn Gly Arg Leu Glu His Leu Arg Gly Ser Ala Leu Gly Phe
 65 70 75 80

Arg Asn Leu Thr Asn Tyr Ile Ala Arg Ser Leu Leu Glu Phe Arg Arg
 85 90 95

Ile Gln Thr Ser Thr Thr Pro Ser Ser Val Lys Ser Arg Phe Arg His
 100 105 110

Pro Ser Ser Ser Arg Thr Thr Met Asn Asp Val Pro Thr His Leu
 115 120 125

<210> 231

<211> 831

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(808)

<223> RXA01998

<400> 231

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gttggggcag taggaagacc ggcgtggaat aatcaggtcc atg ggc atc ttc tcc 115
 Met Gly Ile Phe Ser
 1 5

ggt cgg cag ttc cct cgt gaa atc atc ctg tgg gcg gtg cgg tgg tac 163
 Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr
 10 15 20

tgc cgc tac ggc gtg agc tat cgc gac ctc gaa gag atg atg acc gag 211
 Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu
 25 30 35

cgg gga gtg ccg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa 259
 Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys
 40 45 50

tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct 307
 Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro
 55 60 65

gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355
 Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val
 70 75 80 85

ggg gga aag tgg tgc tac ctc tat cgg gca atc acc gcc ggt agc cag 403
 Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Ser Gln
 90 95 100

acc ctg gac ttc tac ctc tcc ccg aag aga aac gtc gcg gcg gcg aag 451
 Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys
 105 110 115

cgt ttc ctg gcg aag acg ctg cgg tcg aat aaa tcg gca ggc tat ccg 499
 Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys Ser Ala Gly Tyr Pro

120	125	130	
cgg gtg atc agc acc gac aag gcc ccc tca ctc gcc agg gca atc tct			547
Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu Ala Arg Ala Ile Ser			
135	140	145	
gag ctg aag gcg gaa ggc gtc tgt cca tcg acg gtc gag cat cgt cgg			595
Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr Val Glu His Arg Arg			
150	155	160	165
gtg aaa tac ctc aac aac gtc att gaa ggc gac cat ggt cgg tta aag			643
Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys			
	170	175	180
cgg atc ctg ggg ccg aaa ggc gca ttc aaa aac cga acg tct gcc tac			691
Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Thr Ser Ala Tyr			
	185	190	195
cgg acg ttg aaa ggg atg gag gcg atg cac tca ttg cgg aag ggg cag			739
Arg Thr Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Gln			
	200	205	210
ggc acg atg ttt gcc tat ggt cac ccg aat ccg gat gca gtg att gtt			787
Gly Thr Met Phe Ala Tyr Gly His Pro Asn Pro Asp Ala Val Ile Val			
	215	220	225
agc cgg gta ttc gag acg gcc tgacaacaca ggcacatagc gtt			831
Ser Arg Val Phe Glu Thr Ala			
230	235		

<210> 232

<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Gly Ile Phe Ser Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp			
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Ala Val Arg Trp Tyr Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu			
	20	25	30
Glu Met Met Thr Glu Arg Gly Val Pro Val Asp His Thr Thr Ile Tyr			
	35	40	45
Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp			
	50	55	60
Tyr Arg Gln Val Pro Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu			
	65	70	75
Thr Tyr Ile Arg Val Gly Gly Lys Trp Cys Tyr Leu Tyr Arg Ala Ile			
	85	90	95
Thr Ala Gly Ser Gln Thr Leu Asp Phe Tyr Leu Ser Pro Lys Arg Asn			
	100	105	110
Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu Arg Ser Asn Lys			
	115	120	125

Ser Ala Gly Tyr Pro Arg Val Ile Ser Thr Asp Lys Ala Pro Ser Leu
 130 135 140

Ala Arg Ala Ile Ser Glu Leu Lys Ala Glu Gly Val Cys Pro Ser Thr
 145 150 155 160

Val Glu His Arg Arg Val Lys Tyr Leu Asn Asn Val Ile Glu Gly Asp
 165 170 175

His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly Ala Phe Lys Asn
 180 185 190

Arg Thr Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu Ala Met His Ser
 195 200 205

Leu Arg Lys Gly Gln Gly Thr Met Phe Ala Tyr Gly His Pro Asn Pro
 210 215 220

Asp Ala Val Ile Val Ser Arg Val Phe Glu Thr Ala
 225 230 235

<210> 233
 <211> 274
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(274)
 <223> RXA02837

<400> 233
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agagggggcga ggtcgccctga ttggtcggac gaagggtgaa atg aac acc aag ctc 115
 Met Asn Thr Lys Leu
 1 5

cat gct gtg acc gat gcg acg ggg cgt cca atc cgc ttc ttc atg acc 163
 His Ala Val Thr Asp Ala Thr Gly Arg Pro Ile Arg Phe Phe Met Thr
 10 15 20

gcc gga aag gtc agc gac tac atc gga gct atg gct ttg cta ggc agc 211
 Ala Gly Lys Val Ser Asp Tyr Ile Gly Ala Met Ala Leu Leu Gly Ser
 25 30 35

ctg ccc aag gcc ggc tgg ctt cta gcg gat cgg ggc tat gac gcg gac 259
 Leu Pro Lys Ala Gly Trp Leu Leu Ala Asp Arg Gly Tyr Asp Ala Asp
 40 45 50

tgg ttc aga gat gca 274
 Trp Phe Arg Asp Ala
 55

<210> 234
 <211> 58
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 234

Met Asn Thr Lys Leu His Ala Val Thr Asp Ala Thr Gly Arg Pro Ile
 1 5 10 15

Arg Phe Phe Met Thr Ala Gly Lys Val Ser Asp Tyr Ile Gly Ala Met
 20 25 30

Ala Leu Leu Gly Ser Leu Pro Lys Ala Gly Trp Leu Leu Ala Asp Arg
 35 40 45

Gly Tyr Asp Ala Asp Trp Phe Arg Asp Ala
 50 55

<210> 235

<211> 1731

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1708)

<223> RXA00005

<400> 235

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cgaatccttg ctccaaaatc acggcggggt caggggggtga atg cac cac gag caa 115
 Met His His Glu Gln
 1 5

ccc gaa ggg tgc gaa gtg ggc att cgt aga aca atc cca gag gaa agc 163
 Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr Ile Pro Glu Glu Ser
 10 15 20

cgt acg gct ttc ctc gac atg atc aat caa ggt atg tca ggt ctt gct 211
 Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly Met Ser Gly Leu Ala
 25 30 35

gcg tct aca gcg gtc ggg gtc agt gaa ttc acc ggg cga aag tgg gcg 259
 Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr Gly Arg Lys Trp Ala
 40 45 50

aag gcc gcc ggg gtg aaa ctg acc cgc ggc ccg cga ggt ggc aat gct 307
 Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro Arg Gly Gly Asn Ala
 55 60 65

ttt gac acc gcc gag aaa ctt gag att gca gcc agc atg cta gag aaa 355
 Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala Ser Met Leu Glu Lys
 70 75 80 85

gga tgc cta ccc cga gaa atc ggc gag tat gtc ggc atg act cgg gcc 403
 Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val Gly Met Thr Arg Ala
 90 95 100

aat ata tcc cta tgg cgc aaa caa ggc cca gac aag ctt cgc caa cgc 451
 Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp Lys Leu Arg Gln Arg
 105 110 115

gca gcc acc ttg cgc acc ggc aag cga gca gct gaa ttc atc cac gcc 499
 Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala Glu Phe Ile His Ala

120					125					130						
ccg	gtg	atg	ggc	cct	tat	tat	ggg	cca	cgc	aca	ctc	cat	caa	gtg	ttg	547
Pro	Val	Met	Gly	Pro	Tyr	Tyr	Gly	Pro	Arg	Thr	Leu	His	Gln	Val	Leu	
	135						140					145				
cgt	gag	gac	tac	aca	aca	ctg	ttt	gac	gag	tta	tct	gcg	ttg	ggg	ttg	595
Arg	Glu	Asp	Tyr	Thr	Thr	Leu	Phe	Asp	Glu	Leu	Ser	Ala	Leu	Gly	Leu	
150					155					160					165	
cca	gca	cag	gtg	tgt	ggg	gcc	tta	ctt	cat	ctt	gct	cca	cca	cca	tca	643
Pro	Ala	Gln	Val	Cys	Gly	Ala	Leu	Leu	His	Leu	Ala	Pro	Pro	Pro	Ser	
				170					175					180		
tta	cgc	ttt	tct	tat	atg	tcg	tgt	gta	gtg	ccg	tta	ttt	gct	gat	gaa	691
Leu	Arg	Phe	Ser	Tyr	Met	Ser	Cys	Val	Val	Pro	Leu	Phe	Ala	Asp	Glu	
			185					190					195			
atc	aaa	gtc	gta	gga	caa	ggc	aca	cga	tta	tcg	tta	gaa	gag	aaa	atg	739
Ile	Lys	Val	Val	Gly	Gln	Gly	Thr	Arg	Leu	Ser	Leu	Glu	Glu	Lys	Met	
		200					205					210				
atg	atc	caa	cgt	ttc	cat	gac	acc	ggg	gtc	agt	gca	gca	gaa	atc	ggt	787
Met	Ile	Gln	Arg	Phe	His	Asp	Thr	Gly	Val	Ser	Ala	Ala	Glu	Ile	Gly	
	215					220					225					
cga	cgc	ctg	ggt	cgg	tgt	cgg	caa	aca	att	tcc	agg	gaa	ctt	cga	cgt	835
Arg	Arg	Leu	Gly	Arg	Cys	Arg	Gln	Thr	Ile	Ser	Arg	Glu	Leu	Arg	Arg	
230					235					240					245	
ggt	caa	gat	gat	gat	gga	cgt	tat	cgt	gca	cgc	gac	tcc	tat	gaa	ggt	883
Gly	Gln	Asp	Asp	Asp	Gly	Arg	Tyr	Arg	Ala	Arg	Asp	Ser	Tyr	Glu	Gly	
				250					255					260		
gcg	atc	agg	aaa	cta	gcg	cgt	ccg	aaa	aca	ccg	aaa	ctt	gat	gcc	aat	931
Ala	Ile	Arg	Lys	Leu	Ala	Arg	Pro	Lys	Thr	Pro	Lys	Leu	Asp	Ala	Asn	
			265					270					275			
cgt	agg	ctt	cgg	gct	gtg	gtg	gtc	gag	gcg	ttg	aat	aat	aaa	tta	tct	979
Arg	Arg	Leu	Arg	Ala	Val	Val	Val	Glu	Ala	Leu	Asn	Asn	Lys	Leu	Ser	
		280					285					290				
ccg	gag	cag	att	tct	ggt	ctt	tta	gcc	acc	gag	cat	gct	aac	gat	agc	1027
Pro	Glu	Gln	Ile	Ser	Gly	Leu	Leu	Ala	Thr	Glu	His	Ala	Asn	Asp	Ser	
	295					300					305					
tct	atg	cag	att	agt	cat	gaa	act	att	tac	cag	gcg	tta	tat	gtt	caa	1075
Ser	Met	Gln	Ile	Ser	His	Glu	Thr	Ile	Tyr	Gln	Ala	Leu	Tyr	Val	Gln	
310					315					320					325	
ggt	aaa	ggg	gcg	ttg	cgt	gat	gaa	ttg	aag	gtg	gag	aaa	ttt	ctt	cgt	1123
Gly	Lys	Gly	Ala	Leu	Arg	Asp	Glu	Leu	Lys	Val	Glu	Lys	Phe	Leu	Arg	
				330					335					340		
acc	ggt	cgg	aag	gga	cgt	aaa	ccg	cag	tcg	aag	ttg	cca	tcg	aga	ggt	1171
Thr	Gly	Arg	Lys	Gly	Arg	Lys	Pro	Gln	Ser	Lys	Leu	Pro	Ser	Arg	Gly	
			345					350					355			
aag	ccg	tgg	gtg	gag	ggt	gcg	ttg	att	agt	caa	cgc	cca	gca	gaa	gtt	1219
Lys	Pro	Trp	Val	Glu	Gly	Ala	Leu	Ile	Ser	Gln	Arg	Pro	Ala	Glu	Val	
		360					365					370				

gct gat cgt gct gtg cct ggg cac tgg gag ggc gat tta gta att ggt 1267
 Ala Asp Arg Ala Val Pro Gly His Trp Glu Gly Asp Leu Val Ile Gly
 375 380 385

ggt gaa aac caa gcg aca gcg ttg gtg acg ttg gtg gag cgc acg agc 1315
 Gly Glu Asn Gln Ala Thr Ala Leu Val Thr Leu Val Glu Arg Thr Ser
 390 395 400 405

cgg ttg acg ttg att aag cgg ttg ggg gtt aat cat gag gcg tcg act 1363
 Arg Leu Thr Leu Ile Lys Arg Leu Gly Val Asn His Glu Ala Ser Thr
 410 415 420

gtg acg gat gcg ttg gtg gag atg atg ggt gat ttg ccg cag gcg ttg 1411
 Val Thr Asp Ala Leu Val Glu Met Met Gly Asp Leu Pro Gln Ala Leu
 425 430 435

cgt cgg agt ttg acg tgg gat cag ggt gtg gag atg gca gag cat gcg 1459
 Arg Arg Ser Leu Thr Trp Asp Gln Gly Val Glu Met Ala Glu His Ala
 440 445 450

cgg ttt agc gtg gtg acc aag tgt ccg gtg ttt ttc tgt gat cct cat 1507
 Arg Phe Ser Val Val Thr Lys Cys Pro Val Phe Phe Cys Asp Pro His
 455 460 465

tcg ccg tgg cag cgt ggg tcg aat gag aat acg aat gga ttg gtc agg 1555
 Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr Asn Gly Leu Val Arg
 470 475 480 485

gat ttt ttc ccg aag ggc act aat ttt gct aaa gta agt gac gaa gaa 1603
 Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys Val Ser Asp Glu Glu
 490 495 500

gtt cag cgg gca cag gat ctg ctg aat tac cgg ccg cgg aaa atg cat 1651
 Val Gln Arg Ala Gln Asp Leu Leu Asn Tyr Arg Pro Arg Lys Met His
 505 510 515

ggt ttt aaa agc gcg acg cag gta tat gaa aaa atc gta gtt ggt gca 1699
 Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Lys Ile Val Val Gly Ala
 520 525 530

tcc acc gat tgaattcgcc ctaggttgga tgc 1731
 Ser Thr Asp
 535

<210> 236

<211> 536

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

Met His His Glu Gln Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr
 1 5 10 15

Ile Pro Glu Glu Ser Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly
 20 25 30

Met Ser Gly Leu Ala Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr
 35 40 45

Gly Arg Lys Trp Ala Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro
 50 55 60
 Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala
 65 70 75 80
 Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val
 85 90 95
 Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp
 100 105 110
 Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala
 115 120 125
 Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr
 130 135 140
 Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu
 145 150 155 160
 Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu
 165 170 175
 Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro
 180 185 190
 Leu Phe Ala Asp Glu Ile Lys Val Val Gly Gln Gly Thr Arg Leu Ser
 195 200 205
 Leu Glu Glu Lys Met Met Ile Gln Arg Phe His Asp Thr Gly Val Ser
 210 215 220
 Ala Ala Glu Ile Gly Arg Arg Leu Gly Arg Cys Arg Gln Thr Ile Ser
 225 230 235 240
 Arg Glu Leu Arg Arg Gly Gln Asp Asp Asp Gly Arg Tyr Arg Ala Arg
 245 250 255
 Asp Ser Tyr Glu Gly Ala Ile Arg Lys Leu Ala Arg Pro Lys Thr Pro
 260 265 270
 Lys Leu Asp Ala Asn Arg Arg Leu Arg Ala Val Val Val Glu Ala Leu
 275 280 285
 Asn Asn Lys Leu Ser Pro Glu Gln Ile Ser Gly Leu Leu Ala Thr Glu
 290 295 300
 His Ala Asn Asp Ser Ser Met Gln Ile Ser His Glu Thr Ile Tyr Gln
 305 310 315 320
 Ala Leu Tyr Val Gln Gly Lys Gly Ala Leu Arg Asp Glu Leu Lys Val
 325 330 335
 Glu Lys Phe Leu Arg Thr Gly Arg Lys Gly Arg Lys Pro Gln Ser Lys
 340 345 350
 Leu Pro Ser Arg Gly Lys Pro Trp Val Glu Gly Ala Leu Ile Ser Gln
 355 360 365
 Arg Pro Ala Glu Val Ala Asp Arg Ala Val Pro Gly His Trp Glu Gly

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<210> 237
<211> 417
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(394)  
<223> RXA00017
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<400> 237
tcacccaatg tggagaagtt caaaagctga agctggacct gacccccgga tggtaggacac 60

cttgaaacaa gcatgatgct gggaaaggta atctgccacc atg cca cgc aag acc 115
Met Pro Arg Lys Thr
1 5

tac aca gag gag ttc aag cgc gac gct gtc gcg ctc tac gag aac tcc 163
Tyr Thr Glu Glu Phe Lys Arg Asp Ala Val Ala Leu Tyr Glu Asn Ser
10 15 20

gcc ggc acc tcg atc cag aag atc gcc aat gat ctc gga atc aac cga 211
Ala Gly Thr Ser Ile Gln Lys Ile Ala Asn Asp Leu Gly Ile Asn Arg
25 30 35

atg acc ctt aaa aac tgg att act aaa tac ggg gcc aac tca act cca 259
Met Thr Leu Lys Asn Trp Ile Thr Lys Tyr Gly Ala Asn Ser Thr Pro
40 45 50

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cat ggc gct aac acg gcc acc gcg ctg tcc gaa gct gaa cgg atc cgc 307
His Gly Ala Asn Thr Ala Thr Ala Leu Ser Glu Ala Glu Arg Ile Arg
   55                      60                      65

caa ctt gaa aag gaa aat gca ctc ctc cgc gaa gag cgt gac atc ctg 355
Gln Leu Glu Lys Glu Asn Ala Leu Leu Arg Glu Glu Arg Asp Ile Leu
   70                      75                      80                      85

cgg aaa gcg gcc aaa tat ttc gcg gaa gag acg aac tgg tgatccgctt 404
Arg Lys Ala Ala Lys Tyr Phe Ala Glu Glu Thr Asn Trp
          90                      95

ccgattcggtt gat 417

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<210> 238
<211> 98
<212> PRT
<213> Corynebacterium glutamicum

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<400> 238
Met Pro Arg Lys Thr Tyr Thr Glu Glu Phe Lys Arg Asp Ala Val Ala
  1                      5                      10                      15

Leu Tyr Glu Asn Ser Ala Gly Thr Ser Ile Gln Lys Ile Ala Asn Asp
          20                      25                      30

Leu Gly Ile Asn Arg Met Thr Leu Lys Asn Trp Ile Thr Lys Tyr Gly
   35                      40                      45

Ala Asn Ser Thr Pro His Gly Ala Asn Thr Ala Thr Ala Leu Ser Glu
   50                      55                      60

Ala Glu Arg Ile Arg Gln Leu Glu Lys Glu Asn Ala Leu Leu Arg Glu
   65                      70                      75                      80

Glu Arg Asp Ile Leu Arg Lys Ala Ala Lys Tyr Phe Ala Glu Glu Thr
          85                      90                      95

Asn Trp

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<210> 239
<211> 222
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(199)
<223> RXA00057

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<400> 239
tcgcgtcgac gctttcgaac aggtgctgtt ttagaaggga aatagacaac aaatataacc 60

ctacaaatat tatatagaca gcctcggaat gaggcagtca ttg gga tca att ggc 115
          Leu Gly Ser Ile Gly
          1                      5

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acc agt gct gac aac gcg tta gcg gag tcg ttc aac gcc gca ctc agg 163
 Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe Asn Ala Ala Leu Arg
 10 15 20

cgg gaa gtc ctc caa gat tct aag act ttt gcg aac tagttgatct 209
 Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Ala Asn
 25 30

gccgccggga tgt 222

<210> 240

<211> 33

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

Leu Gly Ser Ile Gly Thr Ser Ala Asp Asn Ala Leu Ala Glu Ser Phe
 1 5 10 15

Asn Ala Ala Leu Arg Arg Glu Val Leu Gln Asp Ser Lys Thr Phe Ala
 20 25 30

Asn

<210> 241

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA00227

<400> 241

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ctatccagaa gtaggcttta cagaaagtca ggggtgtggca atg gtg atg cag ggc 115
 Met Val Met Gln Gly
 1 5

att ggt ggt agg aag ctg gcg gcg acg gtg ctg ttg gtt cgg gat ggg 163
 Ile Gly Gly Arg Lys Leu Ala Ala Thr Val Leu Leu Val Arg Asp Gly
 10 15 20

atc atc aat ggg cgt cct gat gtg gag gtt tac att cag gag cgt gtg 211
 Ile Ile Asn Gly Arg Pro Asp Val Glu Val Tyr Ile Gln Glu Arg Val
 25 30 35

tct act atg gct aat ttt cct cgg gcg acg gtg ttt ccg ggt ggg ggt 259
 Ser Thr Met Ala Asn Phe Pro Arg Ala Thr Val Phe Pro Gly Gly Gly
 40 45 50

gtt gat tct cgg gat ttt gcg gat ggt cac ggt aag gaa gtg tgg agg 307
 Val Asp Ser Arg Asp Phe Ala Asp Gly His Gly Lys Glu Val Trp Arg
 55 60 65

gga cct agc gcg gag gag tgg ggt gtg cgt tta ggc gtg gag cct cat 355

Gly 70	Pro	Ser	Ala	Glu	Glu 75	Trp	Gly	Val	Arg	Leu 80	Gly	Val	Glu	Pro	His 85	
ggt	gcg	tat	gcg	ttg	ggt	ttt	gct	gcg	gtt	cgt	gag	ttg	ttt	gaa	gag	403
Val	Ala	Tyr	Ala	Leu	Val	Phe	Ala	Ala	Val	Arg	Glu	Leu	Phe	Glu	Glu	
				90					95					100		
gcc	ggt	acg	ttg	ctt	gcg	gag	cat	acg	gat	ggg	tct	ggg	ttg	gtg	aag	451
Ala	Gly	Thr	Leu	Leu	Ala	Glu	His	Thr	Asp	Gly	Ser	Gly	Leu	Val	Lys	
			105					110					115			
aat	gct	ggg	cag	tat	cac	gga	tat	cgg	gag	ttg	ttg	gag	act	cat	gag	499
Asn	Ala	Gly	Gln	Tyr	His	Gly	Tyr	Arg	Glu	Leu	Leu	Glu	Thr	His	Glu	
		120					125					130				
atg	tcg	ctg	acg	gat	atg	ttg	cag	agt	gag	aat	ttg	gcg	att	cgt	agt	547
Met	Ser	Leu	Thr	Asp	Met	Leu	Gln	Ser	Glu	Asn	Leu	Ala	Ile	Arg	Ser	
						140					145					
gat	ttg	att	gtg	cct	ttt	gcc	agg	tgg	gcg	agc	cct	gag	ggg	aat	agg	595
Asp	Leu	Ile	Val	Pro	Phe	Ala	Arg	Trp	Ala	Ser	Pro	Glu	Gly	Asn	Arg	
150					155				160						165	
gag	cag	ttt	gat	acg	ttt	tct	ttt	gtt	gct	gtg	gag	ccg	gag	ggg	cag	643
Glu	Gln	Phe	Asp	Thr	Phe	Ser	Phe	Val	Ala	Val	Glu	Pro	Glu	Gly	Gln	
				170				175						180		
tgt	gcg	gat	ggg	aat	acg	tcg	gag	gcg	tct	tcg	acg	ggg	tat	ttt	cct	691
Cys	Ala	Asp	Gly	Asn	Thr	Ser	Glu	Ala	Ser	Ser	Thr	Gly	Tyr	Phe	Pro	
			185					190					195			
gca	cgg	ctg	att	ttg	gat	ggg	tgg	cgc	gcc	ggg	ttg	ttg	agg	ttg	gtt	739
Ala	Arg	Leu	Ile	Leu	Asp	Gly	Trp	Arg	Ala	Gly	Leu	Leu	Arg	Leu	Val	
		200					205					210				
att	ccg	acg	tgg	gcg	tcg	ttg	ttt	gag	ttg	tcg	cag	ttt	aag	act	gtg	787
Ile	Pro	Thr	Trp	Ala	Ser	Leu	Phe	Glu	Leu	Ser	Gln	Phe	Lys	Thr	Val	
	215					220					225					
gag	gaa	ttg	ctg	gag	tac	agc	gcg	cag	gtt	gat	atg	tct	cct	gtg	ttg	835
Glu	Glu	Leu	Leu	Glu	Tyr	Ser	Ala	Gln	Val	Asp	Met	Ser	Pro	Val	Leu	
230					235					240					245	
gat	gat	gcg	gtg	gat	aat	ccg	agg	tat	gcg	gag	ttt	tat	cag	gcg	atg	883
Asp	Asp	Ala	Val	Asp	Asn	Pro	Arg	Tyr	Ala	Glu	Phe	Tyr	Gln	Ala	Met	
				250					255					260		
cgc	acg	gaa	cgg	ttt	tgatcattta	aggttcattc	atg									921
Arg	Thr	Glu	Arg	Phe												
				265												

<210> 242

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

Met	Val	Met	Gln	Gly	Ile	Gly	Gly	Arg	Lys	Leu	Ala	Ala	Thr	Val	Leu
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Leu Val Arg Asp Gly Ile Ile Asn Gly Arg Pro Asp Val Glu Val Tyr
 20 25 30
 Ile Gln Glu Arg Val Ser Thr Met Ala Asn Phe Pro Arg Ala Thr Val
 35 40 45
 Phe Pro Gly Gly Gly Val Asp Ser Arg Asp Phe Ala Asp Gly His Gly
 50 55 60
 Lys Glu Val Trp Arg Gly Pro Ser Ala Glu Glu Trp Gly Val Arg Leu
 65 70 75 80
 Gly Val Glu Pro His Val Ala Tyr Ala Leu Val Phe Ala Ala Val Arg
 85 90 95
 Glu Leu Phe Glu Glu Ala Gly Thr Leu Leu Ala Glu His Thr Asp Gly
 100 105 110
 Ser Gly Leu Val Lys Asn Ala Gly Gln Tyr His Gly Tyr Arg Glu Leu
 115 120 125
 Leu Glu Thr His Glu Met Ser Leu Thr Asp Met Leu Gln Ser Glu Asn
 130 135 140
 Leu Ala Ile Arg Ser Asp Leu Ile Val Pro Phe Ala Arg Trp Ala Ser
 145 150 155 160
 Pro Glu Gly Asn Arg Glu Gln Phe Asp Thr Phe Ser Phe Val Ala Val
 165 170 175
 Glu Pro Glu Gly Gln Cys Ala Asp Gly Asn Thr Ser Glu Ala Ser Ser
 180 185 190
 Thr Gly Tyr Phe Pro Ala Arg Leu Ile Leu Asp Gly Trp Arg Ala Gly
 195 200 205
 Leu Leu Arg Leu Val Ile Pro Thr Trp Ala Ser Leu Phe Glu Leu Ser
 210 215 220
 Gln Phe Lys Thr Val Glu Glu Leu Leu Glu Tyr Ser Ala Gln Val Asp
 225 230 235 240
 Met Ser Pro Val Leu Asp Asp Ala Val Asp Asn Pro Arg Tyr Ala Glu
 245 250 255
 Phe Tyr Gln Ala Met Arg Thr Glu Arg Phe
 260 265

<210> 243

<211> 570

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(547)

<223> RXA01819

<400> 243

ggttgggggtc atcaaaggat gcggacatcg ctgtgggggtt gtgtaataat tgcacctgtg 60

<400> 244

Leu	Ile	Leu	Pro	Val	Gln	Glu	Gly	Ile	Ser	Tyr	Phe	Pro	Thr	Pro	Leu
1				5					10					15	
His	Leu	Asn	His	Ile	Gly	Gly	Ser	Arg	Phe	Lys	Lys	Phe	Leu	Val	Lys
			20					25					30		
Ile	Asp	Lys	Thr	Val	Pro	Gln	Asp	Leu	Asp	Val	His	Val	Ile	Cys	Asp
		35					40					45			
Asn	Tyr	Ala	Thr	His	Lys	His	Pro	Thr	Ile	Asn	Thr	Trp	Leu	Val	Lys
	50					55					60				

His Pro Arg Phe His Met His Phe Thr Pro Thr Tyr Ser Ser Trp Ile
65 70 75 80

Asn Gln Val Glu Arg Leu Phe Ala Glu Val Thr Arg Glu Leu Leu Gln
85 90 95

Arg Ser Asp His Arg Ser Val Gln Ala Leu Glu Lys Asp Leu Arg Asn
100 105 110

Trp Val Lys Ala Trp Asn Glu Asp Pro Lys Pro Phe Ile Trp Thr Lys
115 120 125

Thr Ala Glu Glu Ile Leu Ser Ser Ile Ala Arg Tyr Leu Lys Arg Ile
130 135 140

Asn Gly Ala Gly His
145

<210> 245

<211> 879

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(856)

<223> RXN03052

<400> 245

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tttttaaata tccccagcct tcattcctgt aacggtcata atg ccc ttt tct cac 115
Met Pro Phe Ser His
1 5

gac aaa tct gaa ctc ggt ggg gaa acc ccc tac ggg ctt gta cat gtt 163
Asp Lys Ser Glu Leu Gly Gly Glu Thr Pro Tyr Gly Leu Val His Val
10 15 20

aac cct atg gct gaa gtg cga cct gta aaa gca caa acc aac gag ccc 211
Asn Pro Met Ala Glu Val Arg Pro Val Lys Ala Gln Thr Asn Glu Pro
25 30 35

caa gca ctg cag gtt gct gac att caa ccc ttt cac gct gtt att gcg 259
Gln Ala Leu Gln Val Ala Asp Ile Gln Pro Phe His Ala Val Ile Ala
40 45 50

gcc tca aaa caa ttg act ctc atc gac gtt gtc gat gtc tgc ctt gga 307
Ala Ser Lys Gln Leu Thr Leu Ile Asp Val Val Asp Val Cys Leu Gly
55 60 65

aca gtg ttg cga gca tgg gaa gca ctg agc ctg cga tgg gta gac gtg 355
Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu Arg Trp Val Asp Val
70 75 80 85

gtg ctt gac gag gag cat cca aga atc ttt atc cga ggc acc att gtc 403
Val Leu Asp Glu Glu His Pro Arg Ile Phe Ile Arg Gly Thr Ile Val
90 95 100

tac aac aaa gaa aaa ggt aac cac aga caa gat aaa aca aaa acg acc 451
 Tyr Asn Lys Glu Lys Gly Asn His Arg Gln Asp Lys Thr Lys Thr Thr
 105 110 115

 agc agt agg cgt gtc att cag ttg cca gaa att gcc tca gac gtc tta 499
 Ser Ser Arg Arg Val Ile Gln Leu Pro Glu Ile Ala Ser Asp Val Leu
 120 125 130

 cgc aaa aga cat gca ctc tac gcc gaa cat ctc gaa atg gtg ttc cct 547
 Arg Lys Arg His Ala Leu Tyr Ala Glu His Leu Glu Met Val Phe Pro
 135 140 145

 tcc gct aga ggc aca tat att tat gag tcc aat ttc aac aaa ttg ttg 595
 Ser Ala Arg Gly Thr Tyr Ile Tyr Glu Ser Asn Phe Asn Lys Leu Leu
 150 155 160 165

 cga aaa cac cga aag ggt act gca tat gat tgg gtg acc gtg cac agc 643
 Arg Lys His Arg Lys Gly Thr Ala Tyr Asp Trp Val Thr Val His Ser
 170 175 180

 atc agg aaa acc ctt gca tca att gtc tct gag aac ctt gat tcc aag 691
 Ile Arg Lys Thr Leu Ala Ser Ile Val Ser Glu Asn Leu Asp Ser Lys
 185 190 195

 gcc gca tca gac gta ctc ggc cat gct gac tca cga ctc aca gaa cgg 739
 Ala Ala Ser Asp Val Leu Gly His Ala Asp Ser Arg Leu Thr Glu Arg
 200 205 210

 gtc tac atc gct aaa act gac aaa gac gtt ccg att ggt gat gtc gtc 787
 Val Tyr Ile Ala Lys Thr Asp Lys Asp Val Pro Ile Gly Asp Val Val
 215 220 225

 aac caa gcg ctc aaa gag gca cga aaa gtc tcc aaa aag tct cca aat 835
 Asn Gln Ala Leu Lys Glu Ala Arg Lys Val Ser Lys Lys Ser Pro Asn
 230 235 240 245

 aaa gaa gct aaa gaa gaa gaa tagacgcaat agttgcattt tta 879
 Lys Glu Ala Lys Glu Glu Glu
 250

<210> 246

<211> 252

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

Met Pro Phe Ser His Asp Lys Ser Glu Leu Gly Gly Glu Thr Pro Tyr
 1 5 10 15

 Gly Leu Val His Val Asn Pro Met Ala Glu Val Arg Pro Val Lys Ala
 20 25 30

 Gln Thr Asn Glu Pro Gln Ala Leu Gln Val Ala Asp Ile Gln Pro Phe
 35 40 45

 His Ala Val Ile Ala Ala Ser Lys Gln Leu Thr Leu Ile Asp Val Val
 50 55 60

 Asp Val Cys Leu Gly Thr Val Leu Arg Ala Trp Glu Ala Leu Ser Leu
 65 70 75 80

<400> 247																
cacttaatgc	catgaccttg	tgc	atgcata	gtgtcatgac	ctt	gtgcaca	ccccagacct	60								
acaccacagg	catagtccta	ggctgctcac	aattgacatc	atg	cct	aaa	ccc	cta	115							
					Met	Pro	Lys	Pro	Leu							
					1				5							
ccc	cca	gaa	acc	cga	cgc	aag	atc	atc	gat	ttc	gat	ccg	ttc	gca	ccg	163
Pro	Pro	Glu	Thr	Arg	Arg	Lys	Ile	Ile	Asp	Phe	Asp	Pro	Phe	Ala	Pro	
				10					15					20		
aac	agc	ccc	tcg	atc	gaa	gag	ttc	tgc	agt	cgg	cta	aaa	ata	tcg	cgg	211
Asn	Ser	Pro	Ser	Ile	Glu	Glu	Phe	Cys	Ser	Arg	Leu	Lys	Ile	Ser	Arg	
			25					30					35			
cgc	agc	ttc	tac	aac	atc	cgc	aac	cga	tac	caa	caa	gac	gcc	aac	gca	259

Arg Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Asn Ala
 40 45 50
 gca ctg cat tca cac tcc agc gcc cca atc acc gcc cgg cga acg tac 307
 Ala Leu His Ser His Ser Ser Ala Pro Ile Thr Ala Arg Arg Thr Tyr
 55 60 65
 gat gaa tcc atc acc agc acc ttg ctg tcc atc cgc gca cgc ctg aaa 355
 Asp Glu Ser Ile Thr Ser Thr Leu Leu Ser Ile Arg Ala Arg Leu Lys
 70 75 80 85
 gcc caa gga tgg gag tac ggc ccg atc tct att cga ttc gaa ggc atc 403
 Ala Gln Gly Trp Glu Tyr Gly Pro Ile Ser Ile Arg Phe Glu Gly Ile
 90 95 100
 ttc acc cgg gaa ctg act gca ccg att cca tct gtt tca acc att gct 451
 Phe Thr Arg Glu Leu Thr Ala Pro Ile Pro Ser Val Ser Thr Ile Ala
 105 110 115
 cgt ttg tta cgc gcc gca gga gct gtt 478
 Arg Leu Leu Arg Ala Ala Gly Ala Val
 120 125

<210> 248

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Met Pro Lys Pro Leu Pro Pro Glu Thr Arg Arg Lys Ile Ile Asp Phe
 1 5 10 15
 Asp Pro Phe Ala Pro Asn Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg
 20 25 30
 Leu Lys Ile Ser Arg Arg Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln
 35 40 45
 Gln Asp Ala Asn Ala Ala Leu His Ser His Ser Ser Ala Pro Ile Thr
 50 55 60
 Ala Arg Arg Thr Tyr Asp Glu Ser Ile Thr Ser Thr Leu Leu Ser Ile
 65 70 75 80
 Arg Ala Arg Leu Lys Ala Gln Gly Trp Glu Tyr Gly Pro Ile Ser Ile
 85 90 95
 Arg Phe Glu Gly Ile Phe Thr Arg Glu Leu Thr Ala Pro Ile Pro Ser
 100 105 110
 Val Ser Thr Ile Ala Arg Leu Leu Arg Ala Ala Gly Ala Val
 115 120 125

<210> 249

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(634)

<223> RXN02919

<400> 249

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ctgacctaag atctcgagga aatgatgact tcagcgcgga  gtg ccg gtc gat cac 115
                                         Val Pro Val Asp His
                                         1                               5

acc acc atc tac cgc tgg gtc cag aaa tac gcc cct gag ctg gat aag 163
Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala Pro Glu Leu Asp Lys
                        10                               15                               20

cag act cgc tgg tac cgg cag gtt cct gac tgg cag gcc agt tcc tgg 211
Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp Gln Ala Ser Ser Trp
                        25                               30                               35

cgg gtg gat gag acc tat atc cgg gtc ggc ggc acg tgg tgc tat ctc 259
Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly Thr Trp Cys Tyr Leu
                        40                               45                               50

tac cgg gct att acc gcg ggt ggg cag acc ctg gag ttt tat ctc tca 307
Tyr Arg Ala Ile Thr Ala Gly Gln Thr Leu Glu Phe Tyr Leu Ser
                        55                               60                               65

cca aaa cgg aat gtg gct gcg gcc aag cgt ttc ctg gcc aag acg ctg 355
Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe Leu Ala Lys Thr Leu
                        70                               75                               80                               85

cga tcg aat acg aca gcc ggg tcc ccg cgg gtc atc aac acc gac aag 403
Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val Ile Asn Thr Asp Lys
                        90                               95                               100

gca cca gct ctg gcc aag gca ata tcc gag ctg aag gcg gag gga atc 451
Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu Lys Ala Glu Gly Ile
                        105                               110                               115

tgc cct cag acg gtg gag cac cgg cag gtg aaa tac ctc aac aac gtt 499
Cys Pro Gln Thr Val Glu His Arg Gln Val Lys Tyr Leu Asn Asn Val
                        120                               125                               130

atc gag gga gat cat ggc cga ctc aaa aga atc ctg ggg ccg aag gga 547
Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile Leu Gly Pro Lys Gly
                        135                               140                               145

gcg ttc aaa aac cga att tcc gcc tac cgg acg ttg aaa ggg atg gag 595
Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr Leu Lys Gly Met Glu
                        150                               155                               160                               165

gcg atg cat tca ttg cgg aaa ggg tca ggg aac gat gtt tgacctcacg 644
Ala Met His Ser Leu Arg Lys Gly Ser Gly Asn Asp Val
                        170                               175

ggcacccgaa ccc 657

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<210> 250

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

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Val Pro Val Asp His Thr Thr Ile Tyr Arg Trp Val Gln Lys Tyr Ala
  1              5              10              15

Pro Glu Leu Asp Lys Gln Thr Arg Trp Tyr Arg Gln Val Pro Asp Trp
      20              25              30

Gln Ala Ser Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val Gly Gly
      35              40              45

Thr Trp Cys Tyr Leu Tyr Arg Ala Ile Thr Ala Gly Gly Gln Thr Leu
      50              55              60

Glu Phe Tyr Leu Ser Pro Lys Arg Asn Val Ala Ala Ala Lys Arg Phe
      65              70              75              80

Leu Ala Lys Thr Leu Arg Ser Asn Thr Thr Ala Gly Ser Pro Arg Val
      85              90              95

Ile Asn Thr Asp Lys Ala Pro Ala Leu Ala Lys Ala Ile Ser Glu Leu
      100             105             110

Lys Ala Glu Gly Ile Cys Pro Gln Thr Val Glu His Arg Gln Val Lys
      115             120             125

Tyr Leu Asn Asn Val Ile Glu Gly Asp His Gly Arg Leu Lys Arg Ile
      130             135             140

Leu Gly Pro Lys Gly Ala Phe Lys Asn Arg Ile Ser Ala Tyr Arg Thr
      145             150             155             160

Leu Lys Gly Met Glu Ala Met His Ser Leu Arg Lys Gly Ser Gly Asn
      165             170             175

Asp Val

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<210> 251

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN03033

<400> 251

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atcctggcga gggcttagac gaggaggacg ccacctaaac gtg gat gag caa cgc 115
                               Val Asp Glu Gln Arg
                               1              5

gcc ttt gat caa gga ctc aag gaa gaa aac acc ttg atc aca gat ctc 163
Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr Leu Ile Thr Asp Leu
      10              15              20

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acc acc tgt gcc agg ctg agc cat aac aag gca tta cgg ctg atc aag	211
Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala Leu Arg Leu Ile Lys	
25 30 35	
ctg tcg aaa tca acg gcg tat tac cgc aac aag ccg cgt ccc cgt cct	259
Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys Pro Arg Pro Arg Pro	
40 45 50	
gca ccg aaa cct gtc ctg cag gcc gtg cca gca cca aca gca cct ggt	307
Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala Pro Thr Ala Pro Gly	
55 60 65	
gtg gaa ccc aca cca gag cct tgg cag ggg aag gag cca gca gtg tcg	355
Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys Glu Pro Ala Val Ser	
70 75 80 85	
tcg gtg cgt caa gcg ttg gca gaa cac gaa cgc cag ttc att gtt gat	403
Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg Gln Phe Ile Val Asp	
90 95 100	
gcg atc acc gcg tac cca caa ctg agc gtt agt ggg gtg ttt aac atg	451
Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser Gly Val Phe Asn Met	
105 110 115	
ttg ttt aac aaa ggc atc tac cgc gca tca cta cgt aca tgg tgg cgt	499
Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu Arg Thr Trp Trp Arg	
120 125 130	
gtt gcc aag cag cac aag ttg tta cac aaa gac cga gtc agt gcc ctg	547
Val Ala Lys Gln His Lys Leu Leu His Lys Asp Arg Val Ser Ala Leu	
135 140 145	
tcc ccg ggg aaa cga tca cca acg cca ccg gtt aag ccg agg ttg gaa	595
Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val Lys Pro Arg Leu Glu	
150 155 160 165	
gca aca cag cct ggt cag gtg gtg tgt tgg gat gtg acg ttc ttg ccg	643
Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp Val Thr Phe Leu Pro	
170 175 180	
tcg ctg gta cgt ggt aag acc tat gcg ttg cat ctg gcg att gat ttg	691
Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His Leu Ala Ile Asp Leu	
185 190 195	
ttt tcc cgc aag att gtt ggg gcg aag gtc gcg ccg acg gaa aat acc	739
Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala Pro Thr Glu Asn Thr	
200 205 210	
tcc acc gcg gtg gag ttg tta acg cag gtg tta gcg gat aat ccg ggt	787
Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu Ala Asp Asn Pro Gly	
215 220 225	
gtg gtg acg gtg cat tcg gat aat ggg tcg gcg atg aca tcg acg agg	835
Val Val Thr Val His Ser Asp Asn Gly Ser Ala Met Thr Ser Thr Arg	
230 235 240 245	
gtg ccg ccg ttg tta gcg gat cat ggt gtg gcg ttg tcg ttg att ccg	883
Val Arg Arg Leu Leu Ala Asp His Gly Val Ala Leu Ser Leu Ile Arg	
250 255 260	
ccg ccg gtg agt gat gat aat gcg ttt gtg gag tcg gtg ttt cat acg	931

Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu Ser Val Phe His Thr
 265 270 275

ttg aag tat cgg ccg ttt tat ccg aag gtg ttt gca tcg atg gat cag 979
 Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe Ala Ser Met Asp Gln
 280 285 290

gcc cgg gtg tgg gtg gag gag ttt gtg gtg tat tac aac acg gtt cat 1027
 Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr Tyr Asn Thr Val His
 295 300 305

ccg cat tct ggt gtg gct ggg cat act ccg cag tcg gtg ttt gat ggt 1075
 Pro His Ser Gly Val Ala Gly His Thr Pro Gln Ser Val Phe Asp Gly
 310 315 320 325

agt tgg agg gcg gct cat agg ttg cgt gtg cag gcg ttg gat gcc cat 1123
 Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln Ala Leu Asp Ala His
 330 335 340

tac cgg cag ttc ccg cag cgg tat gtg ggg cgg ccg gtg gtt cag gaa 1171
 Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg Pro Val Val Gln Glu
 345 350 355

gtt gct ggt gtg gtg cgt ctt aat ggt gcg cgt gat gat ggg tct gta 1219
 Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg Asp Asp Gly Ser Val
 360 365 370

cag gag agg gtt ggt ggt gta gcg tcg ctg tta agt gct tgagtttagca 1268
 Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu Ser Ala
 375 380 385

tgtgttctta tcg 1281

<210> 252

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

Val Asp Glu Gln Arg Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr
 1 5 10 15

Leu Ile Thr Asp Leu Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala
 20 25 30

Leu Arg Leu Ile Lys Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys
 35 40 45

Pro Arg Pro Arg Pro Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala
 50 55 60

Pro Thr Ala Pro Gly Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys
 65 70 75 80

Glu Pro Ala Val Ser Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg
 85 90 95

Gln Phe Ile Val Asp Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser
 100 105 110

Gly Val Phe Asn Met Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu
 115 120 125
 Arg Thr Trp Trp Arg Val Ala Lys Gln His Lys Leu Leu His Lys Asp
 130 135 140
 Arg Val Ser Ala Leu Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val
 145 150 155 160
 Lys Pro Arg Leu Glu Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp
 165 170 175
 Val Thr Phe Leu Pro Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His
 180 185 190
 Leu Ala Ile Asp Leu Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala
 195 200 205
 Pro Thr Glu Asn Thr Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu
 210 215 220
 Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala
 225 230 235 240
 Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala
 245 250 255
 Leu Ser Leu Ile Arg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu
 260 265 270
 Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe
 275 280 285
 Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr
 290 295 300
 Tyr Asn Thr Val His Pro His Ser Gly Val Ala Gly His Thr Pro Gln
 305 310 315 320
 Ser Val Phe Asp Gly Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln
 325 330 335
 Ala Leu Asp Ala His Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg
 340 345 350
 Pro Val Val Gln Glu Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg
 355 360 365
 Asp Asp Gly Ser Val Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu
 370 375 380
 Ser Ala
 385

<210> 253

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN03035

<400> 253

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atcctggcga gggcttagac gaggaggacg ccacctaaac gtg gat gag caa cgc 115
Val Asp Glu Gln Arg
1 5

gcc ttt gat caa gga ctc aag gaa gaa aac acc ttg atc aca gat ctc 163
Ala Phe Asp Gln Gly Leu Lys Glu Glu Asn Thr Leu Ile Thr Asp Leu
10 15 20

acc acc tgt gcc agg ctg agc cat aac aag gca tta cgg ctg atc aag 211
Thr Thr Cys Ala Arg Leu Ser His Asn Lys Ala Leu Arg Leu Ile Lys
25 30 35

ctg tcg aaa tca acg gcg tat tac cgc aac aag ccg cgt ccc cgt cct 259
Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys Pro Arg Pro Arg Pro
40 45 50

gca ccg aaa cct gtc ctg cag gcc gtg cca gca cca aca gca cct ggt 307
Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala Pro Thr Ala Pro Gly
55 60 65

gtg gaa ccc aca cca gag cct tgg cag ggg aag gag cca gca gtg tcg 355
Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys Glu Pro Ala Val Ser
70 75 80 85

tcg gtg cgt caa gcg ttg gca gaa cac gaa cgc cag ttc att gtt gat 403
Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg Gln Phe Ile Val Asp
90 95 100

gcg atc acc gcg tac cca caa ctg agc gtt agt ggg gtg ttt aac atg 451
Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser Gly Val Phe Asn Met
105 110 115

ttg ttt aac aaa ggc atc tac cgc gca tca cta cgt aca tgg tgg cgt 499
Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu Arg Thr Trp Trp Arg
120 125 130

gtt gcc aag cag cac aag ttg tta cac aaa gac cga gtc agt gcc ctg 547
Val Ala Lys Gln His Lys Leu Leu His Lys Asp Arg Val Ser Ala Leu
135 140 145

tcc ccg ggg aaa cga tca cca acg cca cgg gtt aag ccg agg ttg gaa 595
Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val Lys Pro Arg Leu Glu
150 155 160 165

gca aca cag cct ggt cag gtg gtg tgt tgg gat gtg acg ttc ttg ccg 643
Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp Val Thr Phe Leu Pro
170 175 180

tcg ctg gta cgt ggt aag acc tat gcg ttg cat ctg gcg att gat ttg 691
Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His Leu Ala Ile Asp Leu
185 190 195

ttt tcc cgc aag att gtt ggg gcg aag gtc gcg ccg acg gaa aat acc 739
Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala Pro Thr Glu Asn Thr

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200	205	210	
tcc acc gcg gtg gag ttg tta acg cag gtg tta gcg gat aat ccg ggt Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu Ala Asp Asn Pro Gly 215 220 225			787
gtg gtg acg gtg cat tcg gat aat ggg tcg gcg atg aca tcg acg agg Val Val Thr Val His Ser Asp Asn Gly Ser Ala Met Thr Ser Thr Arg 230 235 240 245			835
gtg cgg cgg ttg tta gcg gat cat ggt gtg gcg ttg tcg ttg att cgg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala Leu Ser Leu Ile Arg 250 255 260			883
ccg cgg gtg agt gat gat aat gcg ttt gtg gag tcg gtg ttt cat acg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu Ser Val Phe His Thr 265 270 275			931
ttg aag tat cgg ccg ttt tat ccg aag gtg ttt gca tcg atg gat cag Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe Ala Ser Met Asp Gln 280 285 290			979
gcc cgg gtg tgg gtg gag gag ttt gtg gtg tat tac aac acg gtt cat Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr Tyr Asn Thr Val His 295 300 305			1027
ccg cat tct ggt gtg gct ggg cat act ccg cag tcg gtg ttt gat ggt Pro His Ser Gly Val Ala Gly His Thr Pro Gln Ser Val Phe Asp Gly 310 315 320 325			1075
agt tgg agg gcg gct cat agg ttg cgt gtg cag gcg ttg gat gcc cat Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln Ala Leu Asp Ala His 330 335 340			1123
tac cgg cag ttc ccg cag cgg tat gtg ggg cgg ccg gtg gtt cag gaa Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg Pro Val Val Gln Glu 345 350 355			1171
gtt gct ggt gtg gtg cgt ctt aat ggt gcg cgt gat gat ggg tct gta Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg Asp Asp Gly Ser Val 360 365 370			1219
cag gag agg gtt ggt ggt gta gcg tcg ctg tta agt gct tgagtttagca Gln Glu Arg Val Gly Gly Val Ala Ser Leu Leu Ser Ala 375 380 385			1268
tgtgttctta tcg			1281

<210> 254

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Val	Asp	Glu	Gln	Arg	Ala	Phe	Asp	Gln	Gly	Leu	Lys	Glu	Glu	Asn	Thr
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Leu	Ile	Thr	Asp	Leu	Thr	Thr	Cys	Ala	Arg	Leu	Ser	His	Asn	Lys	Ala
			20					25					30		

Leu Arg Leu Ile Lys Leu Ser Lys Ser Thr Ala Tyr Tyr Arg Asn Lys
 35 40 45
 Pro Arg Pro Arg Pro Ala Pro Lys Pro Val Leu Gln Ala Val Pro Ala
 50 55 60
 Pro Thr Ala Pro Gly Val Glu Pro Thr Pro Glu Pro Trp Gln Gly Lys
 65 70 75 80
 Glu Pro Ala Val Ser Ser Val Arg Gln Ala Leu Ala Glu His Glu Arg
 85 90 95
 Gln Phe Ile Val Asp Ala Ile Thr Ala Tyr Pro Gln Leu Ser Val Ser
 100 105 110
 Gly Val Phe Asn Met Leu Phe Asn Lys Gly Ile Tyr Arg Ala Ser Leu
 115 120 125
 Arg Thr Trp Trp Arg Val Ala Lys Gln His Lys Leu Leu His Lys Asp
 130 135 140
 Arg Val Ser Ala Leu Ser Pro Gly Lys Arg Ser Pro Thr Pro Arg Val
 145 150 155 160
 Lys Pro Arg Leu Glu Ala Thr Gln Pro Gly Gln Val Val Cys Trp Asp
 165 170 175
 Val Thr Phe Leu Pro Ser Leu Val Arg Gly Lys Thr Tyr Ala Leu His
 180 185 190
 Leu Ala Ile Asp Leu Phe Ser Arg Lys Ile Val Gly Ala Lys Val Ala
 195 200 205
 Pro Thr Glu Asn Thr Ser Thr Ala Val Glu Leu Leu Thr Gln Val Leu
 210 215 220
 Ala Asp Asn Pro Gly Val Val Thr Val His Ser Asp Asn Gly Ser Ala
 225 230 235 240
 Met Thr Ser Thr Arg Val Arg Arg Leu Leu Ala Asp His Gly Val Ala
 245 250 255
 Leu Ser Leu Ile Arg Pro Arg Val Ser Asp Asp Asn Ala Phe Val Glu
 260 265 270
 Ser Val Phe His Thr Leu Lys Tyr Arg Pro Phe Tyr Pro Lys Val Phe
 275 280 285
 Ala Ser Met Asp Gln Ala Arg Val Trp Val Glu Glu Phe Val Val Tyr
 290 295 300
 Tyr Asn Thr Val His Pro His Ser Gly Val Ala Gly His Thr Pro Gln
 305 310 315 320
 Ser Val Phe Asp Gly Ser Trp Arg Ala Ala His Arg Leu Arg Val Gln
 325 330 335
 Ala Leu Asp Ala His Tyr Arg Gln Phe Pro Gln Arg Tyr Val Gly Arg
 340 345 350
 Pro Val Val Gln Glu Val Ala Gly Val Val Arg Leu Asn Gly Ala Arg

[illegible]

ccg cag acc tcg tat gtc gcc gtc cac acg tgc atg cag ggc tgg tca 547
 Pro Gln Thr Ser Tyr Val Ala Val His Thr Cys Met Gln Gly Trp Ser
 135 140 145

 gct acc gcc cgg tgg aca ggg gtg cgg tta cgt gat gtt ttg tgt cat 595
 Ala Thr Ala Arg Trp Thr Gly Val Arg Leu Arg Asp Val Leu Cys His
 150 155 160 165

 gac ctt gtg cac acc cta gac ctt cac cac agg cat agt cct cgg ctg 643
 Asp Leu Val His Thr Leu Asp Leu His His Arg His Ser Pro Arg Leu
 170 175 180

 ctc aca att gag atc ata cct aaa ccc ctg ccc cca gaa acc cga tgc 691
 Leu Thr Ile Glu Ile Ile Pro Lys Pro Leu Pro Pro Glu Thr Arg Cys
 185 190 195

 aag atc atc gat ttc gat ctg ttc gca ccg aac agt ccc tcg atc gaa 739
 Lys Ile Ile Asp Phe Asp Leu Phe Ala Pro Asn Ser Pro Ser Ile Glu
 200 205 210

 gag ttc tgc agt cgg ctt aaa ata tcg cgg cgc agc ttc tac aac atc 787
 Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg Arg Ser Phe Tyr Asn Ile
 215 220 225

 cgc aac cga tac caa caa gat gcc agt gca gcg ctg cat cca cgc tcc 835
 Arg Asn Arg Tyr Gln Gln Asp Ala Ser Ala Ala Leu His Pro Arg Ser
 230 235 240 245

 agc gcc cag atc acc tcc cgg cga aca tac gat gaa tcc atc acc agt 883
 Ser Ala Gln Ile Thr Ser Arg Arg Thr Tyr Asp Glu Ser Ile Thr Ser
 250 255 260

 atc ttg ttg gcc atc cgc gca ccg cct gaa agc cca agg atg gga rta 931
 Ile Leu Leu Ala Ile Arg Ala Pro Pro Glu Ser Pro Arg Met Gly Xaa
 265 270 275

 cgg ycc gat ctc tat ycg att cga agg cat ckc cac cgg gga act gac 979
 Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa His Arg Gly Thr Asp
 280 285 290

 tgc acc gat tcc atc cgt ctc aac tat cgc ttg ctt gtt acg cgc tgc 1027
 Cys Thr Asp Ser Ile Arg Leu Asn Tyr Arg Leu Val Thr Arg Cys
 295 300 305

 agg agc agt cga aag taaccctaag aagcgaccaa agt 1065
 Arg Ser Ser Arg Lys
 310

<210> 256

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 256

Met Val His Met Val Phe Gly Asp Met Asn Thr Asp Arg Ala Ala Gln
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 20 25 30
 Ile Val Leu Arg Tyr Trp Ser Leu Ala Asp Arg Ala Arg Ala Gln Arg
 35 40 45
 Phe Thr Ala Ser Ile Thr Glu Ile Gly Arg Lys Ile Phe Leu Asn Arg
 50 55 60
 Leu Arg Pro Arg Met Ser Arg Gln Asn Thr Tyr Thr Asp Lys Asp Ile
 65 70 75 80
 Ser Gln Phe His Trp Thr Asn Gly Leu Pro Pro Thr Asp Asp Glu Ser
 85 90 95
 Pro Glu Trp Ile Ala Ala Arg Asp Asn Glu Trp Glu Gly Tyr Thr Ile
 100 105 110
 Thr Leu Gly Asp Asp Pro Asn Gly Thr Glu Lys Thr Ile Thr Leu Asp
 115 120 125
 Asp Leu Arg Glu Leu Pro Gln Thr Ser Tyr Val Ala Val His Thr Cys
 130 135 140
 Met Gln Gly Trp Ser Ala Thr Ala Arg Trp Thr Gly Val Arg Leu Arg
 145 150 155 160
 Asp Val Leu Cys His Asp Leu Val His Thr Leu Asp Leu His His Arg
 165 170 175
 His Ser Pro Arg Leu Leu Thr Ile Glu Ile Ile Pro Lys Pro Leu Pro
 180 185 190
 Pro Glu Thr Arg Cys Lys Ile Ile Asp Phe Asp Leu Phe Ala Pro Asn
 195 200 205
 Ser Pro Ser Ile Glu Glu Phe Cys Ser Arg Leu Lys Ile Ser Arg Arg
 210 215 220
 Ser Phe Tyr Asn Ile Arg Asn Arg Tyr Gln Gln Asp Ala Ser Ala Ala
 225 230 235 240
 Leu His Pro Arg Ser Ser Ala Gln Ile Thr Ser Arg Arg Thr Tyr Asp
 245 250 255
 Glu Ser Ile Thr Ser Ile Leu Leu Ala Ile Arg Ala Pro Pro Glu Ser
 260 265 270
 Pro Arg Met Gly Xaa Arg Xaa Asp Leu Tyr Xaa Ile Arg Arg His Xaa
 275 280 285
 His Arg Gly Thr Asp Cys Thr Asp Ser Ile Arg Leu Asn Tyr Arg Leu
 290 295 300
 Leu Val Thr Arg Cys Arg Ser Ser Arg Lys
 305 310

<210> 257

<211> 951

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(928)

<223> RXN03070

<400> 257

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cgaattcgac caagaaaacg taaacaccccc aggagtactc gtg cct gcc ctt cca 115
                               Val Pro Ala Leu Pro
                               1 5

tca tct atc atc gac ccc ctc tgg cgc cag ttc tcc gcc tta atc cca 163
Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe Ser Ala Leu Ile Pro
                               10 15 20

ccg gtt atc atc acc cac cca cta ggg tgc cac cgt gca cgc att gct 211
Pro Val Ile Ile Thr His Pro Leu Gly Cys His Arg Ala Arg Ile Ala
                               25 30 35

gac cgg atc atc gtc gac aaa ctc atc gca gtg ctt gtc ctc ggt gtc 259
Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val Leu Val Leu Gly Val
                               40 45 50

tcc tat atc aag att tcc gat tcc acc tgc tca gcc acc acg ata cgc 307
Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser Ala Thr Thr Ile Arg
                               55 60 65

acc cgc cga gac gag tgg atc act gcc ggg att ttc aag aat tta gaa 355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Lys Asn Leu Glu
                               70 75 80 85

cag atc tgt ctg gag tcc tac gac cgt ttc atc ggg tta gac cta gaa 403
Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile Gly Leu Asp Leu Glu
                               90 95 100

aac tta aat gtt gat ggc tgc att gtt aaa gct ccc tgc ggc gga gag 451
Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala Pro Cys Gly Gly Glu
                               105 110 115

gta gcc ggc aga ttc ccg gtt gac cgg gaa aaa ggc acc aaa cgc tcg 499
Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys Gly Thr Lys Arg Ser
                               120 125 130

tta atg gtc gat gga cat gga atc ccg atc ggg tgc gtg gtc gcc gga 547
Leu Met Val Asp Gly His Gly Ile Pro Ile Gly Cys Val Val Ala Gly
                               135 140 145

gcc aat cgg cat gat tta ccg ttg tta gct gca acc ttg gac acg ctc 595
Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala Thr Leu Asp Thr Leu
                               150 155 160 165

ggc cgg ttt ggg ggc tct ctt ccc gat cag atc acg gtg cat ctc gat 643
Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile Thr Val His Leu Asp
                               170 175 180

gct ggg tat gac tcg aag aaa acc cgc agg cta ctc agc gaa ttt ggt 691
Ala Gly Tyr Asp Ser Lys Lys Thr Arg Arg Leu Leu Ser Glu Phe Gly
                               185 190 195

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tat agc tgg gtg atc agc att aaa ggt gag ccg ctg cag gct ggg act 739
 Tyr Ser Trp Val Ile Ser Ile Lys Gly Glu Pro Leu Gln Ala Gly Thr
 200 205 210

 cgg tgg gtg gtg gag cgt act aac tct tgg cat aac cgg ggt ttt aag 787
 Arg Trp Val Val Glu Arg Thr Asn Ser Trp His Asn Arg Gly Phe Lys
 215 220 225

 aaa ctt agt atc tgc acc gaa cgt tgt acc cgg gtt gtg gaa gcg ttt 835
 Lys Leu Ser Ile Cys Thr Glu Arg Cys Thr Arg Val Val Glu Ala Phe
 230 235 240 245

 atc gct tta gcc aac gcg gtg att att ctg cgt cgg ctt atc aaa cag 883
 Ile Ala Leu Ala Asn Ala Val Ile Ile Leu Arg Arg Leu Ile Lys Gln
 250 255 260

 gcc tgg act agt tac cgc tgg gac acc cga ccg ggc cac aga cct 928
 Ala Trp Thr Ser Tyr Arg Trp Asp Thr Arg Pro Gly His Arg Pro
 265 270 275

 taatctatcc gcgcaatctc taa 951

<210> 258
 <211> 276
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 258
 Val Pro Ala Leu Pro Ser Ser Ile Ile Asp Pro Leu Trp Arg Gln Phe
 1 5 10 15

 Ser Ala Leu Ile Pro Pro Val Ile Ile Thr His Pro Leu Gly Cys His
 20 25 30

 Arg Ala Arg Ile Ala Asp Arg Ile Ile Val Asp Lys Leu Ile Ala Val
 35 40 45

 Leu Val Leu Gly Val Ser Tyr Ile Lys Ile Ser Asp Ser Thr Cys Ser
 50 55 60

 Ala Thr Thr Ile Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
 65 70 75 80

 Phe Lys Asn Leu Glu Gln Ile Cys Leu Glu Ser Tyr Asp Arg Phe Ile
 85 90 95

 Gly Leu Asp Leu Glu Asn Leu Asn Val Asp Gly Cys Ile Val Lys Ala
 100 105 110

 Pro Cys Gly Gly Glu Val Ala Gly Arg Phe Pro Val Asp Arg Glu Lys
 115 120 125

 Gly Thr Lys Arg Ser Leu Met Val Asp Gly His Gly Ile Pro Ile Gly
 130 135 140

 Cys Val Val Ala Gly Ala Asn Arg His Asp Leu Pro Leu Leu Ala Ala
 145 150 155 160

 Thr Leu Asp Thr Leu Gly Arg Phe Gly Gly Ser Leu Pro Asp Gln Ile

165										170					175				
Thr	Val	His	Leu	Asp	Ala	Gly	Tyr	Asp	Ser	Lys	Lys	Thr	Arg	Arg	Leu				
			180					185					190						
Leu	Ser	Glu	Phe	Gly	Tyr	Ser	Trp	Val	Ile	Ser	Ile	Lys	Gly	Glu	Pro				
		195					200					205							
Leu	Gln	Ala	Gly	Thr	Arg	Trp	Val	Val	Glu	Arg	Thr	Asn	Ser	Trp	His				
	210					215					220								
Asn	Arg	Gly	Phe	Lys	Lys	Leu	Ser	Ile	Cys	Thr	Glu	Arg	Cys	Thr	Arg				
225					230					235					240				
Val	Val	Glu	Ala	Phe	Ile	Ala	Leu	Ala	Asn	Ala	Val	Ile	Ile	Leu	Arg				
			245					250						255					
Arg	Leu	Ile	Lys	Gln	Ala	Trp	Thr	Ser	Tyr	Arg	Trp	Asp	Thr	Arg	Pro				
			260					265					270						
Gly	His	Arg	Pro																
		275																	

<210> 259

<211> 742

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(742)

<223> RXN03121

<400> 259

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cgaatctttg	cgctaactgt	agggcggggtt	caggggggtga	atg	cac	cac	gag	caa	115
				Met	His	His	Glu	Gln	
				1				5	

ccc	gaa	ggg	tgc	gaa	gtg	ggc	att	cgt	aga	aca	atc	cca	gag	gaa	agc	163
Pro	Glu	Gly	Cys	Glu	Val	Gly	Ile	Arg	Arg	Thr	Ile	Pro	Glu	Glu	Ser	
			10					15						20		

cgt	acg	gct	ttc	ctc	gac	atg	atc	aat	caa	ggg	atg	tca	ggg	ctt	gct	211
Arg	Thr	Ala	Phe	Leu	Asp	Met	Ile	Asn	Gln	Gly	Met	Ser	Gly	Leu	Ala	
		25						30					35			

gcg	tct	aca	gcg	gtc	ggg	gtc	agt	gaa	ttc	acc	ggg	cga	aag	tgg	gcg	259
Ala	Ser	Thr	Ala	Val	Gly	Val	Ser	Glu	Phe	Thr	Gly	Arg	Lys	Trp	Ala	
		40					45				50					

aag	gcc	gcc	ggg	gtg	aaa	ctg	acc	cgc	ggc	ccg	cga	ggg	ggc	aat	gct	307
Lys	Ala	Ala	Gly	Val	Lys	Leu	Thr	Arg	Gly	Pro	Arg	Gly	Gly	Asn	Ala	
	55					60					65					

ttt	gac	acc	gcc	gag	aaa	ctt	gag	att	gca	gcc	agc	atg	cta	gag	aaa	355
Phe	Asp	Thr	Ala	Glu	Lys	Leu	Glu	Ile	Ala	Ala	Ser	Met	Leu	Glu	Lys	
	70				75				80						85	

gga tgc cta ccc cga gaa atc ggc gag tat gtc ggc atg act cgg gcc 403
 Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val Gly Met Thr Arg Ala
 90 95 100

aat ata tcc cta tgg cgc aaa caa ggc cca gac aag ctt cgc caa cgc 451
 Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp Lys Leu Arg Gln Arg
 105 110 115

gca gcc acc ttg cgc acc ggc aag cga gca gct gaa ttc atc cac gcc 499
 Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala Glu Phe Ile His Ala
 120 125 130

ccg gtg atg ggc cct tat tat ggg cca cgc aca ctc cat caa gtg ttg 547
 Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr Leu His Gln Val Leu
 135 140 145

cgt gag gac tac aca aca ctg ttt gac gag tta tct gcg ttg ggg ttg 595
 Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu Ser Ala Leu Gly Leu
 150 155 160 165

cca gca cag gtg tgt ggg gcc tta ctt cat ctt gct cca cca cca tca 643
 Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu Ala Pro Pro Pro Ser
 170 175 180

tta cgc ttt tct tat atg tcg tgt gta gtg ccg tta ttt gct gat gaa 691
 Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro Leu Phe Ala Asp Glu
 185 190 195

atc aaa atc gta gga caa ggc aca cga tta tcg tta gaa gag aaa atg 739
 Ile Lys Ile Val Gly Gln Gly Thr Arg Leu Ser Leu Glu Glu Lys Met
 200 205 210

atg 742
 Met

<210> 260

<211> 214

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met His His Glu Gln Pro Glu Gly Cys Glu Val Gly Ile Arg Arg Thr
 1 5 10 15

Ile Pro Glu Glu Ser Arg Thr Ala Phe Leu Asp Met Ile Asn Gln Gly
 20 25 30

Met Ser Gly Leu Ala Ala Ser Thr Ala Val Gly Val Ser Glu Phe Thr
 35 40 45

Gly Arg Lys Trp Ala Lys Ala Ala Gly Val Lys Leu Thr Arg Gly Pro
 50 55 60

Arg Gly Gly Asn Ala Phe Asp Thr Ala Glu Lys Leu Glu Ile Ala Ala
 65 70 75 80

Ser Met Leu Glu Lys Gly Cys Leu Pro Arg Glu Ile Gly Glu Tyr Val
 85 90 95

Gly Met Thr Arg Ala Asn Ile Ser Leu Trp Arg Lys Gln Gly Pro Asp
 100 105 110
 Lys Leu Arg Gln Arg Ala Ala Thr Leu Arg Thr Gly Lys Arg Ala Ala
 115 120 125
 Glu Phe Ile His Ala Pro Val Met Gly Pro Tyr Tyr Gly Pro Arg Thr
 130 135 140
 Leu His Gln Val Leu Arg Glu Asp Tyr Thr Thr Leu Phe Asp Glu Leu
 145 150 155 160
 Ser Ala Leu Gly Leu Pro Ala Gln Val Cys Gly Ala Leu Leu His Leu
 165 170 175
 Ala Pro Pro Pro Ser Leu Arg Phe Ser Tyr Met Ser Cys Val Val Pro
 180 185 190
 Leu Phe Ala Asp Glu Ile Lys Ile Val Gly Gln Gly Thr Arg Leu Ser
 195 200 205
 Leu Glu Glu Lys Met Met
 210

<210> 261
 <211> 484
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(484)
 <223> RXN03161

<400> 261
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 Met Gly Ile Phe Ser
 1 5
 ggt cgg cag ttc cct cgt gaa atc atc ctg tgg gcg gtg cgg tgg tac 163
 Gly Arg Gln Phe Pro Arg Glu Ile Ile Leu Trp Ala Val Arg Trp Tyr
 10 15 20
 tgc cgc tac ggc gtg agc tat cgc gac ctc gaa gag atg atg acc gag 211
 Cys Arg Tyr Gly Val Ser Tyr Arg Asp Leu Glu Glu Met Met Thr Glu
 25 30 35
 cgg gga gtg ccg gtc gat cac acc acg atc tac cgc tgg gtc cag aaa 259
 Arg Gly Val Pro Val Asp His Thr Ile Tyr Arg Trp Val Gln Lys
 40 45 50
 tat gct cct gag ctg gat aag aag acc cgg tgg tat cgg caa gtt cct 307
 Tyr Ala Pro Glu Leu Asp Lys Lys Thr Arg Trp Tyr Arg Gln Val Pro
 55 60 65
 gac tgg cag gcc agg tcc tgg cgg gtg gat gag acc tat atc cgg gtc 355
 Asp Trp Gln Ala Arg Ser Trp Arg Val Asp Glu Thr Tyr Ile Arg Val
 70 75 80 85

ttg ccg cag gcg ttg cgt cat agt ttt acg tgq gat cag ggt gtg cag 106

Leu Pro Gln Ala Leu Arg His Ser Phe Thr Trp Asp Gln Gly Val Gln
 5 10 15
 atg gca gag cat gcc cgg tta agc gtg gtg acc aag tgc ccg gtg ttt 154
 Met Ala Glu His Ala Arg Leu Ser Val Val Thr Lys Cys Pro Val Phe
 20 25 30 35
 ttc tgt gat cct cat tcg ccg tgg cag cgt ggg tcg aat gag aat acg 202
 Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn Glu Asn Thr
 40 45 50
 aat gga ttg gtc agg gat ttt ttc ccg aag ggc act aat ttt gct aaa 250
 Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn Phe Ala Lys
 55 60 65
 gta agt gac gaa gaa gtt cag cgg gca cag gat atg ctg aat tac cga 298
 Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Met Leu Asn Tyr Arg
 70 75 80
 ccg cgg aaa atg cat ggt ttt aaa agc gcg acg cag gta tat gaa ata 346
 Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val Tyr Glu Ile
 85 90 95
 atc gta gtt ggt gca tcc acg gat tgaattcgcc taggagattg tgc 393
 Ile Val Val Gly Ala Ser Thr Asp
 100 105

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 <212> PRT
 <213> Corynebacterium glutamicum

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 Gly Val Gln Met Ala Glu His Ala Arg Leu Ser Val Val Thr Lys Cys
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 Pro Val Phe Phe Cys Asp Pro His Ser Pro Trp Gln Arg Gly Ser Asn
 35 40 45
 Glu Asn Thr Asn Gly Leu Val Arg Asp Phe Phe Pro Lys Gly Thr Asn
 50 55 60
 Phe Ala Lys Val Ser Asp Glu Glu Val Gln Arg Ala Gln Asp Met Leu
 65 70 75 80
 Asn Tyr Arg Pro Arg Lys Met His Gly Phe Lys Ser Ala Thr Gln Val
 85 90 95
 Tyr Glu Ile Ile Val Val Gly Ala Ser Thr Asp
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 <212> DNA
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<220>

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<222> (101)..(400)

<223> RXN00083

<400> 265

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                                   Val Leu Ala Leu Pro
                                   1 5

tcc tct atc atc gac ccc ctc tgg tgc cag ttc gcc gcg ctg atc cca 163
Ser Ser Ile Ile Asp Pro Leu Trp Cys Gln Phe Ala Ala Leu Ile Pro
                                   10 15 20

ccc gtg acc gac acc cac cca ctt cgg tgc cac cgc cca cgc atc ccg 211
Pro Val Thr Asp Thr His Pro Leu Arg Cys His Arg Pro Arg Ile Pro
                                   25 30 35

gac cgg atc atc ttc gac aag ctc atc cag gtc ctc gtc ctc ggc gcc 259
Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val Leu Val Leu Gly Ala
                                   40 45 50

tcc tat gcc aag atc gcc gac acg aca tgc tcg gcc acc acc ttg cgc 307
Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser Ala Thr Thr Leu Arg
                                   55 60 65

acc cgc cgg gac gag tgg atc acc gct ggc atc ttc gag cag ctg gaa 355
Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile Phe Glu Gln Leu Glu
                                   70 75 80 85

cag atc tgt ttg gaa ttc tac gac cgt atc gtc gga ctc gat ctc 400
Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val Gly Leu Asp Leu
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<213> Corynebacterium glutamicum

<400> 266

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Ala Ala Leu Ile Pro Pro Val Thr Asp Thr His Pro Leu Arg Cys His
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Arg Pro Arg Ile Pro Asp Arg Ile Ile Phe Asp Lys Leu Ile Gln Val
  35 40 45

Leu Val Leu Gly Ala Ser Tyr Ala Lys Ile Ala Asp Thr Thr Cys Ser
  50 55 60

Ala Thr Thr Leu Arg Thr Arg Arg Asp Glu Trp Ile Thr Ala Gly Ile
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Phe Glu Gln Leu Glu Gln Ile Cys Leu Glu Phe Tyr Asp Arg Ile Val

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85

90

95

Gly Leu Asp Leu
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Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
1 5 10 15

cgg aag ttc aag cgc acg acc ggc agc gat cat acc ttc aac atc gca 96
Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
20 25 30

ccg aac ttt ctg cag cag gac ttt atg gcg agc agg ccg aac cag aag 144
Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
35 40 45

tgg gcg ggc gac atc acc tat gtc tgg acg cgc gag ggc ctg ggt cta 192
Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
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tct ggc cga cat tct tgacctttat ccccgccggg tga 230
Ser Gly Arg His Ser
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<210> 268
<211> 69
<212> PRT
<213> Corynebacterium glutamicum

<400> 268
Arg Val Gly Arg Leu Met Arg Gln Asn Gly Ile Leu Ile Ile Arg Ser
1 5 10 15

Arg Lys Phe Lys Arg Thr Thr Gly Ser Asp His Thr Phe Asn Ile Ala
20 25 30

Pro Asn Phe Leu Gln Gln Asp Phe Met Ala Ser Arg Pro Asn Gln Lys
35 40 45

Trp Ala Gly Asp Ile Thr Tyr Val Trp Thr Arg Glu Gly Leu Gly Leu
50 55 60

Ser Gly Arg His Ser
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<210> 269

<211> 675
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(652)
 <223> RXN02287

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acatctggcc ctcaaaatct tccttttact ggagaccact gtg tac tca att tca 115
                                   Val Tyr Ser Ile Ser
                                   1 5

gaa act atc gcc cga act ctt atg ccc cgc acc gat cac gtt ttc gac 163
Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr Asp His Val Phe Asp
                                   10 15 20

ctg atg ggc aac gga aac gcc tgg ttc gtc gat gcc cta gaa cgc ctc 211
Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp Ala Leu Glu Arg Leu
                                   25 30 35

ggg cga ggc atc atc acc gtc cgc ccc aca gtt gaa acc gtg gcc gcc 259
Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val Glu Thr Val Ala Ala
                                   40 45 50

gcg gac acc tac cac cgc gtc acc cgc cgc ccg gcg gtc gct acc acc 307
Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro Ala Val Ala Thr Thr
                                   55 60 65

acc tat ggt gct ggt ttc acc aac acc atg acc acg ctt gcc gac gtc 355
Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr Thr Leu Ala Asp Val
                                   70 75 80 85

gcc ctc tcc cgt atc cca ctt ctt tta gtt gtg ggc act gcc ccg agc 403
Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val Gly Thr Ala Pro Ser
                                   90 95 100

gcc ggg cct cgc tgt ttc gac att gac cgg caa gga ctc gca cgt gcc 451
Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln Gly Leu Ala Arg Ala
                                   105 110 115

gta ggt gtg gaa acc ttc acc gtg cat gca gat gac gtt gct gcg gta 499
Val Gly Val Glu Thr Phe Thr Val His Ala Asp Asp Val Ala Ala Val
                                   120 125 130

act ctt cag gct tgg aat aat acg ccg gaa aac aca cac gtg atc ctg 547
Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn Thr His Val Ile Leu
                                   135 140 145

gaa atc ccc tat gac cta gca gct gcc aca gcc acc gat cca aca gtg 595
Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala Thr Asp Pro Thr Val
                                   150 155 160 165

act aca tac ctg ctg cgc ccc gga ttt cag aaa ctc ccg atg tca ccg 643
Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys Leu Pro Met Ser Pro
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acc ttg tcc tagctctacg caatgcccaa aat 675

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Thr Leu Ser

<210> 270

<211> 184

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 270

Val Tyr Ser Ile Ser Glu Thr Ile Ala Arg Thr Leu Met Pro Arg Thr
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Asp His Val Phe Asp Leu Met Gly Asn Gly Asn Ala Trp Phe Val Asp
20 25 30

Ala Leu Glu Arg Leu Gly Arg Gly Ile Ile Thr Val Arg Pro Thr Val
35 40 45

Glu Thr Val Ala Ala Ala Asp Thr Tyr His Arg Val Thr Arg Arg Pro
50 55 60

Ala Val Ala Thr Thr Thr Tyr Gly Ala Gly Phe Thr Asn Thr Met Thr
65 70 75 80

Thr Leu Ala Asp Val Ala Leu Ser Arg Ile Pro Leu Leu Leu Val Val
85 90 95

Gly Thr Ala Pro Ser Ala Gly Pro Arg Cys Phe Asp Ile Asp Arg Gln
100 105 110

Gly Leu Ala Arg Ala Val Gly Val Glu Thr Phe Thr Val His Ala Asp
115 120 125

Asp Val Ala Ala Val Thr Leu Gln Ala Trp Asn Asn Thr Pro Glu Asn
130 135 140

Thr His Val Ile Leu Glu Ile Pro Tyr Asp Leu Ala Ala Ala Thr Ala
145 150 155 160

Thr Asp Pro Thr Val Thr Thr Tyr Leu Leu Arg Pro Gly Phe Gln Lys
165 170 175

Leu Pro Met Ser Pro Thr Leu Ser
180

<210> 271

<211> 1431

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1408)

<223> RXN02963

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											Met 1	Lys	Ser	Thr	Gly 5	
aac Asn	atc Ile	atc Ile	gct Ala	gac Asp 10	acc Thr	atc Ile	tgc Cys	cgc Arg	act Thr 15	gcg Ala	gaa Glu	cta Leu	gga Gly	ctc Leu 20	acc Thr	163
atc Ile	acc Thr	ggc Gly	gct Ala 25	tcc Ser	gat Asp	gca Ala	ggg Gly	gat Asp 30	tac Tyr	acc Thr	ctg Leu	atc Ile	gaa Glu 35	gca Ala	gac Asp	211
gca Ala	ctc Leu	gac Asp 40	tac Tyr	acc Thr	tcc Ser	acc Thr	tgc Cys 45	cca Pro	gaa Glu	tgc Cys	tcc Ser	caa Gln 50	cct Pro	ggg Gly	gtg Val	259
ttt Phe	cgt Arg 55	cat His	cac His	acc Thr	cac His	cgg Arg 60	atg Met	ctc Leu	att Ile	gat Asp	tta Leu 65	ccc Pro	atc Ile	gtc Val	ggg Gly	307
ttt Phe 70	ccc Pro	acc Thr	aaa Lys	ctg Leu	ttt Phe 75	atc Ile	cgt Arg	cta Leu	cct Pro	cgc Arg 80	tac Tyr	cgc Arg	tgc Cys	acc Thr	aac Asn 85	355
ccc Pro	aca Thr	tgt Cys	aag Lys	caa Gln 90	aag Lys	tat Tyr	ttc Phe	caa Gln	gca Ala 95	gaa Glu	cta Leu	agc Ser	tgc Cys	gct Ala 100	gac Asp	403
cac His	ggg Gly	aaa Lys	aag Lys 105	gtc Val	acc Thr	cac His	cgg Arg	gtc Val 110	acc Thr	cgc Arg	tgg Trp	att Ile	tta Leu 115	caa Gln	cgc Arg	451
ctt Leu	gct Ala	att Ile 120	gac Asp	cgg Arg	atg Met	agt Ser	gtt Val 125	cac His	gca Ala	acc Thr	gcg Ala	aaa Lys 130	gca Ala	ctt Leu	ggg Gly	499
cta Leu	ggg Gly 135	tgg Trp	gat Asp	tta Leu	acc Thr	tgc Cys 140	caa Gln	cta Leu	gcc Ala	ctc Leu	gat Asp 145	atg Met	tgc Cys	cgt Arg	gag Glu	547
ctg Leu 150	gtc Val	tat Tyr	aac Asn	gat Asp	cct Pro 155	cac His	cat His	ctt Leu	gat Asp	gga Gly 160	gtg Val	tat Tyr	gtc Val	att Ile	ggg Gly 165	595
gtg Val	gat Asp	gag Glu	cat His	aag Lys 170	tgg Trp	tca Ser	cat His	aat Asn	agg Arg	gct Ala	aag Lys	cat His	ggg Gly	gat Asp 180	ggg Gly	643
ttt Phe	gtc Val	acc Thr	gtg Val 185	att Ile	gtc Val	gat Asp	atg Met	acc Thr 190	ggg Gly	cat His	cgg Arg	tat Tyr	gac Asp 195	tca Ser	cgg Arg	691
tgt Cys	cct Pro	gcc Ala 200	cgg Arg	tta Leu	tta Leu	gat Asp	gtc Val 205	gtc Val	cca Pro	ggg Gly	cgt Arg	agt Ser 210	gct Ala	gat Asp	gct Ala	739
tta Leu	cgg Arg 215	tcc Ser	tgg Trp	ctt Leu	ggc Gly	tcc Ser 220	cgc Arg	ggg Gly	gaa Glu	cag Gln	ttc Phe 225	cgc Arg	aat Asn	cag Gln	ata Ile	787
cgg Arg	atc Ile	gtg Val	tcc Ser	atg Met	gat Asp	gga Gly	ttc Phe	caa Gln	ggc Gly	tac Tyr	gcc Ala	aca Thr	gca Ala	agt Ser	aaa Lys	835

230	235	240	245	
gaa ctc att cct tct gct cgt cgc gtg atg gat cca ttc cat gtt gtg				883
Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp Pro Phe His Val Val				
	250	255	260	
cgg ctt gct ggt gac aag ctc acc gcc tgc cgg caa cgc ctc cag cgg				931
Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg Gln Arg Leu Gln Arg				
	265	270	275	
gag aaa tac cag cgt cgt ggt tta agc cag gat ccg ttg tat aaa aac				979
Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp Pro Leu Tyr Lys Asn				
	280	285	290	
cgg aag acc ttg ttg acc acg cac aag tgg ttg agt cct cgt cag caa				1027
Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu Ser Pro Arg Gln Gln				
	295	300	305	
gaa agc ttg gag cag ttg tgg gcg tat gac aaa gac tac ggg gcg tta				1075
Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys Asp Tyr Gly Ala Leu				
	310	315	320	325
aag ctt gcg tgg ctt gcg tat cag gcg att att gat tgt tat cag atg				1123
Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile Asp Cys Tyr Gln Met				
	330	335	340	
ggt aat aag cgt gaa gcg aag aag aaa atg cgg acc att att gat cag				1171
Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg Thr Ile Ile Asp Gln				
	345	350	355	
ctt cgg gtg ttg aag ggg ccg aat aag gaa ctc gcg cag ttg ggt cgt				1219
Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu Ala Gln Leu Gly Arg				
	360	365	370	
agt ttg ttt aaa cga ctt ggt gat gtg ttg gcg tat ttc gat gtt ggt				1267
Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala Tyr Phe Asp Val Gly				
	375	380	385	
gtc tcc aac ggt ccg gtc gaa gcg atc aac gga cgg ttg gag cat ttg				1315
Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly Arg Leu Glu His Leu				
	390	395	400	405
cgt ggg att gct cta ggt ttc cgt aat ttg aac cac tac att ctg cgg				1363
Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn His Tyr Ile Leu Arg				
	410	415	420	
tgc ctt atc cat tca ggg cag ttg gtc cat aag atc aat gca ctc				1408
Cys Leu Ile His Ser Gly Gln Leu Val His Lys Ile Asn Ala Leu				
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<211> 436

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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 20 25 30
 Leu Ile Glu Ala Asp Ala Leu Asp Tyr Thr Ser Thr Cys Pro Glu Cys
 35 40 45
 Ser Gln Pro Gly Val Phe Arg His His Thr His Arg Met Leu Ile Asp
 50 55 60
 Leu Pro Ile Val Gly Phe Pro Thr Lys Leu Phe Ile Arg Leu Pro Arg
 65 70 75 80
 Tyr Arg Cys Thr Asn Pro Thr Cys Lys Gln Lys Tyr Phe Gln Ala Glu
 85 90 95
 Leu Ser Cys Ala Asp His Gly Lys Lys Val Thr His Arg Val Thr Arg
 100 105 110
 Trp Ile Leu Gln Arg Leu Ala Ile Asp Arg Met Ser Val His Ala Thr
 115 120 125
 Ala Lys Ala Leu Gly Leu Gly Trp Asp Leu Thr Cys Gln Leu Ala Leu
 130 135 140
 Asp Met Cys Arg Glu Leu Val Tyr Asn Asp Pro His His Leu Asp Gly
 145 150 155 160
 Val Tyr Val Ile Gly Val Asp Glu His Lys Trp Ser His Asn Arg Ala
 165 170 175
 Lys His Gly Asp Gly Phe Val Thr Val Ile Val Asp Met Thr Gly His
 180 185 190
 Arg Tyr Asp Ser Arg Cys Pro Ala Arg Leu Leu Asp Val Val Pro Gly
 195 200 205
 Arg Ser Ala Asp Ala Leu Arg Ser Trp Leu Gly Ser Arg Gly Glu Gln
 210 215 220
 Phe Arg Asn Gln Ile Arg Ile Val Ser Met Asp Gly Phe Gln Gly Tyr
 225 230 235 240
 Ala Thr Ala Ser Lys Glu Leu Ile Pro Ser Ala Arg Arg Val Met Asp
 245 250 255
 Pro Phe His Val Val Arg Leu Ala Gly Asp Lys Leu Thr Ala Cys Arg
 260 265 270
 Gln Arg Leu Gln Arg Glu Lys Tyr Gln Arg Arg Gly Leu Ser Gln Asp
 275 280 285
 Pro Leu Tyr Lys Asn Arg Lys Thr Leu Leu Thr Thr His Lys Trp Leu
 290 295 300
 Ser Pro Arg Gln Gln Glu Ser Leu Glu Gln Leu Trp Ala Tyr Asp Lys
 305 310 315 320
 Asp Tyr Gly Ala Leu Lys Leu Ala Trp Leu Ala Tyr Gln Ala Ile Ile
 325 330 335

Asp Cys Tyr Gln Met Gly Asn Lys Arg Glu Ala Lys Lys Lys Met Arg
 340 345 350
 Thr Ile Ile Asp Gln Leu Arg Val Leu Lys Gly Pro Asn Lys Glu Leu
 355 360 365
 Ala Gln Leu Gly Arg Ser Leu Phe Lys Arg Leu Gly Asp Val Leu Ala
 370 375 380
 Tyr Phe Asp Val Gly Val Ser Asn Gly Pro Val Glu Ala Ile Asn Gly
 385 390 395 400
 Arg Leu Glu His Leu Arg Gly Ile Ala Leu Gly Phe Arg Asn Leu Asn
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 His Tyr Ile Leu Arg Cys Leu Ile His Ser Gly Gln Leu Val His Lys
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 Ile Asn Ala Leu
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 <212> DNA
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<220>
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 <222> (101)..(2764)
 <223> RXA02788

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 Val Gln Thr His Glu
 1 5
 atc agg gag cgt ttt acc aat cac ttc gtc aat gcc ggt cac cag gcg 163
 Ile Arg Glu Arg Phe Thr Asn His Phe Val Asn Ala Gly His Gln Ala
 10 15 20
 gta cct agc gcg tca ctg att ctc gac gac cct aac ctg ctg ttc gtt 211
 Val Pro Ser Ala Ser Leu Ile Leu Asp Asp Pro Asn Leu Leu Phe Val
 25 30 35
 aac gca ggc atg gtt cca ttc aag ccg tac ttc ctg ggc cag cag acc 259
 Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe Leu Gly Gln Gln Thr
 40 45 50
 cca cct ttt gaa aac ggc act gcg act tcc att cag aag tgt gtt cgt 307
 Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile Gln Lys Cys Val Arg
 55 60 65
 acc ctg gat atc gaa gaa gtg ggt atc acc act cgc cac aat acc ttc 355
 Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr Arg His Asn Thr Phe
 70 75 80 85
 ttc cag atg gca ggt aac ttc tcc ttc ggc cag tac ttc aaa gaa ggc 403
 Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln Tyr Phe Lys Glu Gly

				90					95					100		
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Ala	Ile	Thr	His	Ala	Trp	Gly	Leu	Leu	Thr	Gly	Ser	Val	Ala	Asp	Gly	
			105												115	
ggc	ttt	ggc	ctt	gat	cca	gag	cgc	ctc	tgg	gtc	act	gtg	tac	ctc	gat	499
Gly	Phe	Gly	Leu	Asp	Pro	Glu	Arg	Leu	Trp	Val	Thr	Val	Tyr	Leu	Asp	
		120					125								130	
gat	gac	gag	gct	gca	gag	atc	tgg	gaa	aag	aag	atc	ggc	gtc	cca	tca	547
Asp	Asp	Glu	Ala	Ala	Glu	Ile	Trp	Glu	Lys	Lys	Ile	Gly	Val	Pro	Ser	
		135					140								145	
gag	cgc	atc	cag	cgc	ctg	ggt	atg	gct	gac	aac	tac	tgg	tcc	atg	ggt	595
Glu	Arg	Ile	Gln	Arg	Leu	Gly	Met	Ala	Asp	Asn	Tyr	Trp	Ser	Met	Gly	
150					155					160					165	
gta	cca	gga	cct	tgt	ggc	cct	tgc	tcc	gag	atc	tac	tac	gac	cgc	ggc	643
Val	Pro	Gly	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Ile	Tyr	Tyr	Asp	Arg	Gly	
			170							175					180	
gag	aag	tac	ggc	aag	gaa	ggc	ggc	cct	gtc	gct	gac	gac	aac	cgc	tac	691
Glu	Lys	Tyr	Gly	Lys	Glu	Gly	Gly	Pro	Val	Ala	Asp	Asp	Asn	Arg	Tyr	
			185							190					195	
atg	gag	atc	tgg	aac	ctg	gtc	ttc	atg	gag	aag	gaa	cgc	gga	cag	ggt	739
Met	Glu	Ile	Trp	Asn	Leu	Val	Phe	Met	Glu	Lys	Glu	Arg	Gly	Gln	Gly	
		200					205								210	
att	ggc	aag	gac	aac	ttc	gac	atc	ctt	ggc	gat	ctt	cca	aag	aag	aac	787
Ile	Gly	Lys	Asp	Asn	Phe	Asp	Ile	Leu	Gly	Asp	Leu	Pro	Lys	Lys	Asn	
		215				220									225	
atc	gat	acc	ggc	atg	ggc	gtc	gag	cgc	gtt	gcc	tgc	atc	ctc	cag	gat	835
Ile	Asp	Thr	Gly	Met	Gly	Val	Glu	Arg	Val	Ala	Cys	Ile	Leu	Gln	Asp	
230					235					240					245	
gtt	gaa	aac	gtc	tac	gaa	acc	gac	ctg	ctg	cgc	cca	gtc	atc	gac	gtt	883
Val	Glu	Asn	Val	Tyr	Glu	Thr	Asp	Leu	Leu	Arg	Pro	Val	Ile	Asp	Val	
			250							255					260	
gca	gag	acc	ctg	acc	gga	acc	aag	tat	ggt	tct	gac	aac	acc	tct	gac	931
Ala	Glu	Thr	Leu	Thr	Gly	Thr	Lys	Tyr	Gly	Ser	Asp	Asn	Thr	Ser	Asp	
			265							270					275	
att	cgc	ttc	cgc	gtt	atc	gcc	gac	cac	tct	cgt	acc	ggc	atg	atg	ctc	979
Ile	Arg	Phe	Arg	Val	Ile	Ala	Asp	His	Ser	Arg	Thr	Gly	Met	Met	Leu	
		280					285								290	
atc	ctc	gat	ggt	gtt	acc	cca	ggc	aac	gaa	ggc	cgt	gga	tac	atc	ctg	1027
Ile	Leu	Asp	Gly	Val	Thr	Pro	Gly	Asn	Glu	Gly	Arg	Gly	Tyr	Ile	Leu	
		295				300					305					
cgc	cgc	ctg	ctt	cgc	cgc	att	atc	cgt	tcc	gca	cgt	ctg	ctc	ggt	gct	1075
Arg	Arg	Leu	Leu	Arg	Arg	Ile	Ile	Arg	Ser	Ala	Arg	Leu	Leu	Gly	Ala	
310					315					320					325	
act	ggt	gag	acc	atg	gag	cag	ttc	atg	aac	acc	atc	atg	gac	acc	atg	1123
Thr	Gly	Glu	Thr	Met	Glu	Gln	Phe	Met	Asn	Thr	Ile	Met	Asp	Thr	Met	
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acc ccg tcc tac cca gaa atc gcc gac aac cgt gag cgc atc atg cgt	1171
Thr Pro Ser Tyr Pro Glu Ile Ala Asp Asn Arg Glu Arg Ile Met Arg	
345 350 355	
gtg gct gtc acc gaa gag cgc gct ttc ttg aag act ctg gtc tct gga	1219
Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys Thr Leu Val Ser Gly	
360 365 370	
acc cac ctc ttc gaa gag gct gca acc tcc atc aag gct gca gga tcc	1267
Thr His Leu Phe Glu Glu Ala Ala Thr Ser Ile Lys Ala Ala Gly Ser	
375 380 385	
acc aag gtt gcc ggt gct cag gca ttc gca ctg cac gac acc tac ggt	1315
Thr Lys Val Ala Gly Ala Gln Ala Phe Ala Leu His Asp Thr Tyr Gly	
390 395 400 405	
ttc ccc atc gac ctc acc ctc gaa atg gct gca gaa gca ggc ctt gag	1363
Phe Pro Ile Asp Leu Thr Leu Glu Met Ala Ala Glu Ala Gly Leu Glu	
410 415 420	
gtt gac gtt gaa ggc ttt gat tcc ctc atg gca gag cag cgc tcc cgt	1411
Val Asp Val Glu Gly Phe Asp Ser Leu Met Ala Glu Gln Arg Ser Arg	
425 430 435	
gca aag gct gac agc cag gca aag aag cac ggc cac acc gac ttg agc	1459
Ala Lys Ala Asp Ser Gln Ala Lys Lys His Gly His Thr Asp Leu Ser	
440 445 450	
atc tac cgc gaa tgg gtc gac aac aac cca acc gta ttc acc ggc ttt	1507
Ile Tyr Arg Glu Trp Val Asp Asn Asn Pro Thr Val Phe Thr Gly Phe	
455 460 465	
gag gaa ctg gat tcc cag tcc aag gtc ctc gga cta ctt tcc gat ggt	1555
Glu Glu Leu Asp Ser Gln Ser Lys Val Leu Gly Leu Leu Ser Asp Gly	
470 475 480 485	
gcc aag att tct gaa gcc aca gaa ggt caa gaa gtt gag gtc atc ctc	1603
Ala Lys Ile Ser Glu Ala Thr Glu Gly Gln Glu Val Glu Val Ile Leu	
490 495 500	
gac cag tca cct ctg tac gca gaa tca ggt gga cag ctc ggc gat cgt	1651
Asp Gln Ser Pro Leu Tyr Ala Glu Ser Gly Gly Gln Leu Gly Asp Arg	
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ggt cag atc ctg ctc gga gac acc gtg ctt gat gtc cat gac gtg cag	1699
Gly Gln Ile Leu Leu Gly Asp Thr Val Leu Asp Val His Asp Val Gln	
520 525 530	
aag atc ggt aag aaa ctg tgg gtt cac aag gca ctc gtg gca aac ggt	1747
Lys Ile Gly Lys Lys Leu Trp Val His Lys Ala Leu Val Ala Asn Gly	
535 540 545	
gga ctt gcg gta ggt gat gaa gtg gtg gca agc gtc gat aag caa tgg	1795
Gly Leu Ala Val Gly Asp Glu Val Val Ala Ser Val Asp Lys Gln Trp	
550 555 560 565	
cgc cat gct gca cgc cag gca cac acc gca acc cac ctg att cat gcc	1843
Arg His Ala Ala Arg Gln Ala His Thr Ala Thr His Leu Ile His Ala	
570 575 580	

gct ctg cgg cag gtt ctt gga cca act gcc ctc cag gca gga tcc atg	1891
Ala Leu Arg Gln Val Leu Gly Pro Thr Ala Leu Gln Ala Gly Ser Met	
585 590 595	
aac aag cca ggc tac ctg cgc ttc gac ttc aac tac acc gag cag ctc	1939
Asn Lys Pro Gly Tyr Leu Arg Phe Asp Phe Asn Tyr Thr Glu Gln Leu	
600 605 610	
acc cca gca caa gtc gag caa atc cag gcg atc acc aac gaa gcc gtg	1987
Thr Pro Ala Gln Val Glu Gln Ile Gln Ala Ile Thr Asn Glu Ala Val	
615 620 625	
gac acc gac tgg gct gtc aac acc gtg gaa acc tca ctc gag gaa gcc	2035
Asp Thr Asp Trp Ala Val Asn Thr Val Glu Thr Ser Leu Glu Glu Ala	
630 635 640 645	
aag gca atg ggt gcg atg gcg ctc ttc ggc gaa aac tac gga agc acc	2083
Lys Ala Met Gly Ala Met Ala Leu Phe Gly Glu Asn Tyr Gly Ser Thr	
650 655 660	
gtg cgc gtt gtg gaa atc ggc gga cct ttc tcc atg gaa ctc tgt ggc	2131
Val Arg Val Val Glu Ile Gly Gly Pro Phe Ser Met Glu Leu Cys Gly	
665 670 675	
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Gly Thr His Val Ala His Ser Ser Gln Ile Gly Pro Val Ala Leu Leu	
680 685 690	
ggt gaa tca tcc atc ggc tcc ggc gtg cgc cgc atc gag gcc tac tcc	2227
Gly Glu Ser Ser Ile Gly Ser Gly Val Arg Arg Ile Glu Ala Tyr Ser	
695 700 705	
ggc ctg aac tcc ttc aac tac ctg tcc aag gaa cgc gca ctc gcc gag	2275
Gly Leu Asn Ser Phe Asn Tyr Leu Ser Lys Glu Arg Ala Leu Ala Glu	
710 715 720 725	
ggt ttg gca agc tcc ctg aag gct cca tcc gag gaa ctt cca gag cgc	2323
Gly Leu Ala Ser Ser Leu Lys Ala Pro Ser Glu Glu Leu Pro Glu Arg	
730 735 740	
gtc gca cag ctg gta gac aag ctg aag gca gca gag aag gaa atc gaa	2371
Val Ala Gln Leu Val Asp Lys Leu Lys Ala Ala Glu Lys Glu Ile Glu	
745 750 755	
gcc ctg cac cgt cag cag ctc atg gca caa acc gca gac ctg ttg aac	2419
Ala Leu His Arg Gln Gln Leu Met Ala Gln Thr Ala Asp Leu Leu Asn	
760 765 770	
aac gct caa gag atc ggt ggc gtc acc acc ttg ctg ctg cgc gtc aag	2467
Asn Ala Gln Glu Ile Gly Gly Val Thr Thr Leu Leu Arg Val Lys	
775 780 785	
gac aac acc aac gcc ggt gac ctg cgc acc atc gca acc acc ctg aag	2515
Asp Asn Thr Asn Ala Gly Asp Leu Arg Thr Ile Ala Thr Thr Leu Lys	
790 795 800 805	
gac aag ctc ggc gac cgc gaa ggc gtc ttg gtt att gcc tcc gac aac	2563
Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val Ile Ala Ser Asp Asn	
810 815 820	
gcc ggc aag gtt cca ttc gtg gta gct gca acc aag gcc gct gtg gct	2611

Ala Gly Lys Val Pro Phe Val Val Ala Ala Thr Lys Ala Ala Val Ala
 825 830 835

cgc gga gct cac tcc ggc aac ctg gtt aag ctc gtt ggt tcc tac atc 2659
 Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu Val Gly Ser Tyr Ile
 840 845 850

gac ggt cgc ggt ggc ggc aag gct gac ctc gca caa gga tcc ggc gcc 2707
 Asp Gly Arg Gly Gly Gly Lys Ala Asp Leu Ala Gln Gly Ser Gly Ala
 855 860 865

aac att gct ggc ctg gaa tcc gca ttc ggc gca gtc cgc gct gag atc 2755
 Asn Ile Ala Gly Leu Glu Ser Ala Phe Gly Ala Val Arg Ala Glu Ile
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<211> 888

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

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Asn Leu Leu Phe Val Asn Ala Gly Met Val Pro Phe Lys Pro Tyr Phe
 35 40 45

Leu Gly Gln Gln Thr Pro Pro Phe Glu Asn Gly Thr Ala Thr Ser Ile
 50 55 60

Gln Lys Cys Val Arg Thr Leu Asp Ile Glu Glu Val Gly Ile Thr Thr
 65 70 75 80

Arg His Asn Thr Phe Phe Gln Met Ala Gly Asn Phe Ser Phe Gly Gln
 85 90 95

Tyr Phe Lys Glu Gly Ala Ile Thr His Ala Trp Gly Leu Leu Thr Gly
 100 105 110

Ser Val Ala Asp Gly Gly Phe Gly Leu Asp Pro Glu Arg Leu Trp Val
 115 120 125

Thr Val Tyr Leu Asp Asp Asp Glu Ala Ala Glu Ile Trp Glu Lys Lys
 130 135 140

Ile Gly Val Pro Ser Glu Arg Ile Gln Arg Leu Gly Met Ala Asp Asn
 145 150 155 160

Tyr Trp Ser Met Gly Val Pro Gly Pro Cys Gly Pro Cys Ser Glu Ile
 165 170 175

Tyr Tyr Asp Arg Gly Glu Lys Tyr Gly Lys Glu Gly Gly Pro Val Ala
 180 185 190

Asp Asp Asn Arg Tyr Met Glu Ile Trp Asn Leu Val Phe Met Glu Lys
 195 200 205
 Glu Arg Gly Gln Gly Ile Gly Lys Asp Asn Phe Asp Ile Leu Gly Asp
 210 215 220
 Leu Pro Lys Lys Asn Ile Asp Thr Gly Met Gly Val Glu Arg Val Ala
 225 230 235 240
 Cys Ile Leu Gln Asp Val Glu Asn Val Tyr Glu Thr Asp Leu Leu Arg
 245 250 255
 Pro Val Ile Asp Val Ala Glu Thr Leu Thr Gly Thr Lys Tyr Gly Ser
 260 265 270
 Asp Asn Thr Ser Asp Ile Arg Phe Arg Val Ile Ala Asp His Ser Arg
 275 280 285
 Thr Gly Met Met Leu Ile Leu Asp Gly Val Thr Pro Gly Asn Glu Gly
 290 295 300
 Arg Gly Tyr Ile Leu Arg Arg Leu Leu Arg Arg Ile Ile Arg Ser Ala
 305 310 315 320
 Arg Leu Leu Gly Ala Thr Gly Glu Thr Met Glu Gln Phe Met Asn Thr
 325 330 335
 Ile Met Asp Thr Met Thr Pro Ser Tyr Pro Glu Ile Ala Asp Asn Arg
 340 345 350
 Glu Arg Ile Met Arg Val Ala Val Thr Glu Glu Arg Ala Phe Leu Lys
 355 360 365
 Thr Leu Val Ser Gly Thr His Leu Phe Glu Glu Ala Ala Thr Ser Ile
 370 375 380
 Lys Ala Ala Gly Ser Thr Lys Val Ala Gly Ala Gln Ala Phe Ala Leu
 385 390 395 400
 His Asp Thr Tyr Gly Phe Pro Ile Asp Leu Thr Leu Glu Met Ala Ala
 405 410 415
 Glu Ala Gly Leu Glu Val Asp Val Glu Gly Phe Asp Ser Leu Met Ala
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 Glu Gln Arg Ser Arg Ala Lys Ala Asp Ser Gln Ala Lys Lys His Gly
 435 440 445
 His Thr Asp Leu Ser Ile Tyr Arg Glu Trp Val Asp Asn Asn Pro Thr
 450 455 460
 Val Phe Thr Gly Phe Glu Glu Leu Asp Ser Gln Ser Lys Val Leu Gly
 465 470 475 480
 Leu Leu Ser Asp Gly Ala Lys Ile Ser Glu Ala Thr Glu Gly Gln Glu
 485 490 495
 Val Glu Val Ile Leu Asp Gln Ser Pro Leu Tyr Ala Glu Ser Gly Gly
 500 505 510

Gln Leu Gly Asp Arg Gly Gln Ile Leu Leu Gly Asp Thr Val Leu Asp
 515 520 525
 Val His Asp Val Gln Lys Ile Gly Lys Lys Leu Trp Val His Lys Ala
 530 535 540
 Leu Val Ala Asn Gly Gly Leu Ala Val Gly Asp Glu Val Val Ala Ser
 545 550 555 560
 Val Asp Lys Gln Trp Arg His Ala Ala Arg Gln Ala His Thr Ala Thr
 565 570 575
 His Leu Ile His Ala Ala Leu Arg Gln Val Leu Gly Pro Thr Ala Leu
 580 585 590
 Gln Ala Gly Ser Met Asn Lys Pro Gly Tyr Leu Arg Phe Asp Phe Asn
 595 600 605
 Tyr Thr Glu Gln Leu Thr Pro Ala Gln Val Glu Gln Ile Gln Ala Ile
 610 615 620
 Thr Asn Glu Ala Val Asp Thr Asp Trp Ala Val Asn Thr Val Glu Thr
 625 630 635 640
 Ser Leu Glu Glu Ala Lys Ala Met Gly Ala Met Ala Leu Phe Gly Glu
 645 650 655
 Asn Tyr Gly Ser Thr Val Arg Val Val Glu Ile Gly Gly Pro Phe Ser
 660 665 670
 Met Glu Leu Cys Gly Gly Thr His Val Ala His Ser Ser Gln Ile Gly
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 Pro Val Ala Leu Leu Gly Glu Ser Ser Ile Gly Ser Gly Val Arg Arg
 690 695 700
 Ile Glu Ala Tyr Ser Gly Leu Asn Ser Phe Asn Tyr Leu Ser Lys Glu
 705 710 715 720
 Arg Ala Leu Ala Glu Gly Leu Ala Ser Ser Leu Lys Ala Pro Ser Glu
 725 730 735
 Glu Leu Pro Glu Arg Val Ala Gln Leu Val Asp Lys Leu Lys Ala Ala
 740 745 750
 Glu Lys Glu Ile Glu Ala Leu His Arg Gln Gln Leu Met Ala Gln Thr
 755 760 765
 Ala Asp Leu Leu Asn Asn Ala Gln Glu Ile Gly Gly Val Thr Thr Leu
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 Leu Leu Arg Val Lys Asp Asn Thr Asn Ala Gly Asp Leu Arg Thr Ile
 785 790 795 800
 Ala Thr Thr Leu Lys Asp Lys Leu Gly Asp Arg Glu Gly Val Leu Val
 805 810 815
 Ile Ala Ser Asp Asn Ala Gly Lys Val Pro Phe Val Val Ala Ala Thr
 820 825 830
 Lys Ala Ala Val Ala Arg Gly Ala His Ser Gly Asn Leu Val Lys Leu

835 840 845

Val Gly Ser Tyr Ile Asp Gly Arg Gly Gly Gly Lys Ala Asp Leu Ala
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Gln Gly Ser Gly Ala Asn Ile Ala Gly Leu Glu Ser Ala Phe Gly Ala
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Val Arg Ala Glu Ile Glu Ala Leu
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<223> RXN00975

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attctgtgcg acgggtgtac ctcggtctaga atttctcccc atg aca cca gct gat 115
Met Thr Pro Ala Asp
1 5

ctc gca aca ttg att aaa gag acc gcg gta gag gtt ttg acc tcc cgc 163
Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu Val Leu Thr Ser Arg
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gag ctc gat act tct gtt ctt ccg gag cag gta gtt gtg gag cgt ccg 211
Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val Val Glu Arg Pro
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cgt aac cca gag cac ggc gat tac gcc acc aac att gca ttg cag gtg 259
Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn Ile Ala Leu Gln Val
40 45 50

gct aaa aag gtc ggt cag aac cct cgg gat ttg gct acc tgg ctg gca 307
Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu Ala Thr Trp Leu Ala
55 60 65

gag gca ttg gct gca gat gac gcc att gat tct gct gaa att gct ggc 355
Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser Ala Glu Ile Ala Gly
70 75 80 85

cca ggc ttt ttg aac att cgc ctt gct gca gca gca cag ggt gaa att 403
Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala Gln Gly Glu Ile
90 95 100

gtg gcc aag att ctg gca cag ggc gag act ttc gga aac tcc gat cac 451
Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe Gly Asn Ser Asp His
105 110 115

ctt tcc cac ttg gac gtg aac ctc gag ttc gtt tct gca aac cca acc 499
Leu Ser His Leu Asp Val Asn Leu Glu Phe Val Ser Ala Asn Pro Thr
120 125 130

gga cct att cac ctt ggc gga acc cgc tgg gct gcc gtg ggt gac tct	547
Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala Val Gly Asp Ser	
135 140 145	
ttg ggt cgt gtg ctg gag gct tcc tcc gcg aaa gtg acc cgc gaa tac	595
Leu Gly Arg Val Leu Glu Ala Ser Ser Ala Lys Val Thr Arg Glu Tyr	
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tac ttc aac gat cac ggt cgc cag atc gat cgt ttc gct ttg tcc ctt	643
Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg Phe Ala Leu Ser Leu	
170 175 180	
ctt gca gcg gcg aag ggc gag cca acg cca gaa gac ggt tat ggc ggc	691
Leu Ala Ala Ala Lys Gly Glu Pro Thr Pro Glu Asp Gly Tyr Gly Gly	
185 190 195	
gaa tac att aag gaa att gcg gag gca atc gtc gaa aag cat cct gaa	739
Glu Tyr Ile Lys Glu Ile Ala Glu Ala Ile Val Glu Lys His Pro Glu	
200 205 210	
gcg ttg gct ttg gag cct gcc gca acc cag gag ctt ttc cgc gct gaa	787
Ala Leu Ala Leu Glu Pro Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu	
215 220 225	
ggc gtg gag atg atg ttc gag cac atc aaa tct tcc ctg cat gag ttc	835
Gly Val Glu Met Met Phe Glu His Ile Lys Ser Ser Leu His Glu Phe	
230 235 240 245	
ggc acc gat ttc gat gtc tac tac cac gag aac tcc ctg ttc gag tcc	883
Gly Thr Asp Phe Asp Val Tyr Tyr His Glu Asn Ser Leu Phe Glu Ser	
250 255 260	
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Gly Ala Val Asp Lys Ala Val Gln Val Leu Lys Asp Asn Gly Asn Leu	
265 270 275	
tac gaa aac gag ggc gct tgg tgg ctg cgt tcc acc gaa ttc ggc gat	979
Tyr Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr Glu Phe Gly Asp	
280 285 290	
gac aaa gac cgc gtg gtg atc aag tct gac ggc gac gca gcc tac atc	1027
Asp Lys Asp Arg Val Val Ile Lys Ser Asp Gly Asp Ala Ala Tyr Ile	
295 300 305	
gct ggc gat atc gcg tac gtg gct gat aag ttc tcc cgc gga cac aac	1075
Ala Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser Arg Gly His Asn	
310 315 320 325	
cta aac atc tac atg ttg ggt gct gac cac cat ggt tac atc gcg cgc	1123
Leu Asn Ile Tyr Met Leu Gly Ala Asp His His Gly Tyr Ile Ala Arg	
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ctg aag gca gcg gcg gcg gca ctt ggc tac aag cca gaa ggc gtt gaa	1171
Leu Lys Ala Ala Ala Ala Ala Leu Gly Tyr Lys Pro Glu Gly Val Glu	
345 350 355	
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Val Leu Ile Gly Gln Met Val Asn Leu Leu Arg Asp Gly Lys Ala Val	
360 365 370	
cgt atg tcc aag cgt gca ggc acc gtg gtc acc cta gat gac ctc gtt	1267

Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr Leu Asp Asp Leu Val
 375 380 385
 gaa gca atc ggc atc gat gcg gcg cgt tac tcc ctg atc cgt tcc tcc 1315
 Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser Leu Ile Arg Ser Ser
 390 395 400 405
 gtg gat tct tcc ctg gat atc gat ctc ggc ctg tgg gaa tcc cag tcc 1363
 Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu Trp Glu Ser Gln Ser
 410 415 420
 tcc gac aac cct gtg tac tac gtg cag tac gga cac gct cgt ctg tgc 1411
 Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly His Ala Arg Leu Cys
 425 430 435
 tcc atc gcg cgc aag gca gag acc ttg ggt gtc acc gag gaa ggc gca 1459
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 440 445 450
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 Asp Leu Ser Leu Leu Thr His Asp Arg Glu Gly Asp Leu Ile Arg Thr
 455 460 465
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 Leu Gly Glu Phe Pro Ala Val Val Lys Ala Ala Ala Asp Leu Arg Glu
 470 475 480 485
 cca cac cgc att gcc cgc tat gct gag gaa tta gct gga act ttc cac 1603
 Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu Ala Gly Thr Phe His
 490 495 500
 cgc ttc tac gat tcc tgc cac atc ctt cca aag gtt gat gag gat acg 1651
 Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys Val Asp Glu Asp Thr
 505 510 515
 gca cca atc cac aca gca cgt ctg gca ctt gca gca gca acc cgc cag 1699
 Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala Ala Ala Thr Arg Gln
 520 525 530
 acc ctc gct aac gcc ctg cac ctg gtt ggc gtt tcc gca ccg gag aag 1747
 Thr Leu Ala Asn Ala Leu His Leu Val Gly Val Ser Ala Pro Glu Lys
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 Met
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<210> 276

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

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Val Val Glu Arg Pro Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn

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Ala	Glu	Ile	Ala	Gly	Pro	Gly	Phe	Leu	Asn	Ile	Arg	Leu	Ala	Ala	Ala
				85					90					95	
Ala	Gln	Gly	Glu	Ile	Val	Ala	Lys	Ile	Leu	Ala	Gln	Gly	Glu	Thr	Phe
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Gly	Asn	Ser	Asp	His	Leu	Ser	His	Leu	Asp	Val	Asn	Leu	Glu	Phe	Val
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Ser	Ala	Asn	Pro	Thr	Gly	Pro	Ile	His	Leu	Gly	Gly	Thr	Arg	Trp	Ala
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Ala	Val	Gly	Asp	Ser	Leu	Gly	Arg	Val	Leu	Glu	Ala	Ser	Ser	Ala	Lys
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Val	Thr	Arg	Glu	Tyr	Tyr	Phe	Asn	Asp	His	Gly	Arg	Gln	Ile	Asp	Arg
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Phe	Ala	Leu	Ser	Leu	Leu	Ala	Ala	Ala	Lys	Gly	Glu	Pro	Thr	Pro	Glu
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Asp	Gly	Tyr	Gly	Gly	Glu	Tyr	Ile	Lys	Glu	Ile	Ala	Glu	Ala	Ile	Val
		195					200					205			
Glu	Lys	His	Pro	Glu	Ala	Leu	Ala	Leu	Glu	Pro	Ala	Ala	Thr	Gln	Glu
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Leu	Phe	Arg	Ala	Glu	Gly	Val	Glu	Met	Met	Phe	Glu	His	Ile	Lys	Ser
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Ser	Leu	His	Glu	Phe	Gly	Thr	Asp	Phe	Asp	Val	Tyr	Tyr	His	Glu	Asn
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		275					280					285			
Thr	Glu	Phe	Gly	Asp	Asp	Lys	Asp	Arg	Val	Val	Ile	Lys	Ser	Asp	Gly
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Ser	Arg	Gly	His	Asn	Leu	Asn	Ile	Tyr	Met	Leu	Gly	Ala	Asp	His	His
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Gly	Tyr	Ile	Ala	Arg	Leu	Lys	Ala	Ala	Ala	Ala	Ala	Leu	Gly	Tyr	Lys
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Pro	Glu	Gly	Val	Glu	Val	Leu	Ile	Gly	Gln	Met	Val	Asn	Leu	Leu	Arg
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Asp Gly Lys Ala Val Arg Met Ser Lys Arg Ala Gly Thr Val Val Thr
 370 375 380
 Leu Asp Asp Leu Val Glu Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser
 385 390 395 400
 Leu Ile Arg Ser Ser Val Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu
 405 410 415
 Trp Glu Ser Gln Ser Ser Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly
 420 425 430
 His Ala Arg Leu Cys Ser Ile Ala Arg Lys Ala Glu Thr Leu Gly Val
 435 440 445
 Thr Glu Glu Gly Ala Asp Leu Ser Leu Leu Thr His Asp Arg Glu Gly
 450 455 460
 Asp Leu Ile Arg Thr Leu Gly Glu Phe Pro Ala Val Val Lys Ala Ala
 465 470 475 480
 Ala Asp Leu Arg Glu Pro His Arg Ile Ala Arg Tyr Ala Glu Glu Leu
 485 490 495
 Ala Gly Thr Phe His Arg Phe Tyr Asp Ser Cys His Ile Leu Pro Lys
 500 505 510
 Val Asp Glu Asp Thr Ala Pro Ile His Thr Ala Arg Leu Ala Leu Ala
 515 520 525
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<211> 877

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(877)

<223> FRXA00975

<400> 277

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gcc gca acc caa gag ctt ttc cgc gct gaa ggc gtg gag atg atg ttc 163
 Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu Gly Val Glu Met Met Phe
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gag cac atc aaa tct tcc ctg cat gag ttc ggc acc gat ttc gat gtc 211
 Glu His Ile Lys Ser Ser Leu His Glu Phe Gly Thr Asp Phe Asp Val

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Tyr	Tyr	His	Glu	Asn	Ser	Leu	Phe	Glu	Ser	Gly	Ala	Val	Asp	Lys	Ala					
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gtg	cag	gtg	ctg	aag	gac	aac	ggc	aac	ctg	tac	gaa	aac	gag	ggc	gct	307				
Val	Gln	Val	Leu	Lys	Asp	Asn	Gly	Asn	Leu	Tyr	Glu	Asn	Glu	Gly	Ala					
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Trp	Trp	Leu	Arg	Ser	Thr	Glu	Phe	Gly	Asp	Asp	Lys	Asp	Arg	Val	Val					
	70				75					80					85					
atc	aag	tct	gac	ggc	gac	gca	gcc	tac	atc	gct	ggc	gat	atc	gcg	tac	403				
Ile	Lys	Ser	Asp	Gly	Asp	Ala	Ala	Tyr	Ile	Ala	Gly	Asp	Ile	Ala	Tyr					
				90					95					100						
gtg	gct	gat	aag	ttc	tcc	cgc	gga	cac	aac	cta	aac	atc	tac	atg	ttg	451				
Val	Ala	Asp	Lys	Phe	Ser	Arg	Gly	His	Asn	Leu	Asn	Ile	Tyr	Met	Leu					
			105					110					115							
ggt	gct	gac	cac	cat	ggt	tac	atc	gcg	cgc	ctg	aag	gca	gcg	gcg	gcg	499				
Gly	Ala	Asp	His	His	Gly	Tyr	Ile	Ala	Arg	Leu	Lys	Ala	Ala	Ala	Ala					
		120					125					130								
gca	ctt	ggc	tac	aag	cca	gaa	ggc	gtt	gaa	gtc	ctg	att	ggc	cag	atg	547				
Ala	Leu	Gly	Tyr	Lys	Pro	Glu	Gly	Val	Glu	Val	Leu	Ile	Gly	Gln	Met					
	135					140					145									
gtg	aac	ctg	ctt	cgc	gac	ggc	aag	gca	gtg	cgt	atg	tcc	aag	cgt	gca	595				
Val	Asn	Leu	Leu	Arg	Asp	Gly	Lys	Ala	Val	Arg	Met	Ser	Lys	Arg	Ala					
	150				155					160				165						
ggc	acc	gtg	gtc	acc	cta	gat	gac	ctc	gtt	gaa	gca	atc	ggc	atc	gat	643				
Gly	Thr	Val	Val	Thr	Leu	Asp	Asp	Leu	Val	Glu	Ala	Ile	Gly	Ile	Asp					
				170					175					180						
gcg	gcg	cgt	tac	tcc	ctg	atc	cgt	tcc	tcc	gtg	gat	tct	tcc	ctg	gat	691				
Ala	Ala	Arg	Tyr	Ser	Leu	Ile	Arg	Ser	Ser	Val	Asp	Ser	Ser	Leu	Asp					
			185					190					195							
atc	gat	ctc	ggc	ctg	tgg	gaa	tcc	cag	tcc	tcc	gac	aac	cct	gtg	tac	739				
Ile	Asp	Leu	Gly	Leu	Trp	Glu	Ser	Gln	Ser	Ser	Asp	Asn	Pro	Val	Tyr					
		200					205					210								
tac	gtg	cag	tac	gga	cac	gct	cgt	ctg	tgc	tcc	atc	gcg	cgc	aag	gca	787				
Tyr	Val	Gln	Tyr	Gly	His	Ala	Arg	Leu	Cys	Ser	Ile	Ala	Arg	Lys	Ala					
	215					220					225									
gag	acc	ttg	ggt	gtc	acc	gag	gaa	ggc	gca	gac	cta	tct	cta	ctg	acc	835				
Glu	Thr	Leu	Gly	Val	Thr	Glu	Glu	Gly	Ala	Asp	Leu	Ser	Leu	Leu	Thr					
	230				235					240					245					
cac	gac	cgc	gaa	ggt	gat	ctc	atc	cgc	aca	ctc	gga	gag	ttc			877				
His	Asp	Arg	Glu	Gly	Asp	Leu	Ile	Arg	Thr	Leu	Gly	Glu	Phe							
				250					255											

<210> 278

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 278

Leu Ala Leu Glu Pro Ala Ala Thr Gln Glu Leu Phe Arg Ala Glu Gly
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 Val Glu Met Met Phe Glu His Ile Lys Ser Ser Leu His Glu Phe Gly
 20 25 30
 Thr Asp Phe Asp Val Tyr Tyr His Glu Asn Ser Leu Phe Glu Ser Gly
 35 40 45
 Ala Val Asp Lys Ala Val Gln Val Leu Lys Asp Asn Gly Asn Leu Tyr
 50 55 60
 Glu Asn Glu Gly Ala Trp Trp Leu Arg Ser Thr Glu Phe Gly Asp Asp
 65 70 75 80
 Lys Asp Arg Val Val Ile Lys Ser Asp Gly Asp Ala Ala Tyr Ile Ala
 85 90 95
 Gly Asp Ile Ala Tyr Val Ala Asp Lys Phe Ser Arg Gly His Asn Leu
 100 105 110
 Asn Ile Tyr Met Leu Gly Ala Asp His His Gly Tyr Ile Ala Arg Leu
 115 120 125
 Lys Ala Ala Ala Ala Ala Leu Gly Tyr Lys Pro Glu Gly Val Glu Val
 130 135 140
 Leu Ile Gly Gln Met Val Asn Leu Leu Arg Asp Gly Lys Ala Val Arg
 145 150 155 160
 Met Ser Lys Arg Ala Gly Thr Val Val Thr Leu Asp Asp Leu Val Glu
 165 170 175
 Ala Ile Gly Ile Asp Ala Ala Arg Tyr Ser Leu Ile Arg Ser Ser Val
 180 185 190
 Asp Ser Ser Leu Asp Ile Asp Leu Gly Leu Trp Glu Ser Gln Ser Ser
 195 200 205
 Asp Asn Pro Val Tyr Tyr Val Gln Tyr Gly His Ala Arg Leu Cys Ser
 210 215 220
 Ile Ala Arg Lys Ala Glu Thr Leu Gly Val Thr Glu Glu Gly Ala Asp
 225 230 235 240
 Leu Ser Leu Leu Thr His Asp Arg Glu Gly Asp Leu Ile Arg Thr Leu
 245 250 255
 Gly Glu Phe

<210> 279

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> FRXA00976

<400> 279

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attctgtgcg acgggtgtac ctcggtctaga atttctcccc atg aca cca gct gat 115
Met Thr Pro Ala Asp
1 5

ctc gca aca ttg att aaa gag acc gcg gta gag gtt ttg acc tcc cgc 163
Leu Ala Thr Leu Ile Lys Glu Thr Ala Val Glu Val Leu Thr Ser Arg
10 15 20

gag ctc gat act tct gtt ctt ccg gag cag gta gtt gtg gag cgt ccg 211
Glu Leu Asp Thr Ser Val Leu Pro Glu Gln Val Val Val Glu Arg Pro
25 30 35

cgt aac cca gag cac ggc gat tac gcc acc aac att gca ttg cag gtg 259
Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn Ile Ala Leu Gln Val
40 45 50

gct aaa aag gtc ggt cag aac cct cgg gat ttg gct acc tgg ctg gca 307
Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu Ala Thr Trp Leu Ala
55 60 65

gag gca ttg gct gca gat gac gcc att gat tct gct gaa att gct ggc 355
Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser Ala Glu Ile Ala Gly
70 75 80 85

cca ggc ttt ttg aac att cgc ctt gct gca gca gca cag ggt gaa att 403
Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala Gln Gly Glu Ile
90 95 100

gtg gcc aag att ctg gca cag ggc gag act ttc gga aac tcc gat cac 451
Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe Gly Asn Ser Asp His
105 110 115

ctt tcc cac ttg gac gtg aac ctc gag ttc gtt tct gca aac cca acc 499
Leu Ser His Leu Asp Val Asn Leu Glu Phe Val Ser Ala Asn Pro Thr
120 125 130

gga cct att cac ctt ggc gga acc cgc tgg gct gcc gtg ggt gac tct 547
Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala Ala Val Gly Asp Ser
135 140 145

ttg ggt cgt gtg ctg gag gct tcc ggc gcg aaa gtg acc cgc gaa tac 595
Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys Val Thr Arg Glu Tyr
150 155 160 165

tac ttc aac gat cac ggt cgc cag atc gat cgt ttc gct ttg tcg agt 643
Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg Phe Ala Leu Ser Ser
170 175 180

tct tgc agc ggc gaa ggg cga gcc aac gcc aga aga cgg tta tgg cgg 691
Ser Cys Ser Gly Glu Gly Arg Ala Asn Ala Arg Arg Arg Leu Trp Arg
185 190 195

cga ata cat taaggaaatt gcggaggcaa tcg 723

Arg Ile His
200

<210> 280
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 280
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20 25 30
Val Val Glu Arg Pro Arg Asn Pro Glu His Gly Asp Tyr Ala Thr Asn
35 40 45
Ile Ala Leu Gln Val Ala Lys Lys Val Gly Gln Asn Pro Arg Asp Leu
50 55 60
Ala Thr Trp Leu Ala Glu Ala Leu Ala Ala Asp Asp Ala Ile Asp Ser
65 70 75 80
Ala Glu Ile Ala Gly Pro Gly Phe Leu Asn Ile Arg Leu Ala Ala Ala
85 90 95
Ala Gln Gly Glu Ile Val Ala Lys Ile Leu Ala Gln Gly Glu Thr Phe
100 105 110
Gly Asn Ser Asp His Leu Ser His Leu Asp Val Asn Leu Glu Phe Val
115 120 125
Ser Ala Asn Pro Thr Gly Pro Ile His Leu Gly Gly Thr Arg Trp Ala
130 135 140
Ala Val Gly Asp Ser Leu Gly Arg Val Leu Glu Ala Ser Gly Ala Lys
145 150 155 160
Val Thr Arg Glu Tyr Tyr Phe Asn Asp His Gly Arg Gln Ile Asp Arg
165 170 175
Phe Ala Leu Ser Ser Ser Cys Ser Gly Glu Gly Arg Ala Asn Ala Arg
180 185 190
Arg Arg Leu Trp Arg Arg Ile His
195 200

<210> 281
<211> 1804
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> RXN01730

<400> 281

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catcgactga tcaaaaccaa gcggaaggac ttccaccaac gtg ctg cgc act cat 115
Val Leu Arg Thr His
1 5

ctc tca ggc gag ctt cgt aaa gaa aac gca ggc cag tca gtt act ctg 163
Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly Gln Ser Val Thr Leu
10 15 20

acc ggc tgg gtc aat cgt cgc cgt gac cac ggt ggc gtg atc ttc atc 211
Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly Gly Val Ile Phe Ile
25 30 35

gat ctt cgc gac cgt act ggc att gcc cag gtt gtt ttc cgc aat gag 259
Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val Val Phe Arg Asn Glu
40 45 50

gac gtt gct gag cgt gca cac gca ctg cgc agc gaa ttc gtc cta cgc 307
Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser Glu Phe Val Leu Arg
55 60 65

gtc acc ggc gtc gtc gaa gag cgc cca gaa ggc tct caa aac cct aac 355
Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly Ser Gln Asn Pro Asn
70 75 80 85

ctt gca tcc ggc gac att gaa gtc agc gtc acc gaa ttt gag gta ctc 403
Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr Glu Phe Glu Val Leu
90 95 100

aac gag tcc gct cca ctt cct ttc cag atc gag gat tcc tcc tct gct 451
Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu Asp Ser Ser Ser Ala
105 110 115

ggt gaa gtc ggc gaa gag acc cgt ctg aag tac cgc tac ctg gac ctg 499
Gly Glu Val Gly Glu Glu Thr Arg Leu Lys Tyr Arg Tyr Leu Asp Leu
120 125 130

cgt cgc cca gtt cag gcg aac gcc ctg cgt ctg cgt tct gct gcc aac 547
Arg Arg Pro Val Gln Ala Asn Ala Leu Arg Leu Arg Ser Ala Ala Asn
135 140 145

aag gct gca cgc acc gtg ctg gac agc cac gat ttc acc gag atc gag 595
Lys Ala Ala Arg Thr Val Leu Asp Ser His Asp Phe Thr Glu Ile Glu
150 155 160 165

acc cca acc ttg act cgt tcc acc cca gaa ggc gca cgt gac ttc ctg 643
Thr Pro Thr Leu Thr Arg Ser Thr Pro Glu Gly Ala Arg Asp Phe Leu
170 175 180

gtg cca gct cgt ctg cgc cca ggc act ttc tac gca ttg cca cag tcc 691
Val Pro Ala Arg Leu Arg Pro Gly Thr Phe Tyr Ala Leu Pro Gln Ser
185 190 195

cca cag ctg ttc aag cag ctg ctg cag gtt gct ggc atg gag cgc tac 739
Pro Gln Leu Phe Lys Gln Leu Leu Gln Val Ala Gly Met Glu Arg Tyr
200 205 210

tac cag atc gct cgt tgc tac cgc gat gag gat ttc cgt gca gac cgt 787
Tyr Gln Ile Ala Arg Cys Tyr Arg Asp Glu Asp Phe Arg Ala Asp Arg
215 220 225

cag cca gag ttc acc cag ctg gac gtt gaa atg tcc ttc gtg gac cag	835
Gln Pro Glu Phe Thr Gln Leu Asp Val Glu Met Ser Phe Val Asp Gln	
230 235 240 245	
gat gat gtc atc gca ctg ggc gag gag atc atc tct gag gtg tgg aag	883
Asp Asp Val Ile Ala Leu Gly Glu Glu Ile Ile Ser Glu Val Trp Lys	
250 255 260	
ttg atc gga tat gag atc aag act cca atc cca cgc atg acc tac gcc	931
Leu Ile Gly Tyr Glu Ile Lys Thr Pro Ile Pro Arg Met Thr Tyr Ala	
265 270 275	
gat gca atg cgt cgc tac ggc tcc gac aag cca gac ctg cgc ttc gac	979
Asp Ala Met Arg Arg Tyr Gly Ser Asp Lys Pro Asp Leu Arg Phe Asp	
280 285 290	
atc gaa atc acc gag tgc acc gag ttc ttc cag gac acc aca ttc cgt	1027
Ile Glu Ile Thr Glu Cys Thr Glu Phe Phe Gln Asp Thr Thr Phe Arg	
295 300 305	
gtg ttc aag aac gaa tat gtc ggc gca gtt gtc atg acc ggt ggt gct	1075
Val Phe Lys Asn Glu Tyr Val Gly Ala Val Val Met Thr Gly Gly Ala	
310 315 320 325	
tcc cag cct cgc cgt cag ctc gac gca tgg cag gaa tgg gcc aag cag	1123
Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln Glu Trp Ala Lys Gln	
330 335 340	
cgc ggt gct aag gga ctt gct tac atc ctc gtt ggt gaa gac ggc gag	1171
Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val Gly Glu Asp Gly Glu	
345 350 355	
ctg tcc gga cct gtg gct aag aac atc acc gac gct gag cgc gca gga	1219
Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp Ala Glu Arg Ala Gly	
360 365 370	
atc gca gct cac gtt ggc gca cag cca ggc gac tgc atc ttc ttc gca	1267
Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp Cys Ile Phe Phe Ala	
375 380 385	
gca gga gac acc aag tct tcc ctc gca ctg ctc ggt gca gct cgt ggc	1315
Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu Gly Ala Ala Arg Gly	
390 395 400 405	
gag atc gct aag aag ctc gac ctg atc aag gaa ggc gac tgg gca ttc	1363
Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu Gly Asp Trp Ala Phe	
410 415 420	
acc tgg atc gtt gac gct cca atg ttc gag cca gca gca gac gcc acc	1411
Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro Ala Ala Asp Ala Thr	
425 430 435	
gca tcc ggt gac gtt gca ctg ggt aac tcc aag tgg acc gca gtc cac	1459
Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys Trp Thr Ala Val His	
440 445 450	
cac gcc ttc acc tca cct aag cca gag ttc ctg gac aac ttt gac acc	1507
His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu Asp Asn Phe Asp Thr	
455 460 465	

aac cca ggt gac gca ctt gct tat gca tac gac atc gtg tgc aac ggc 1555
 Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp Ile Val Cys Asn Gly
 470 475 480 485

 aat gaa atc ggt ggc ggt tcc atc cgt atc cac cag cgc gac gtt cag 1603
 Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His Gln Arg Asp Val Gln
 490 495 500

 gaa cgc gtt ttc gag gtt atg ggc atc acc ggt gaa gaa gca cgc gag 1651
 Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly Glu Glu Ala Arg Glu
 505 510 515

 aag ttc ggc ttc ctg ctt gac gcc ttc gca ttc ggc gca cct cca cac 1699
 Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe Gly Ala Pro Pro His
 520 525 530

 ggc gga atc gca ttc ggc tgg gac cgc atc gtg tcc ctg ctg ggc ggc 1747
 Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val Ser Leu Leu Gly Gly
 535 540 545

 ttt gac tcc atc cgc gac gtc atc gcg ttc cct aag tcc ggt ggc gga 1795
 Phe Asp Ser Ile Arg Asp Val Ile Ala Phe Pro Lys Ser Gly Gly Gly
 550 555 560 565

 atc gac ccc 1804
 Ile Asp Pro

<210> 282

<211> 568

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Leu Arg Thr His Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly
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 Gln Ser Val Thr Leu Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly
 20 25 30

 Gly Val Ile Phe Ile Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val
 35 40 45

 Val Phe Arg Asn Glu Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser
 50 55 60

 Glu Phe Val Leu Arg Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly
 65 70 75 80

 Ser Gln Asn Pro Asn Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr
 85 90 95

 Glu Phe Glu Val Leu Asn Glu Ser Ala Pro Leu Pro Phe Gln Ile Glu
 100 105 110

 Asp Ser Ser Ser Ala Gly Glu Val Gly Glu Glu Thr Arg Leu Lys Tyr
 115 120 125

 Arg Tyr Leu Asp Leu Arg Arg Pro Val Gln Ala Asn Ala Leu Arg Leu
 130 135 140

Arg	Ser	Ala	Ala	Asn	Lys	Ala	Ala	Arg	Thr	Val	Leu	Asp	Ser	His	Asp	
145					150					155					160	
Phe	Thr	Glu	Ile	Glu	Thr	Pro	Thr	Leu	Thr	Arg	Ser	Thr	Pro	Glu	Gly	
				165					170					175		
Ala	Arg	Asp	Phe	Leu	Val	Pro	Ala	Arg	Leu	Arg	Pro	Gly	Thr	Phe	Tyr	
			180					185					190			
Ala	Leu	Pro	Gln	Ser	Pro	Gln	Leu	Phe	Lys	Gln	Leu	Leu	Gln	Val	Ala	
		195					200					205				
Gly	Met	Glu	Arg	Tyr	Tyr	Gln	Ile	Ala	Arg	Cys	Tyr	Arg	Asp	Glu	Asp	
	210					215					220					
Phe	Arg	Ala	Asp	Arg	Gln	Pro	Glu	Phe	Thr	Gln	Leu	Asp	Val	Glu	Met	
225					230					235					240	
Ser	Phe	Val	Asp	Gln	Asp	Asp	Val	Ile	Ala	Leu	Gly	Glu	Glu	Ile	Ile	
				245					250					255		
Ser	Glu	Val	Trp	Lys	Leu	Ile	Gly	Tyr	Glu	Ile	Lys	Thr	Pro	Ile	Pro	
			260					265					270			
Arg	Met	Thr	Tyr	Ala	Asp	Ala	Met	Arg	Arg	Tyr	Gly	Ser	Asp	Lys	Pro	
		275					280					285				
Asp	Leu	Arg	Phe	Asp	Ile	Glu	Ile	Thr	Glu	Cys	Thr	Glu	Phe	Phe	Gln	
	290					295					300					
Asp	Thr	Thr	Phe	Arg	Val	Phe	Lys	Asn	Glu	Tyr	Val	Gly	Ala	Val	Val	
305					310					315					320	
Met	Thr	Gly	Gly	Ala	Ser	Gln	Pro	Arg	Arg	Gln	Leu	Asp	Ala	Trp	Gln	
				325					330					335		
Glu	Trp	Ala	Lys	Gln	Arg	Gly	Ala	Lys	Gly	Leu	Ala	Tyr	Ile	Leu	Val	
			340					345					350			
Gly	Glu	Asp	Gly	Glu	Leu	Ser	Gly	Pro	Val	Ala	Lys	Asn	Ile	Thr	Asp	
		355					360					365				
Ala	Glu	Arg	Ala	Gly	Ile	Ala	Ala	His	Val	Gly	Ala	Gln	Pro	Gly	Asp	
						375					380					
Cys	Ile	Phe	Phe	Ala	Ala	Gly	Asp	Thr	Lys	Ser	Ser	Leu	Ala	Leu	Leu	
385					390					395					400	
Gly	Ala	Ala	Arg	Gly	Glu	Ile	Ala	Lys	Lys	Leu	Asp	Leu	Ile	Lys	Glu	
				405					410					415		
Gly	Asp	Trp	Ala	Phe	Thr	Trp	Ile	Val	Asp	Ala	Pro	Met	Phe	Glu	Pro	
			420					425					430			
Ala	Ala	Asp	Ala	Thr	Ala	Ser	Gly	Asp	Val	Ala	Leu	Gly	Asn	Ser	Lys	
		435					440					445				
Trp	Thr	Ala	Val	His	His	Ala	Phe	Thr	Ser	Pro	Lys	Pro	Glu	Phe	Leu	
	450					455					460					

Asp Asn Phe Asp Thr Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp
 465 470 475 480
 Ile Val Cys Asn Gly Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His
 485 490 495
 Gln Arg Asp Val Gln Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly
 500 505 510
 Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe
 515 520 525
 Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val
 530 535 540
 Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe Pro
 545 550 555 560
 Lys Ser Gly Gly Gly Ile Asp Pro
 565

<210> 283
 <211> 1777
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1777)
 <223> FRXA01730

<400> 283
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 catcgactga tcaaaaccaa gcggaaggac ttccaccaac gtg ctg cgc act cat 115
 Val Leu Arg Thr His
 1 5
 ctc tca ggc gag ctt cgt aaa gaa aac gca ggc cag tca gtt act ctg 163
 Leu Ser Gly Glu Leu Arg Lys Glu Asn Ala Gly Gln Ser Val Thr Leu
 10 15 20
 acc ggc tgg gtc aat cgt cgc cgt gac cac ggt ggc gtg atc ttc atc 211
 Thr Gly Trp Val Asn Arg Arg Arg Asp His Gly Gly Val Ile Phe Ile
 25 30 35
 gat ctt cgc gac cgt act ggc att gcc cag gtt gtt ttc cgc aat gag 259
 Asp Leu Arg Asp Arg Thr Gly Ile Ala Gln Val Val Phe Arg Asn Glu
 40 45 50
 gac gtt gct gag cgt gca cac gca ctg cgc agc gaa ttc gtc cta cgc 307
 Asp Val Ala Glu Arg Ala His Ala Leu Arg Ser Glu Phe Val Leu Arg
 55 60 65
 gtc acc ggc gtc gtc gaa gag cgc cca gaa ggc tct caa aac cct aac 355
 Val Thr Gly Val Val Glu Glu Arg Pro Glu Gly Ser Gln Asn Pro Asn
 70 75 80 85
 ctt gca tcc ggc gac att gaa gtc agc gtc acc gaa ttt gag gta ctc 403
 Leu Ala Ser Gly Asp Ile Glu Val Ser Val Thr Glu Phe Glu Val Leu

										90											95											100	
aac	gag	tcc	gct	cca	ctt	cct	ttc	cag	atc	gag	gat	tcc	tcc	tct	gct	451																	
Asn	Glu	Ser	Ala	Pro	Leu	Pro	Phe	Gln	Ile	Glu	Asp	Ser	Ser	Ser	Ala																		
			105				110				115																						
ggt	gaa	gtc	ggc	gaa	gag	acc	cgt	ctg	aag	tac	cgc	tac	ctg	gac	ctg	499																	
Gly	Glu	Val	Gly	Glu	Glu	Thr	Arg	Leu	Lys	Tyr	Arg	Tyr	Leu	Asp	Leu																		
			120				125				130																						
cgt	cgc	cca	gtt	cag	gcg	aac	gcc	ctg	cgt	ctg	cgt	tct	gct	gcc	aac	547																	
Arg	Arg	Pro	Val	Gln	Ala	Asn	Ala	Leu	Arg	Leu	Arg	Ser	Ala	Ala	Asn																		
			135				140				145																						
aag	gct	gca	cgc	acc	gtg	ctg	gac	agc	cac	gat	ttc	acc	gag	atc	gag	595																	
Lys	Ala	Ala	Arg	Thr	Val	Leu	Asp	Ser	His	Asp	Phe	Thr	Glu	Ile	Glu																		
150				155				160					165																				
acc	cca	acc	ttg	act	cgt	tcc	acc	cca	gaa	ggc	gca	cgt	gac	ttc	ctg	643																	
Thr	Pro	Thr	Leu	Thr	Arg	Ser	Thr	Pro	Glu	Gly	Ala	Arg	Asp	Phe	Leu																		
			170				175				180																						
gtg	cca	gct	cgt	ctg	cgc	cca	ggc	act	ttc	tac	gca	ttg	cca	cag	tcc	691																	
Val	Pro	Ala	Arg	Leu	Arg	Pro	Gly	Thr	Phe	Tyr	Ala	Leu	Pro	Gln	Ser																		
			185				190				195																						
cca	cag	ctg	ttc	aag	cag	ctg	ctg	cag	gtt	gct	ggc	atg	gag	cgc	tac	739																	
Pro	Gln	Leu	Phe	Lys	Gln	Leu	Leu	Gln	Val	Ala	Gly	Met	Glu	Arg	Tyr																		
			200				205				210																						
tac	cag	atc	gct	cgt	tgc	tac	cgc	gat	gag	gat	ttc	cgt	gca	gac	cgt	787																	
Tyr	Gln	Ile	Ala	Arg	Cys	Tyr	Arg	Asp	Glu	Asp	Phe	Arg	Ala	Asp	Arg																		
			215				220				225																						
cag	cca	gag	ttc	acc	cag	ctg	gac	gtt	gaa	atg	tcc	ttc	gtg	gac	cag	835																	
Gln	Pro	Glu	Phe	Thr	Gln	Leu	Asp	Val	Glu	Met	Ser	Phe	Val	Asp	Gln																		
230				235				240					245																				
gat	gat	gtc	atc	gca	ctg	ggc	gag	gag	atc	atc	tct	gag	gtg	tgg	aag	883																	
Asp	Asp	Val	Ile	Ala	Leu	Gly	Glu	Glu	Ile	Ile	Ser	Glu	Val	Trp	Lys																		
			250				255					260																					
ttg	atc	gga	tat	gag	atc	aag	act	cca	atc	cca	cgc	atg	acc	tac	gcc	931																	
Leu	Ile	Gly	Tyr	Glu	Ile	Lys	Thr	Pro	Ile	Pro	Arg	Met	Thr	Tyr	Ala																		
			265				270				275																						
gat	gca	atg	cgt	cgc	tac	ggc	tcc	gac	aag	cca	gac	ctg	cgc	ttc	gac	979																	
Asp	Ala	Met	Arg	Arg	Tyr	Gly	Ser	Asp	Lys	Pro	Asp	Leu	Arg	Phe	Asp																		
			280				285				290																						
atc	gaa	atc	acc	gag	tgc	acc	gag	ttc	ttc	cag	gac	acc	aca	ttc	cgt	1027																	
Ile	Glu	Ile	Thr	Glu	Cys	Thr	Glu	Phe	Phe	Gln	Asp	Thr	Thr	Phe	Arg																		
			295				300				305																						
gtg	ttc	aag	aac	gaa	tat	gtc	ggc	gca	gtt	gtc	atg	acc	ggt	ggt	gct	1075																	
Val	Phe	Lys	Asn	Glu	Tyr	Val	Gly	Ala	Val	Val	Met	Thr	Gly	Gly	Ala																		
310				315				320					325																				
tcc	cag	cct	cgc	cgt	cag	ctc	gac	gca	tgg	cag	gaa	tgg	gcc	aag	cag	1123																	
Ser	Gln	Pro	Arg	Arg	Gln	Leu	Asp	Ala	Trp	Gln	Glu	Trp	Ala	Lys	Gln																		
			330				335				340																						

cgc ggt gct aag gga ctt gct tac atc ctc gtt ggt gaa gac ggc gag	1171
Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val Gly Glu Asp Gly Glu	
345 350 355	
ctg tcc gga cct gtg gct aag aac atc acc gac gct gag cgc gca gga	1219
Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp Ala Glu Arg Ala Gly	
360 365 370	
atc gca gct cac gtt ggc gca cag cca ggc gac tgc atc ttc ttc gca	1267
Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp Cys Ile Phe Phe Ala	
375 380 385	
gca gga gac acc aag tct tcc ctc gca ctg ctc ggt gca gct cgt ggc	1315
Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu Gly Ala Ala Arg Gly	
390 395 400 405	
gag atc gct aag aag ctc gac ctg atc aag gaa ggc gac tgg gca ttc	1363
Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu Gly Asp Trp Ala Phe	
410 415 420	
acc tgg atc gtt gac gct cca atg ttc gag cca gca gca gac gcc acc	1411
Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro Ala Ala Asp Ala Thr	
425 430 435	
gca tcc ggt gac gtt gca ctg ggt aac tcc aag tgg acc gca gtc cac	1459
Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys Trp Thr Ala Val His	
440 445 450	
cac gcc ttc acc tca cct aag cca gag ttc ctg gac aac ttt gac acc	1507
His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu Asp Asn Phe Asp Thr	
455 460 465	
aac cca ggt gac gca ctt gct tat gca tac gac atc gtg tgc aac ggc	1555
Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp Ile Val Cys Asn Gly	
470 475 480 485	
aat gaa atc ggt ggc ggt tcc atc cgt atc cac cag cgc gac gtt cag	1603
Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His Gln Arg Asp Val Gln	
490 495 500	
gaa cgc gtt ttc gag gtt atg ggc atc acc ggt gaa gaa gca cgc gag	1651
Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly Glu Glu Ala Arg Glu	
505 510 515	
aag ttc ggc ttc ctg ctt gac gcc ttc gca ttc ggc gca cct cca cac	1699
Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe Gly Ala Pro Pro His	
520 525 530	
ggc gga atc gca ttc ggc tgg gac cgc atc gtg tcc ctg ctg ggc ggc	1747
Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val Ser Leu Leu Gly Gly	
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Phe Asp Ser Ile Arg Asp Val Ile Ala Phe	
550 555	

<210> 284

<211> 559

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

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			20					25					30		
Gly	Val	Ile	Phe	Ile	Asp	Leu	Arg	Asp	Arg	Thr	Gly	Ile	Ala	Gln	Val
		35					40					45			
Val	Phe	Arg	Asn	Glu	Asp	Val	Ala	Glu	Arg	Ala	His	Ala	Leu	Arg	Ser
	50					55					60				
Glu	Phe	Val	Leu	Arg	Val	Thr	Gly	Val	Val	Glu	Glu	Arg	Pro	Glu	Gly
65					70					75					80
Ser	Gln	Asn	Pro	Asn	Leu	Ala	Ser	Gly	Asp	Ile	Glu	Val	Ser	Val	Thr
				85					90					95	
Glu	Phe	Glu	Val	Leu	Asn	Glu	Ser	Ala	Pro	Leu	Pro	Phe	Gln	Ile	Glu
			100					105					110		
Asp	Ser	Ser	Ser	Ala	Gly	Glu	Val	Gly	Glu	Glu	Thr	Arg	Leu	Lys	Tyr
		115					120					125			
Arg	Tyr	Leu	Asp	Leu	Arg	Arg	Pro	Val	Gln	Ala	Asn	Ala	Leu	Arg	Leu
	130					135					140				
Arg	Ser	Ala	Ala	Asn	Lys	Ala	Ala	Arg	Thr	Val	Leu	Asp	Ser	His	Asp
145					150					155					160
Phe	Thr	Glu	Ile	Glu	Thr	Pro	Thr	Leu	Thr	Arg	Ser	Thr	Pro	Glu	Gly
				165					170					175	
Ala	Arg	Asp	Phe	Leu	Val	Pro	Ala	Arg	Leu	Arg	Pro	Gly	Thr	Phe	Tyr
			180					185					190		
Ala	Leu	Pro	Gln	Ser	Pro	Gln	Leu	Phe	Lys	Gln	Leu	Leu	Gln	Val	Ala
		195					200					205			
Gly	Met	Glu	Arg	Tyr	Tyr	Gln	Ile	Ala	Arg	Cys	Tyr	Arg	Asp	Glu	Asp
	210					215					220				
Phe	Arg	Ala	Asp	Arg	Gln	Pro	Glu	Phe	Thr	Gln	Leu	Asp	Val	Glu	Met
225					230					235					240
Ser	Phe	Val	Asp	Gln	Asp	Asp	Val	Ile	Ala	Leu	Gly	Glu	Glu	Ile	Ile
				245					250					255	
Ser	Glu	Val	Trp	Lys	Leu	Ile	Gly	Tyr	Glu	Ile	Lys	Thr	Pro	Ile	Pro
			260					265					270		
Arg	Met	Thr	Tyr	Ala	Asp	Ala	Met	Arg	Arg	Tyr	Gly	Ser	Asp	Lys	Pro
		275					280					285			
Asp	Leu	Arg	Phe	Asp	Ile	Glu	Ile	Thr	Glu	Cys	Thr	Glu	Phe	Phe	Gln
	290					295					300				
Asp	Thr	Thr	Phe	Arg	Val	Phe	Lys	Asn	Glu	Tyr	Val	Gly	Ala	Val	Val

305	310	315	320
Met Thr Gly Gly Ala Ser Gln Pro Arg Arg Gln Leu Asp Ala Trp Gln	325	330	335
Glu Trp Ala Lys Gln Arg Gly Ala Lys Gly Leu Ala Tyr Ile Leu Val	340	345	350
Gly Glu Asp Gly Glu Leu Ser Gly Pro Val Ala Lys Asn Ile Thr Asp	355	360	365
Ala Glu Arg Ala Gly Ile Ala Ala His Val Gly Ala Gln Pro Gly Asp	370	375	380
Cys Ile Phe Phe Ala Ala Gly Asp Thr Lys Ser Ser Leu Ala Leu Leu	385	390	400
Gly Ala Ala Arg Gly Glu Ile Ala Lys Lys Leu Asp Leu Ile Lys Glu	405	410	415
Gly Asp Trp Ala Phe Thr Trp Ile Val Asp Ala Pro Met Phe Glu Pro	420	425	430
Ala Ala Asp Ala Thr Ala Ser Gly Asp Val Ala Leu Gly Asn Ser Lys	435	440	445
Trp Thr Ala Val His His Ala Phe Thr Ser Pro Lys Pro Glu Phe Leu	450	455	460
Asp Asn Phe Asp Thr Asn Pro Gly Asp Ala Leu Ala Tyr Ala Tyr Asp	465	470	475
Ile Val Cys Asn Gly Asn Glu Ile Gly Gly Gly Ser Ile Arg Ile His	485	490	495
Gln Arg Asp Val Gln Glu Arg Val Phe Glu Val Met Gly Ile Thr Gly	500	505	510
Glu Glu Ala Arg Glu Lys Phe Gly Phe Leu Leu Asp Ala Phe Ala Phe	515	520	525
Gly Ala Pro Pro His Gly Gly Ile Ala Phe Gly Trp Asp Arg Ile Val	530	535	540
Ser Leu Leu Gly Gly Phe Asp Ser Ile Arg Asp Val Ile Ala Phe	545	550	555

<210> 285

<211> 1503

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1480)

<223> RXA00314

<400> 285

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	Val Thr Leu Arg Ile	
	1 5	
ttt gac acc ggt acc cgt acg ctt cga gat ttt aaa cct gtt caa cca	163	
Phe Asp Thr Gly Thr Arg Thr Leu Arg Asp Phe Lys Pro Val Gln Pro		
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ggt cat gcc tcg gtg tac ctg tgt ggt gcc acc ccg caa tct tca ccc	211	
Gly His Ala Ser Val Tyr Leu Cys Gly Ala Thr Pro Gln Ser Ser Pro		
	25 30 35	
cac att gga cat gtt cgt tca gca gta gcg ttt gat att ttg cgc cgc	259	
His Ile Gly His Val Arg Ser Ala Val Ala Phe Asp Ile Leu Arg Arg		
	40 45 50	
tgg ctc atg gct aag gga ctt gat gtg gca ttt gtt cgc aat gtc act	307	
Trp Leu Met Ala Lys Gly Leu Asp Val Ala Phe Val Arg Asn Val Thr		
	55 60 65	
gat atc gat gac aag att ctc acc aag gca tct gaa aat ggt cgc cct	355	
Asp Ile Asp Asp Lys Ile Leu Thr Lys Ala Ser Glu Asn Gly Arg Pro		
	70 75 80 85	
tgg tgg gaa tgg gtg tcc acc tat gaa cgt gaa ttc acc tgg acg tac	403	
Trp Trp Glu Trp Val Ser Thr Tyr Glu Arg Glu Phe Thr Trp Thr Tyr		
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aac acg ttg ggt gtg ctt cct cca tca acg gag cct cgt gca aca ggc	451	
Asn Thr Leu Gly Val Leu Pro Pro Ser Thr Glu Pro Arg Ala Thr Gly		
	105 110 115	
cac gtc act cag atg att aag tac atg cag cgc ttg att gat aac ggc	499	
His Val Thr Gln Met Ile Lys Tyr Met Gln Arg Leu Ile Asp Asn Gly		
	120 125 130	
ttt gct tac gcc gtt gat ggc tct gtg tac ttt gat gtc gca gcg tgg	547	
Phe Ala Tyr Ala Val Asp Gly Ser Val Tyr Phe Asp Val Ala Ala Trp		
	135 140 145	
tcc aag gct gaa gga tct gac tat ggt tct ttg tcc gga aac cgt gtt	595	
Ser Lys Ala Glu Gly Ser Asp Tyr Gly Ser Leu Ser Gly Asn Arg Val		
	150 155 160 165	
gaa gat atg gag cag ggc gag ccc gat aac ttt ggt aag cgg ggg cca	643	
Glu Asp Met Glu Gln Gly Glu Pro Asp Asn Phe Gly Lys Arg Gly Pro		
	170 175 180	
cag gac ttt gct ctg tgg aag gct gcc aaa ccg ggt gag ccg tca tgg	691	
Gln Asp Phe Ala Leu Trp Lys Ala Ala Lys Pro Gly Glu Pro Ser Trp		
	185 190 195	
cca acc cct tgg gga gac ggc cgg ccg ggt tgg cat ttg gaa tgc tct	739	
Pro Thr Pro Trp Gly Asp Gly Arg Pro Gly Trp His Leu Glu Cys Ser		
	200 205 210	
gcc atg gcc acc tac tat ttg ggt gag caa ttt gat att cac tgt ggt	787	
Ala Met Ala Thr Tyr Tyr Leu Gly Glu Gln Phe Asp Ile His Cys Gly		
	215 220 225	
ggt ttg gat ctg caa ttt cca cac cat gaa aat gaa att gcc cag gca	835	

Gly 230	Leu	Asp	Leu	Gln	Phe 235	Pro	His	His	Glu	Asn 240	Glu	Ile	Ala	Gln	Ala 245	
cat	gcg	gct	ggc	gat	aaa	ttt	gcc	aac	tac	tgg	atg	cac	aat	cac	tgg	883
His	Ala	Ala	Gly	Asp 250	Lys	Phe	Ala	Asn	Tyr 255	Trp	Met	His	Asn	His	Trp 260	
gta	aca	atg	gcc	ggc	gag	aaa	atg	tcc	aag	tct	ttg	ggc	aat	gtt	ttg	931
Val	Thr	Met	Ala 265	Gly	Glu	Lys	Met	Ser 270	Lys	Ser	Leu	Gly	Asn	Val	Leu	
gct	gtg	ccg	gaa	atg	cta	aag	cag	gtt	cgt	cct	gtc	gag	ctt	cgt	tat	979
Ala	Val	Pro 280	Glu	Met	Leu	Lys	Gln	Val	Arg	Pro	Val	Glu	Leu	Arg	Tyr	
tac	ctt	ggg	tct	gcc	cat	tac	cgt	tcc	gtc	ctt	gag	tat	tcc	gag	agc	1027
Tyr	Leu	Gly 295	Ser	Ala	His	Tyr 300	Arg	Ser	Val	Leu	Glu 305	Tyr	Ser	Glu	Ser	
gct	ttg	agt	gaa	gct	gcg	gtg	ggc	tac	cgt	cgc	att	gag	tct	ttc	ctt	1075
Ala	Leu	Ser	Glu	Ala	Ala 315	Val	Gly	Tyr	Arg	Arg	Ile	Glu	Ser	Phe	Leu 325	
gag	cgt	gtg	ggg	gat	gtt	gag	gta	ggc	gag	tgg	acg	cca	ggc	ttt	gaa	1123
Glu	Arg	Val	Gly 330	Asp	Val	Glu	Val	Gly	Glu 335	Trp	Thr	Pro	Gly	Phe	Glu 340	
gtt	gcg	atg	gat	gag	gat	att	gca	gtt	cct	aag	gct	ttg	gct	gaa	atc	1171
Val	Ala	Met	Asp 345	Glu	Asp	Ile	Ala	Val	Pro 350	Lys	Ala	Leu	Ala	Glu	Ile 355	
cat	aac	gct	gtc	cgc	gag	ggc	aat	gct	gcc	ttg	gat	aag	ggc	gat	cgt	1219
His	Asn	Ala 360	Val	Arg	Glu	Gly	Asn	Ala	Ala	Leu	Asp	Lys	Gly	Asp	Arg 370	
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Glu	Ala	Ala	Glu	Lys	Leu	Ala 380	Ser	Ser	Val	Arg	Ala 385	Met	Thr	Gly	Val	
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Leu	Gly	Phe	Asp	Pro	Val 395	Glu	Trp	Gly	Ser	Asp 400	Ala	Gly	Ala	Asp	Gly 405	
aag	gca	gat	aag	gcg	ctt	gat	gtg	ctg	att	tct	tcg	gag	ctt	gag	cgt	1363
Lys	Ala	Asp	Lys	Ala 410	Leu	Asp	Val	Leu	Ile 415	Ser	Ser	Glu	Leu	Glu	Arg 420	
cgt	gca	act	gct	cgt	gct	gag	aag	aat	tgg	gcg	gtt	gct	gat	gag	gtt	1411
Arg	Ala	Thr	Ala 425	Arg	Ala	Glu	Lys	Asn 430	Trp	Ala	Val	Ala	Asp	Glu	Val 435	
cga	gat	cgt	ctt	gcc	gat	gct	ggc	att	gag	gtt	gtg	gat	acc	gca	gat	1459
Arg	Asp	Arg	Leu 440	Ala	Asp	Ala	Gly	Ile 445	Glu	Val	Val	Asp	Thr	Ala	Asp 450	
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Gly	Ala	Thr	Trp	Lys	Leu	Gln 460										
455																

<211> 460

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 286

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			20					25					30		
Pro	Gln	Ser	Ser	Pro	His	Ile	Gly	His	Val	Arg	Ser	Ala	Val	Ala	Phe
		35					40					45			
Asp	Ile	Leu	Arg	Arg	Trp	Leu	Met	Ala	Lys	Gly	Leu	Asp	Val	Ala	Phe
	50					55					60				
Val	Arg	Asn	Val	Thr	Asp	Ile	Asp	Asp	Lys	Ile	Leu	Thr	Lys	Ala	Ser
65					70					75					80
Glu	Asn	Gly	Arg	Pro	Trp	Trp	Glu	Trp	Val	Ser	Thr	Tyr	Glu	Arg	Glu
				85					90					95	
Phe	Thr	Trp	Thr	Tyr	Asn	Thr	Leu	Gly	Val	Leu	Pro	Pro	Ser	Thr	Glu
			100					105					110		
Pro	Arg	Ala	Thr	Gly	His	Val	Thr	Gln	Met	Ile	Lys	Tyr	Met	Gln	Arg
		115					120					125			
Leu	Ile	Asp	Asn	Gly	Phe	Ala	Tyr	Ala	Val	Asp	Gly	Ser	Val	Tyr	Phe
	130					135					140				
Asp	Val	Ala	Ala	Trp	Ser	Lys	Ala	Glu	Gly	Ser	Asp	Tyr	Gly	Ser	Leu
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Ser	Gly	Asn	Arg	Val	Glu	Asp	Met	Glu	Gln	Gly	Glu	Pro	Asp	Asn	Phe
				165					170					175	
Gly	Lys	Arg	Gly	Pro	Gln	Asp	Phe	Ala	Leu	Trp	Lys	Ala	Ala	Lys	Pro
			180					185					190		
Gly	Glu	Pro	Ser	Trp	Pro	Thr	Pro	Trp	Gly	Asp	Gly	Arg	Pro	Gly	Trp
		195					200					205			
His	Leu	Glu	Cys	Ser	Ala	Met	Ala	Thr	Tyr	Tyr	Leu	Gly	Glu	Gln	Phe
	210					215					220				
Asp	Ile	His	Cys	Gly	Gly	Leu	Asp	Leu	Gln	Phe	Pro	His	His	Glu	Asn
225					230					235					240
Glu	Ile	Ala	Gln	Ala	His	Ala	Ala	Gly	Asp	Lys	Phe	Ala	Asn	Tyr	Trp
				245					250					255	
Met	His	Asn	His	Trp	Val	Thr	Met	Ala	Gly	Glu	Lys	Met	Ser	Lys	Ser
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Leu	Gly	Asn	Val	Leu	Ala	Val	Pro	Glu	Met	Leu	Lys	Gln	Val	Arg	Pro
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Val	Glu	Leu	Arg	Tyr	Tyr	Leu	Gly	Ser	Ala	His	Tyr	Arg	Ser	Val	Leu
	290					295					300				

Glu Tyr Ser Glu Ser Ala Leu Ser Glu Ala Ala Val Gly Tyr Arg Arg
 305 310 315 320
 Ile Glu Ser Phe Leu Glu Arg Val Gly Asp Val Glu Val Gly Glu Trp
 325 330 335
 Thr Pro Gly Phe Glu Val Ala Met Asp Glu Asp Ile Ala Val Pro Lys
 340 345 350
 Ala Leu Ala Glu Ile His Asn Ala Val Arg Glu Gly Asn Ala Ala Leu
 355 360 365
 Asp Lys Gly Asp Arg Glu Ala Ala Glu Lys Leu Ala Ser Ser Val Arg
 370 375 380
 Ala Met Thr Gly Val Leu Gly Phe Asp Pro Val Glu Trp Gly Ser Asp
 385 390 395 400
 Ala Gly Ala Asp Gly Lys Ala Asp Lys Ala Leu Asp Val Leu Ile Ser
 405 410 415
 Ser Glu Leu Glu Arg Arg Ala Thr Ala Arg Ala Glu Lys Asn Trp Ala
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 Val Ala Asp Glu Val Arg Asp Arg Leu Ala Asp Ala Gly Ile Glu Val
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 450 455 460

<210> 287

<211> 1383

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1360)

<223> RXA02204

<400> 287

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 Met Gln Ser Trp Pro
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aca cct gaa gta cct gct ctc gct ggc acg cct gtg cct ttg gaa ttg 163
 Thr Pro Glu Val Pro Ala Leu Ala Gly Thr Pro Val Pro Leu Glu Leu
 10 15 20

ttc gac act gca gat cag gaa gta cgc ctg gtt gaa acc cca cct gcc 211
 Phe Asp Thr Ala Asp Gln Glu Val Arg Leu Val Glu Thr Pro Pro Ala
 25 30 35

gga tcc gac aca ccg gtt ggc atg tac gtc tgt ggc atc act ccc tac 259
 Gly Ser Asp Thr Pro Val Gly Met Tyr Val Cys Gly Ile Thr Pro Tyr
 40 45 50

gac tcc aca cac ttg ggg cac gcg gcg aca tac ctc gct ttc gat ctg Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr Leu Ala Phe Asp Leu 55 60 65	307
atc tac cgc atc ctg ctg gac aat gat cac gat gtc cac tac gtc caa Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp Val His Tyr Val Gln 70 75 80 85	355
aac atc acc gat gtc gat gac cct ctg ttt gaa cgc gca gcc cgc gac Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu Arg Ala Ala Arg Asp 90 95 100	403
ggc gtc gac tgg cgc gac ctc ggc acc agc caa atc aac ctc ttc cgc Gly Val Asp Trp Arg Asp Leu Gly Thr Ser Gln Ile Asn Leu Phe Arg 105 110 115	451
agc gat atg gaa gcc ctg agc atc att ccg ccg aag gac tac atc ggt Ser Asp Met Glu Ala Leu Ser Ile Ile Pro Pro Lys Asp Tyr Ile Gly 120 125 130	499
gcg att gag tcc atc gac gaa gtc att gag atg gtc aag acg ctt ctc Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met Val Lys Thr Leu Leu 135 140 145	547
gac gaa ggc gcc gcg tac atc gtc gag gac gcc gaa tat cca gat gtc Asp Glu Gly Ala Ala Tyr Ile Val Glu Asp Ala Glu Tyr Pro Asp Val 150 155 160 165	595
tac gca tca atc aac gcc aca gac aaa ttt ggc tac gag tcc aat tac Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly Tyr Glu Ser Asn Tyr 170 175 180	643
gac gca gcg acc atg gct gag ttc ttc gca gaa cgc ggc ggc gac cca Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu Arg Gly Gly Asp Pro 185 190 195	691
gag cgt ccc ggc aag aaa aac ccc atg gat gcc ctc ctg tgg cgc gca Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala Leu Leu Trp Arg Ala 200 205 210	739
gcc cgc gaa ggt gaa cca agc tgg gaa tcc cca ttc ggc gca ggt cgt Ala Arg Glu Gly Glu Pro Ser Trp Glu Ser Pro Phe Gly Ala Gly Arg 215 220 225	787
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cac agc ttt gat atc caa ggt ggc ggc tct gac ctg atc ttc cct cac His Ser Phe Asp Ile Gln Gly Gly Gly Ser Asp Leu Ile Phe Pro His 250 255 260	883
cac gag ttc tcc gca gcg cac gcc gaa gca gct cac ggt gtc gag cgc His Glu Phe Ser Ala Ala His Ala Glu Ala Ala His Gly Val Glu Arg 265 270 275	931
atg gct aag cac tac gtc cac gct ggc atg ata tcc caa gat ggc gtg Met Ala Lys His Tyr Val His Ala Gly Met Ile Ser Gln Asp Gly Val 280 285 290	979
aaa atg tcc aag tct ttg ggc aac ctg gaa ttt gtt tcc cgc ctc acc	1027

Lys Met Ser Lys Ser Leu Gly Asn Leu Glu Phe Val Ser Arg Leu Thr
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 gct gca ggc cac gag ccc ggc gcg atc cgc ctc ggt gtt ttt gcc aac 1075
 Ala Ala Gly His Glu Pro Gly Ala Ile Arg Leu Gly Val Phe Ala Asn
 310 315 320 325
 cat tac cgt ggc aac cgt gat tgg aac gca gag agc ctc gcc acc gca 1123
 His Tyr Arg Gly Asn Arg Asp Trp Asn Ala Glu Ser Leu Ala Thr Ala
 330 335 340
 gaa cag cgt cta gca acc tgg cgt gaa gca gca cga gct gca acc aat 1171
 Glu Gln Arg Leu Ala Thr Trp Arg Glu Ala Ala Arg Ala Ala Thr Asn
 345 350 355
 agg gaa gat gcc att gca gtt gtc gag cag ctt cgt gca cac cta tct 1219
 Arg Glu Asp Ala Ile Ala Val Val Glu Gln Leu Arg Ala His Leu Ser
 360 365 370
 gct gac ctt gat act ccc ggc gcg ctc gcc gcg gta gat aat tgg gca 1267
 Ala Asp Leu Asp Thr Pro Gly Ala Leu Ala Ala Val Asp Asn Trp Ala
 375 380 385
 gcg ggt atc gac acc acg acc gat tca aaa gag ttc acc gag gta gga 1315
 Ala Gly Ile Asp Thr Thr Asp Ser Lys Glu Phe Thr Glu Val Gly
 390 395 400 405
 aac atc gtg gtc gca gcc att gat gcc ctc ctg ggc gtg cag ctc 1360
 Asn Ile Val Val Ala Ala Ile Asp Ala Leu Leu Gly Val Gln Leu
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<211> 420

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

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 20 25 30
 Glu Thr Pro Pro Ala Gly Ser Asp Thr Pro Val Gly Met Tyr Val Cys
 35 40 45
 Gly Ile Thr Pro Tyr Asp Ser Thr His Leu Gly His Ala Ala Thr Tyr
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 Leu Ala Phe Asp Leu Ile Tyr Arg Ile Leu Leu Asp Asn Asp His Asp
 65 70 75 80
 Val His Tyr Val Gln Asn Ile Thr Asp Val Asp Asp Pro Leu Phe Glu
 85 90 95
 Arg Ala Ala Arg Asp Gly Val Asp Trp Arg Asp Leu Gly Thr Ser Gln
 100 105 110

Ile Asn Leu Phe Arg Ser Asp Met Glu Ala Leu Ser Ile Ile Pro Pro
 115 120 125
 Lys Asp Tyr Ile Gly Ala Ile Glu Ser Ile Asp Glu Val Ile Glu Met
 130 135 140
 Val Lys Thr Leu Leu Asp Glu Gly Ala Ala Tyr Ile Val Glu Asp Ala
 145 150 155 160
 Glu Tyr Pro Asp Val Tyr Ala Ser Ile Asn Ala Thr Asp Lys Phe Gly
 165 170 175
 Tyr Glu Ser Asn Tyr Asp Ala Ala Thr Met Ala Glu Phe Phe Ala Glu
 180 185 190
 Arg Gly Gly Asp Pro Glu Arg Pro Gly Lys Lys Asn Pro Met Asp Ala
 195 200 205
 Leu Leu Trp Arg Ala Ala Arg Glu Gly Glu Pro Ser Trp Glu Ser Pro
 210 215 220
 Phe Gly Ala Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ala Ile Ala
 225 230 235 240
 Thr Asn Arg Leu Gly His Ser Phe Asp Ile Gln Gly Gly Gly Ser Asp
 245 250 255
 Leu Ile Phe Pro His His Glu Phe Ser Ala Ala His Ala Glu Ala Ala
 260 265 270
 His Gly Val Glu Arg Met Ala Lys His Tyr Val His Ala Gly Met Ile
 275 280 285
 Ser Gln Asp Gly Val Lys Met Ser Lys Ser Leu Gly Asn Leu Glu Phe
 290 295 300
 Val Ser Arg Leu Thr Ala Ala Gly His Glu Pro Gly Ala Ile Arg Leu
 305 310 315 320
 Gly Val Phe Ala Asn His Tyr Arg Gly Asn Arg Asp Trp Asn Ala Glu
 325 330 335
 Ser Leu Ala Thr Ala Glu Gln Arg Leu Ala Thr Trp Arg Glu Ala Ala
 340 345 350
 Arg Ala Ala Thr Asn Arg Glu Asp Ala Ile Ala Val Val Glu Gln Leu
 355 360 365
 Arg Ala His Leu Ser Ala Asp Leu Asp Thr Pro Gly Ala Leu Ala Ala
 370 375 380
 Val Asp Asn Trp Ala Ala Gly Ile Asp Thr Thr Thr Asp Ser Lys Glu
 385 390 395 400
 Phe Thr Glu Val Gly Asn Ile Val Val Ala Ala Ile Asp Ala Leu Leu
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 Gly Val Gln Leu
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 <223> RXA01124

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 cgt ttc tgc cca tcg ccc acc ggc acc cca cac gtt gga ctt gtg cgc 96
 Arg Phe Cys Pro Ser Pro Thr Gly Thr Pro His Val Gly Leu Val Arg
 20 25 30
 acc gcg ctg ttc aac tgg gca tat gct cgc cac act gga ggc aag tta 144
 Thr Ala Leu Phe Asn Trp Ala Tyr Ala Arg His Thr Gly Gly Lys Leu
 35 40 45
 gtt ttc cgc att gag gac act gac gct gcc cgc gat tcc gag gag tct 192
 Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser
 50 55 60
 tac tcc gcc atc atc gat tcc ctg cgc tgg ttg gga atg gac tgg gat 240
 Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp
 65 70 75 80
 gag ggt gtg gaa aag ggc ggc ccg cat gag ccc tac cgc cag tcg cag 288
 Glu Gly Val Glu Lys Gly Gly Pro His Glu Pro Tyr Arg Gln Ser Gln
 85 90 95
 cgc aag gac atc tat cag gat gtg ttg aag cag ctt atc gac gcc ggt 336
 Arg Lys Asp Ile Tyr Gln Asp Val Leu Lys Gln Leu Ile Asp Ala Gly
 100 105 110
 gaa gtc tac cca gct tat tcc acc gcg gaa gag gtt gag gag cga cac 384
 Glu Val Tyr Pro Ala Tyr Ser Thr Ala Glu Glu Val Glu Glu Arg His
 115 120 125
 aag gct gct ggc cgc gat cca aag ctc ggc tac gac aac ttt gac cgt 432
 Lys Ala Ala Gly Arg Asp Pro Lys Leu Gly Tyr Asp Asn Phe Asp Arg
 130 135 140
 gat ctc acc gaa gag cag gtc gca gca ttt gag gct gag ggg cgt aag 480
 Asp Leu Thr Glu Glu Gln Val Ala Ala Phe Glu Ala Glu Gly Arg Lys
 145 150 155 160
 cct gtg tgg cgt ctg cgc atg cca gag cag gat tgg aag tgg act gac 528
 Pro Val Trp Arg Leu Arg Met Pro Glu Gln Asp Trp Lys Trp Thr Asp
 165 170 175
 ctg gtc cgc ggt gaa gtt gag ttc aag tcg ttc acc cag cct gac ttc 576
 Leu Val Arg Gly Glu Val Glu Phe Lys Ser Phe Thr Gln Pro Asp Phe
 180 185 190
 gtg gtt gct cgt tcc aac ggt gag cct ttg tac acc ctg gtc aac cct 624
 Val Val Ala Arg Ser Asn Gly Glu Pro Leu Tyr Thr Leu Val Asn Pro

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cgc att ggc gtg gca aag gcc acc cca gcc ttt ggt cac ctg cca ttt Arg Ile Gly Val Ala Lys Ala Thr Pro Ala Phe Gly His Leu Pro Phe 245 250 255			768
gtg atg ggt gag ggc aac aag aag ctg tct aag cgt gat cca cag tcc Val Met Gly Glu Gly Asn Lys Lys Leu Ser Lys Arg Asp Pro Gln Ser 260 265 270			816
agc ctg ttc aac cac cgt gac aac ggc atc atc cca gag ggc atg ctc Ser Leu Phe Asn His Arg Asp Asn Gly Ile Ile Pro Glu Gly Met Leu 275 280 285			864
aac tac ctg gcg ctg ctg ggt tgg tca ctg tct gct gat cag gac att Asn Tyr Leu Ala Leu Leu Gly Trp Ser Leu Ser Ala Asp Gln Asp Ile 290 295 300			912
ttc ggt gtc gat gag ttg atc gct aac ttt gat gtc gct gac gtg ttg Phe Gly Val Asp Glu Leu Ile Ala Asn Phe Asp Val Ala Asp Val Leu 305 310 315 320			960
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gat cac atc cga ctt ctg gag cct aag gat ttc gag gct cgc ctg cgc Asp His Ile Arg Leu Leu Glu Pro Lys Asp Phe Glu Ala Arg Leu Arg 340 345 350			1056
gcg tac atg act gag tac acc gag ttc cca gcg gat tac cca gct gag Ala Tyr Met Thr Glu Tyr Thr Glu Phe Pro Ala Asp Tyr Pro Ala Glu 355 360 365			1104
aag ttt gcc att gct gcg gag ctg gtt cag acc cgc atc aag gtg ctc Lys Phe Ala Ile Ala Ala Glu Leu Val Gln Thr Arg Ile Lys Val Leu 370 375 380			1152
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ctg gtg ttc aat gag aag gct gcc aag aag aac ctc aag gag acc gct Leu Val Phe Asn Glu Lys Ala Ala Lys Lys Asn Leu Lys Glu Thr Ala 405 410 415			1248
gtt gag cct ctc aac gcc ggt atc gca gcg ctg gag gca gtg gag gag Val Glu Pro Leu Asn Ala Gly Ile Ala Ala Leu Glu Ala Val Glu Glu 420 425 430			1296
tgg acc act cca aac att gaa gca gca ttg aac aag gct ctc att gag Trp Thr Thr Pro Asn Ile Glu Ala Ala Leu Asn Lys Ala Leu Ile Glu 435 440 445			1344

gat cta ggc ctg aag cct cgc gtg gcg ttc ggt gcg ttg cgc att ggt 1392
 Asp Leu Gly Leu Lys Pro Arg Val Ala Phe Gly Ala Leu Arg Ile Gly
 450 455 460

atc tcc ggc gag gct gta tcc cca cca ctg ttt gag tcc atg gag ctt 1440
 Ile Ser Gly Glu Ala Val Ser Pro Pro Leu Phe Glu Ser Met Glu Leu
 465 470 475 480

ttg ggc aag gaa tcc acg ttg gtt cgt ctg aag gtt act cgt gag cag 1488
 Leu Gly Lys Glu Ser Thr Leu Val Arg Leu Lys Val Thr Arg Glu Gln
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<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Thr Ala Leu Phe Asn Trp Ala Tyr Ala Arg His Thr Gly Gly Lys Leu
 35 40 45

Val Phe Arg Ile Glu Asp Thr Asp Ala Ala Arg Asp Ser Glu Glu Ser
 50 55 60

Tyr Ser Ala Ile Ile Asp Ser Leu Arg Trp Leu Gly Met Asp Trp Asp
 65 70 75 80

Glu Gly Val Glu Lys Gly Gly Pro His Glu Pro Tyr Arg Gln Ser Gln
 85 90 95

Arg Lys Asp Ile Tyr Gln Asp Val Leu Lys Gln Leu Ile Asp Ala Gly
 100 105 110

Glu Val Tyr Pro Ala Tyr Ser Thr Ala Glu Glu Val Glu Glu Arg His
 115 120 125

Lys Ala Ala Gly Arg Asp Pro Lys Leu Gly Tyr Asp Asn Phe Asp Arg
 130 135 140

Asp Leu Thr Glu Glu Gln Val Ala Ala Phe Glu Ala Glu Gly Arg Lys
 145 150 155 160

Pro Val Trp Arg Leu Arg Met Pro Glu Gln Asp Trp Lys Trp Thr Asp
 165 170 175

Leu Val Arg Gly Glu Val Glu Phe Lys Ser Phe Thr Gln Pro Asp Phe
 180 185 190

Val Val Ala Arg Ser Asn Gly Glu Pro Leu Tyr Thr Leu Val Asn Pro

195						200						205					
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Arg	Ile	Gly	Val	Ala	Lys	Ala	Thr	Pro	Ala	Phe	Gly	His	Leu	Pro	Phe		
245						250						255					
Val	Met	Gly	Glu	Gly	Asn	Lys	Lys	Leu	Ser	Lys	Arg	Asp	Pro	Gln	Ser		
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Ser	Leu	Phe	Asn	His	Arg	Asp	Asn	Gly	Ile	Ile	Pro	Glu	Gly	Met	Leu		
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Asn	Tyr	Leu	Ala	Leu	Leu	Gly	Trp	Ser	Leu	Ser	Ala	Asp	Gln	Asp	Ile		
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Phe	Gly	Val	Asp	Glu	Leu	Ile	Ala	Asn	Phe	Asp	Val	Ala	Asp	Val	Leu		
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Gly	Asn	Pro	Ala	Arg	Phe	Asp	Gln	Lys	Lys	Leu	Glu	Ala	Ile	Asn	Ala		
325						330						335					
Asp	His	Ile	Arg	Leu	Leu	Glu	Pro	Lys	Asp	Phe	Glu	Ala	Arg	Leu	Arg		
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Ala	Tyr	Met	Thr	Glu	Tyr	Thr	Glu	Phe	Pro	Ala	Asp	Tyr	Pro	Ala	Glu		
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Lys	Phe	Ala	Ile	Ala	Ala	Glu	Leu	Val	Gln	Thr	Arg	Ile	Lys	Val	Leu		
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Ser	Glu	Ala	Trp	Asp	Leu	Leu	Lys	Phe	Leu	Val	Thr	Ala	Asp	Glu	Asp		
385						390						395					
Leu	Val	Phe	Asn	Glu	Lys	Ala	Ala	Lys	Lys	Asn	Leu	Lys	Glu	Thr	Ala		
405						410						415					
Val	Glu	Pro	Leu	Asn	Ala	Gly	Ile	Ala	Ala	Leu	Glu	Ala	Val	Glu	Glu		
420						425						430					
Trp	Thr	Thr	Pro	Asn	Ile	Glu	Ala	Ala	Leu	Asn	Lys	Ala	Leu	Ile	Glu		
435						440						445					
Asp	Leu	Gly	Leu	Lys	Pro	Arg	Val	Ala	Phe	Gly	Ala	Leu	Arg	Ile	Gly		
450						455						460					
Ile	Ser	Gly	Glu	Ala	Val	Ser	Pro	Pro	Leu	Phe	Glu	Ser	Met	Glu	Leu		
465						470						475					
Leu	Gly	Lys	Glu	Ser	Thr	Leu	Val	Arg	Leu	Lys	Val	Thr	Arg	Glu	Gln		
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500																	

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 <222> (101)..(736)
 <223> RXN00458

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                                         Met Ala Gly Arg Tyr
                                         1           5

gca cca tca cca agc ggc gac ctt cac ttt ggc aac ctc cgc aca gca 163
Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala
                        10                15                20

ctg ctg gcc tgg ctg ttc gcg cgc tcc gaa gga aaa aaa ttc ctc atg 211
Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met
                        25                30                35

cgg gtc gaa gac atc gat gaa caa cgc tca tcc aag gaa tcc gcc gaa 259
Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Ser Lys Glu Ser Ala Glu
                        40                45                50

agc caa ctc gca gac cta tcc gcc ctg ggt ctc gat tgg gat ggc gac 307
Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp
                        55                60                65

gtc ctc tac caa tcc aca cgc tac gac gcc tac cgc gca gcc ctt gaa 355
Val Leu Tyr Gln Ser Thr Arg Tyr Asp Ala Tyr Arg Ala Ala Leu Glu
                        70                75                80                85

aaa cta gac acc tac gaa tgt tat tgc tcg cgc cgg gac atc caa gaa 403
Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg Arg Asp Ile Gln Glu
                        90                95                100

gcc tcg cgg gca ccc cat gtg gct ccg gga gtg tat ccg gga acg tgt 451
Ala Ser Arg Ala Pro His Val Ala Pro Gly Val Tyr Pro Gly Thr Cys
                        105                110                115

agg gga ttg aag gag gag gaa cgc gtc gaa aag cgt gca acc ttg gct 499
Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys Arg Ala Thr Leu Ala
                        120                125                130

gcg caa aac cgg cac ccc gcc att cgc ctg cgc gcg cag gta acc tcg 547
Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg Ala Gln Val Thr Ser
                        135                140                145

ttt gat ttt cac gac cga ctt cgc ggc cca caa act ggc ccc gta gac 595
Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln Thr Gly Pro Val Asp
                        150                155                160                165

gat ttc att ctg ctc cgc ggc ggg cag gaa ccc gga tgg gca tac aac 643
Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro Gly Trp Ala Tyr Asn
                        170                175                180

tta act gtc gtc gtc gac gat gcc tac caa ggc gtt gac cag gta gtc 691
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Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly Val Asp Gln Val Val
 185 190 195

cgc ggc gac gac cta ctc gaa ttc ggc gcg cgc caa gct acc ttg 736
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<210> 292
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 <213> Corynebacterium glutamicum

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 20 25 30

Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Ser
 35 40 45

Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu
 50 55 60

Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg Tyr Asp Ala Tyr
 65 70 75 80

Arg Ala Ala Leu Glu Lys Leu Asp Thr Tyr Glu Cys Tyr Cys Ser Arg
 85 90 95

Arg Asp Ile Gln Glu Ala Ser Arg Ala Pro His Val Ala Pro Gly Val
 100 105 110

Tyr Pro Gly Thr Cys Arg Gly Leu Lys Glu Glu Glu Arg Val Glu Lys
 115 120 125

Arg Ala Thr Leu Ala Ala Gln Asn Arg His Pro Ala Ile Arg Leu Arg
 130 135 140

Ala Gln Val Thr Ser Phe Asp Phe His Asp Arg Leu Arg Gly Pro Gln
 145 150 155 160

Thr Gly Pro Val Asp Asp Phe Ile Leu Leu Arg Gly Gly Gln Glu Pro
 165 170 175

Gly Trp Ala Tyr Asn Leu Thr Val Val Val Asp Asp Ala Tyr Gln Gly
 180 185 190

Val Asp Gln Val Val Arg Gly Asp Asp Leu Leu Glu Phe Gly Ala Arg
 195 200 205

Gln Ala Thr Leu
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<222> (101)..(328)

<223> FRXA00458

<400> 293

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                                         Met Ala Gly Arg Tyr
                                         1 5

gca cca tca cca agc ggc gac ctt cac ttt ggc aac ctc cgc aca gca 163
Ala Pro Ser Pro Ser Gly Asp Leu His Phe Gly Asn Leu Arg Thr Ala
                        10 15 20

ctg ctg gcc tgg ctg ttc gcg cgc tcc gaa gga aaa aaa ttc ctc atg 211
Leu Leu Ala Trp Leu Phe Ala Arg Ser Glu Gly Lys Lys Phe Leu Met
                        25 30 35

cgg gtc gaa gac atc gat gaa caa cgc tca ttc aag gaa tcc gcc gaa 259
Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe Lys Glu Ser Ala Glu
                        40 45 50

agc caa ctc gca gac cta tcc gcc ctg ggt ctc gat tgg gat ggc gac 307
Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu Asp Trp Asp Gly Asp
                        55 60 65

gtc ctc tac caa tcc aca cgc 328
Val Leu Tyr Gln Ser Thr Arg
70 75

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<210> 294

<211> 76

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

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20 25 30

Lys Lys Phe Leu Met Arg Val Glu Asp Ile Asp Glu Gln Arg Ser Phe
35 40 45

Lys Glu Ser Ala Glu Ser Gln Leu Ala Asp Leu Ser Ala Leu Gly Leu
50 55 60

Asp Trp Asp Gly Asp Val Leu Tyr Gln Ser Thr Arg
65 70 75

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<223> RXA00069

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                                         1                               5

atc atc gac acc gtg gtt aac ctg tgt aaa cga cgt gga ctg gtg tac  163
Ile Ile Asp Thr Val Val Asn Leu Cys Lys Arg Arg Gly Leu Val Tyr
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ccc tgt ggt gag atc tac ggc ggt acc cgc tct gcg tgg gac tac ggc  211
Pro Cys Gly Glu Ile Tyr Gly Gly Thr Arg Ser Ala Trp Asp Tyr Gly
                        25                        30                        35

ccg ctg ggt gtg gag ctg aag gaa aac atc aag cgc cag tgg tgg cgt  259
Pro Leu Gly Val Glu Leu Lys Glu Asn Ile Lys Arg Gln Trp Trp Arg
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tct atg gtt act tcc cgc cca gat gtt gtg ggt gtt gat act tct gtc  307
Ser Met Val Thr Ser Arg Pro Asp Val Val Gly Val Asp Thr Ser Val
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atc ctt cct cgc cag gtg tgg gta act tcc ggc cac gtt gag gtc ttc  355
Ile Leu Pro Arg Gln Val Trp Val Thr Ser Gly His Val Glu Val Phe
                        70                        75                        80                        85

act gac cca ctg gtt gag tct ttg aac acc cac aag cgt tac cgt gcg  403
Thr Asp Pro Leu Val Glu Ser Leu Asn Thr His Lys Arg Tyr Arg Ala
                        90                        95                        100

gac cac ctg ctg gag cag tac gaa gag aag cat ggt cac cca cct gta  451
Asp His Leu Leu Glu Gln Tyr Glu Glu Lys His Gly His Pro Pro Val
                        105                        110                        115

aac ggc ttg gct gac atc aac gat cca gag acc ggc cag cca ggt aac  499
Asn Gly Leu Ala Asp Ile Asn Asp Pro Glu Thr Gly Gln Pro Gly Asn
                        120                        125                        130

tgg act gag cct aag gcg ttc tct ggt ctt ctg aag act ttc ttg gga  547
Trp Thr Glu Pro Lys Ala Phe Ser Gly Leu Leu Lys Thr Phe Leu Gly
                        135                        140                        145

cct gtg gac gac gaa gag ggt ctg cac tac ctg cgc cct gaa act gct  595
Pro Val Asp Asp Glu Glu Gly Leu His Tyr Leu Arg Pro Glu Thr Ala
                        150                        155                        160                        165

cag ggt atc ttc gtg aac ttc aag aac gtg atg aac act tca cgt atg  643
Gln Gly Ile Phe Val Asn Phe Lys Asn Val Met Asn Thr Ser Arg Met
                        170                        175                        180

aag cca cct ttc ggt atc gcg aac atc ggt aag tct ttc cgt aac gag  691
Lys Pro Pro Phe Gly Ile Ala Asn Ile Gly Lys Ser Phe Arg Asn Glu
                        185                        190                        195

atc acc cca ggt aac ttc att ttc cgt act cgt gag ttc gag cag atg  739

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Glu	Met	Glu	Phe	Phe	Val	Lys	Pro	Gly	Glu	Asp	Glu	Glu	Trp	His	Gln		
	215					220					225						
cac	tgg	att	gat	act	cgc	ctg	cag	tgg	tac	atc	aac	ctg	ggc	att	aag	835	
His	Trp	Ile	Asp	Thr	Arg	Leu	Gln	Trp	Tyr	Ile	Asn	Leu	Gly	Ile	Lys		
	230				235					240					245		
cct	gag	aac	ctg	cgt	ctg	tac	gag	cac	cct	cag	gag	aag	ctg	tct	cac	883	
Pro	Glu	Asn	Leu	Arg	Leu	Tyr	Glu	His	Pro	Gln	Glu	Lys	Leu	Ser	His		
				250					255					260			
tac	tcc	aag	cgc	act	ggt	gat	att	gag	tac	gca	ttc	aac	ttt	gct	aac	931	
Tyr	Ser	Lys	Arg	Thr	Val	Asp	Ile	Glu	Tyr	Ala	Phe	Asn	Phe	Ala	Asn		
			265					270					275				
acc	aag	tgg	ggc	gag	ttg	gag	ggg	atc	gcg	aac	cgt	act	gat	tac	gat	979	
Thr	Lys	Trp	Gly	Glu	Leu	Glu	Gly	Ile	Ala	Asn	Arg	Thr	Asp	Tyr	Asp		
		280					285					290					
ctt	cgc	gtg	cac	tct	gag	ggc	tct	ggt	gag	gac	ctg	tca	ttc	ttc	gat	1027	
Leu	Arg	Val	His	Ser	Glu	Gly	Ser	Gly	Glu	Asp	Leu	Ser	Phe	Phe	Asp		
	295					300					305						
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Asp	Glu	Ala	Pro	Asn	Ser	Lys	Gly	Gly	Val	Asp	Lys	Arg	Val	Val	Leu		
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Lys	Leu	Asp	Arg	Arg	Leu	Ala	Pro	Val	Lys	Val	Ala	Val	Leu	Pro	Leu		
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Ser	Lys	Lys	Asp	Thr	Leu	Thr	Pro	Leu	Ala	Glu	Lys	Leu	Ala	Ala	Glu		
		375				380					385						
ctg	cgt	gaa	ttc	tgg	aac	ggt	gat	tac	gac	act	tca	ggt	gcg	att	ggt	1315	
Leu	Arg	Glu	Phe	Trp	Asn	Val	Asp	Tyr	Asp	Thr	Ser	Gly	Ala	Ile	Gly		
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cgc	cgt	tac	cgt	cgt	cag	gac	gag	atc	ggt	act	cca	ttc	tgc	gtc	acc	1363	
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Val	Asp	Phe	Asp	Ser	Leu	Glu	Asp	Asn	Ala	Val	Thr	Val	Arg	Glu	Arg		
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Asp	Thr	Met	Glu	Gln	Val	Arg	Val	Pro	Leu	Asp	Glu	Leu	Gln	Gly	Tyr		

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 Arg Gln Trp Trp Arg Ser Met Val Thr Ser Arg Pro Asp Val Val Gly
 50 55 60
 Val Asp Thr Ser Val Ile Leu Pro Arg Gln Val Trp Val Thr Ser Gly
 65 70 75 80
 His Val Glu Val Phe Thr Asp Pro Leu Val Glu Ser Leu Asn Thr His
 85 90 95
 Lys Arg Tyr Arg Ala Asp His Leu Leu Glu Gln Tyr Glu Glu Lys His
 100 105 110
 Gly His Pro Pro Val Asn Gly Leu Ala Asp Ile Asn Asp Pro Glu Thr
 115 120 125
 Gly Gln Pro Gly Asn Trp Thr Glu Pro Lys Ala Phe Ser Gly Leu Leu
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 Lys Thr Phe Leu Gly Pro Val Asp Asp Glu Glu Gly Leu His Tyr Leu
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 Arg Pro Glu Thr Ala Gln Gly Ile Phe Val Asn Phe Lys Asn Val Met
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 Asn Thr Ser Arg Met Lys Pro Pro Phe Gly Ile Ala Asn Ile Gly Lys
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 Ser Phe Arg Asn Glu Ile Thr Pro Gly Asn Phe Ile Phe Arg Thr Arg
 195 200 205
 Glu Phe Glu Gln Met Glu Met Glu Phe Phe Val Lys Pro Gly Glu Asp
 210 215 220
 Glu Glu Trp His Gln His Trp Ile Asp Thr Arg Leu Gln Trp Tyr Ile
 225 230 235 240
 Asn Leu Gly Ile Lys Pro Glu Asn Leu Arg Leu Tyr Glu His Pro Gln
 245 250 255

Glu Lys Leu Ser His Tyr Ser Lys Arg Thr Val Asp Ile Glu Tyr Ala
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 Phe Asn Phe Ala Asn Thr Lys Trp Gly Glu Leu Glu Gly Ile Ala Asn
 275 280 285
 Arg Thr Asp Tyr Asp Leu Arg Val His Ser Glu Gly Ser Gly Glu Asp
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 Leu Ser Phe Phe Asp Gln Glu Thr Asn Glu Arg Trp Ile Pro Phe Val
 305 310 315 320
 Ile Glu Pro Ala Ala Gly Leu Gly Arg Ala Met Met Met Phe Leu Met
 325 330 335
 Asp Ala Tyr His Glu Asp Glu Ala Pro Asn Ser Lys Gly Gly Val Asp
 340 345 350
 Lys Arg Val Val Leu Lys Leu Asp Arg Arg Leu Ala Pro Val Lys Val
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 Ala Val Leu Pro Leu Ser Lys Lys Asp Thr Leu Thr Pro Leu Ala Glu
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 Lys Leu Ala Ala Glu Leu Arg Glu Phe Trp Asn Val Asp Tyr Asp Thr
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 Ser Gly Ala Ile Gly Arg Arg Tyr Arg Arg Gln Asp Glu Ile Gly Thr
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<223> RXA01852

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 Val Ser Gln Asn Lys
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 Ser Lys Ser Glu Lys Leu Gln Ser Phe Ala Ala Pro Lys Gly Val Pro
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Asp Tyr Ala Pro Pro Lys Ser Ala Ala Phe Leu Ala Val Arg Asp Ala	
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Phe Val Asn Gln Ala His Lys Ala Gly Phe Glu His Ile Glu Leu Pro	
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Ile Phe Glu Asp Thr Gly Leu Phe Ala Arg Gly Val Gly Glu Ser Thr	
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Asp Val Val Ser Lys Glu Met Tyr Thr Phe Ala Asp Arg Gly Glu Arg	
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Ser Val Thr Leu Arg Pro Glu Gly Thr Ala Gly Val Met Arg Ala Val	
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Ile Glu His Ser Leu Asp Arg Gly Gln Leu Pro Val Lys Leu Asn Tyr	
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Cys Arg Pro Glu Tyr Arg Gln Lys Leu Gln Asp Phe Leu Phe Ala Leu	
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Phe	Val	His	Asp	Gly	Leu	Gly	Ala	Gln	Ser	Gly	Ile	Gly	Gly	Gly	Gly	
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Pro	Leu	Gly	Lys	Asp	Ala	Lys	Lys	Ala	Leu	Ala	Gly	Ile	Val	Asn	Thr	
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Leu	Lys	Gly	Ala	Met	Lys	Gly	Ala	Asp	Arg	Ser	Asn	Ala	Leu	Tyr	Thr	
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gat	atg	cgt	gcg	cat	gag	cag	cac	gat	gtc	gca	ttg	gac	gag	gtt	gtg	1363
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gcc	ttt	ttg	cag	ggg	aaa	ctt	att	taaataattc	ataagtaaaa	aac						1410
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<213> Corynebacterium glutamicum

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Ala	Val	Arg	Asp	Ala	Phe	Val	Asn	Gln	Ala	His	Lys	Ala	Gly	Phe	Glu	
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His	Ile	Glu	Leu	Pro	Ile	Phe	Glu	Asp	Thr	Gly	Leu	Phe	Ala	Arg	Gly	
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Asp	Arg	Gly	Glu	Arg 85	Ser	Val	Thr	Leu	Arg 90	Pro	Glu	Gly	Thr	Ala 95	Gly
Val	Met	Arg	Ala 100	Val	Ile	Glu	His	Ser 105	Leu	Asp	Arg	Gly	Gln 110	Leu	Pro
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Ala 130	Gly	Arg	Tyr	Arg	Gln	Leu 135	Gln	Gln	Val	Gly	Val 140	Glu	Ala	Ile	Gly
Val 145	Asp	Asp	Pro	Ala	Leu 150	Asp	Ala	Glu	Ile	Ile 155	Ala	Leu	Ala	Asp	Arg 160
Ser	Tyr	Arg	Ser	Leu 165	Gly	Leu	Gln	Asp	Phe 170	Arg	Leu	Glu	Leu	Thr	Ser 175
Leu	Gly	Asp	Arg 180	His	Cys	Arg	Pro	Glu 185	Tyr	Arg	Gln	Lys	Leu 190	Gln	Asp
Phe	Leu	Phe 195	Ala	Leu	Pro	Leu	Asp 200	Glu	Glu	Thr	Arg	Lys 205	Arg	Ala	Glu
Ile	Asn 210	Pro	Leu	Arg	Val	Leu 215	Asp	Asp	Lys	Arg	Pro	Glu	Val	Gln	Glu
Met 225	Thr	Ala	Asp	Ala	Pro 230	Leu	Met	Leu	Asp	His 235	Leu	Asp	Ala	Glu	Cys 240
Arg	Glu	His	Phe	Glu 245	Thr	Val	Thr	Gly	Leu 250	Leu	Asp	Asp	Met	Gly 255	Val
Pro	Tyr	Val	Ile 260	Asn	Pro	Arg	Met	Val 265	Arg	Gly	Leu	Asp	Tyr 270	Tyr	Thr
Lys	Thr	Cys 275	Phe	Glu	Phe	Val	His 280	Asp	Gly	Leu	Gly	Ala 285	Gln	Ser	Gly
Ile 290	Gly	Gly	Gly	Gly	Arg	Tyr 295	Asp	Gly	Leu	Met	Ala 300	Gln	Leu	Gly	Gly
Gln 305	Asp	Leu	Ser	Gly	Ile 310	Gly	Tyr	Gly	Leu	Gly 315	Val	Asp	Arg	Thr	Met 320
Leu	Ala	Leu	Glu	Ala 325	Glu	Gly	Val	Thr	Val 330	Gly	Ala	Glu	Arg	Arg 335	Val
Asp	Val	Tyr	Gly 340	Val	Pro	Leu	Gly	Lys 345	Asp	Ala	Lys	Lys	Ala 350	Leu	Ala
Gly	Ile	Val	Asn	Thr	Leu	Arg	Ala 360	Ala	Gly	Ile	Ser	Thr	Asp	Met	Ser
Tyr 370	Gly	Asp	Arg	Gly	Leu	Lys 375	Gly	Ala	Met	Lys	Gly 380	Ala	Asp	Arg	Ser

Asn Ala Leu Tyr Thr Leu Val Leu Gly Glu Gln Glu Leu Glu Asn Asn
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Leu Phe Leu Ala Thr
1 5

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Arg Pro Cys Arg Gly Tyr Arg Val Pro Arg Val Phe Ser Trp Asp Thr
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His Gly Leu Pro Ala Glu Leu Glu Ala Glu Lys Gln Leu Gly Ile Lys
25 30 35

gac aag ggc gag atc gag gcc atg ggt ctt gcc aag ttc aac gag tac 259
Asp Lys Gly Glu Ile Glu Ala Met Gly Leu Ala Lys Phe Asn Glu Tyr
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Cys Ala Thr Ser Val Leu Gln Tyr Thr Lys Glu Trp Glu Glu Tyr Val
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Thr Arg Gln Ala Arg Trp Val Asp Phe Glu Asn Gly Tyr Lys Thr Met
70 75 80 85

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105 110 115

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Ala Glu His Thr Pro Leu Ser Asn Gln Glu Thr Arg Leu Asp Asp Ser
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Tyr Lys Leu Arg Gln Asp Pro Thr Leu Thr Val Thr Phe Pro Val Thr

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Gln Phe Gly Lys Trp Leu Glu Gly Ala Arg Asp Trp Asn Ile Ser Arg	
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Ser Arg Tyr Trp Gly Ser Pro Ile Pro Ala Trp Val Ser Asp Asn Asp	
410 415 420	
gaa tac cca cgc gtt gat gtt tat ggt tcc ctc gat gag ctt gag gct	1411
Glu Tyr Pro Arg Val Asp Val Tyr Gly Ser Leu Asp Glu Leu Glu Ala	
425 430 435	
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Asp Phe Gly Val Arg Pro Lys Ser Leu His Arg Pro Asp Ile Asp Glu	
440 445 450	
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Leu Thr Arg Pro Asn Pro Asp Asp Pro Thr Gly Lys Ser Thr Met Arg	
455 460 465	
cgc gtc acc gat gtt ttg gac gtg tgg ttc gac tcc ggt tcc atg ccg	1555
Arg Val Thr Asp Val Leu Asp Val Trp Phe Asp Ser Gly Ser Met Pro	
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Phe Ala Gln Val His Tyr Pro Phe Glu Asn Lys Glu Trp Phe Asp Thr	
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His Ala Pro Ala Asp Phe Ile Val Glu Tyr Ile Gly Gln Thr Arg Gly	
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Trp Phe Tyr Leu Leu His Val Leu Ser Thr Ala Leu Phe Asp Arg Pro	
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Ala Phe Lys Lys Val Val Ala His Gly Ile Val Leu Gly Asp Asp Gly	
535 540 545	
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Leu Lys Met Ser Lys Ser Lys Gly Asn Tyr Pro Asn Val Asn Glu Val	
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Leu Gln Leu Tyr Thr Ser Lys Asn Ala Thr Trp Ser Val Asp Ser Thr	
615 620 625	

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Leu	Val	Arg	Asn	Phe	Cys	Asp	Ala	Leu	Thr	Asn	Trp	Tyr	Val	Arg	Arg	
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Ser	Arg	Asp	Arg	Phe	Trp	Ala	Gly	Asp	Glu	Ala	His	Pro	Glu	Ala	Phe	
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Asn	Thr	Leu	Tyr	Thr	Val	Leu	Glu	Thr	Leu	Thr	Arg	Val	Ala	Ala	Pro	
	695					700					705					
ctg	ctg	cca	atg	acc	acc	gaa	gtg	atc	tgg	cgt	gga	ctg	acc	ggc	gag	2275
Leu	Leu	Pro	Met	Thr	Thr	Glu	Val	Ile	Trp	Arg	Gly	Leu	Thr	Gly	Glu	
710					715				720					725		
cgt	tct	gtg	cac	ctg	act	gat	ttc	cca	tcc	gct	gag	tct	ttc	cca	gca	2323
Arg	Ser	Val	His	Leu	Thr	Asp	Phe	Pro	Ser	Ala	Glu	Ser	Phe	Pro	Ala	
				730					735					740		
gat	gct	gat	ttg	gtt	cgc	acc	atg	gat	gag	atc	cgt	ggc	gtg	tgc	tct	2371
Asp	Ala	Asp	Leu	Val	Arg	Thr	Met	Asp	Glu	Ile	Arg	Gly	Val	Cys	Ser	
			745					750					755			
gcg	gct	tcc	tct	gtt	cgt	aag	gct	cac	aag	ctg	cgt	aac	cgt	ctg	cca	2419
Ala	Ala	Ser	Ser	Val	Arg	Lys	Ala	His	Lys	Leu	Arg	Asn	Arg	Leu	Pro	
		760					765					770				
ctt	cca	ggc	ctg	act	gtt	gct	ctt	cca	gac	tct	gct	cgc	ctg	gca	gac	2467
Leu	Pro	Gly	Leu	Thr	Val	Ala	Leu	Pro	Asp	Ser	Ala	Arg	Leu	Ala	Asp	
	775					780					785					
ttc	gct	tcg	atc	atc	cgc	gat	gag	gtc	aac	gtg	aag	aac	gtg	gat	ctg	2515
Phe	Ala	Ser	Ile	Ile	Arg	Asp	Glu	Val	Asn	Val	Lys	Asn	Val	Asp	Leu	
790					795					800					805	
acc	tct	gac	gtg	gat	tcc	gtg	gga	acc	ttc	gag	gtt	gtt	gtt	aac	gct	2563
Thr	Ser	Asp	Val	Asp	Ser	Val	Gly	Thr	Phe	Glu	Val	Val	Val	Asn	Ala	
				810					815					820		
aag	gtt	gca	ggt	cct	cgc	ttg	ggc	aag	gac	gtc	cag	cgc	gtg	atc	aag	2611
Lys	Val	Ala	Gly	Pro	Arg	Leu	Gly	Lys	Asp	Val	Gln	Arg	Val	Ile	Lys	
			825					830					835			
gct	gtg	aag	gct	ggc	aac	tac	acc	cgc	gaa	ggc	gac	gtc	gtt	gtt	gcc	2659
Ala	Val	Lys	Ala	Gly	Asn	Tyr	Thr	Arg	Glu	Gly	Asp	Val	Val	Val	Ala	
		840					845					850				
gat	ggc	atc	gag	ctc	aac	gag	ggt	gaa	ttc	acc	gag	cgt	ctc	gta	gca	2707
Asp	Gly	Ile	Glu	Leu	Asn	Glu	Gly	Glu	Phe	Thr	Glu	Arg	Leu	Val	Ala	
	855					860					865					
gca	aac	cct	gat	tcc	acc	gcg	cag	atc	gac	ggc	gtg	gat	gga	ctc	gtg	2755

Ala Asn Pro Asp Ser Thr Ala Gln Ile Asp Gly Val Asp Gly Leu Val
 870 875 880 885

gtt ctg gac atg gaa gtc acg gaa gaa ctt gaa gca gaa ggc tgg gca 2803
 Val Leu Asp Met Glu Val Thr Glu Glu Leu Glu Ala Glu Gly Trp Ala
 890 895 900

gcg gac gcg atc cgt ggc ctg cag gat gct cga aag aac tcc ggc ttt 2851
 Ala Asp Ala Ile Arg Gly Leu Gln Asp Ala Arg Lys Asn Ser Gly Phe
 905 910 915

gag gtt tct gac cgc att tct gtt gtc gtc agc gtt cct gag gac aag 2899
 Glu Val Ser Asp Arg Ile Ser Val Val Val Ser Val Pro Glu Asp Lys
 920 925 930

aag gaa tgg atc acc act cac gct gat cac atc gca gcg gaa gtt ttg 2947
 Lys Glu Trp Ile Thr Thr His Ala Asp His Ile Ala Ala Glu Val Leu
 935 940 945

gca acc tcc ttt gag atc gtc act gat gcc ctc gac ggc gaa acc cac 2995
 Ala Thr Ser Phe Glu Ile Val Thr Asp Ala Leu Asp Gly Glu Thr His
 950 955 960 965

gac att gtc gct ggt gtg acc gcg aag gtt act aag aac taagagttgt 3044
 Asp Ile Val Ala Gly Val Thr Ala Lys Val Thr Lys Asn
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<212> PRT

<213> Corynebacterium glutamicum

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Phe Ser Trp Asp Thr His Gly Leu Pro Ala Glu Leu Glu Ala Glu Lys
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Gln Leu Gly Ile Lys Asp Lys Gly Glu Ile Glu Ala Met Gly Leu Ala
 35 40 45

Lys Phe Asn Glu Tyr Cys Ala Thr Ser Val Leu Gln Tyr Thr Lys Glu
 50 55 60

Trp Glu Glu Tyr Val Thr Arg Gln Ala Arg Trp Val Asp Phe Glu Asn
 65 70 75 80

Gly Tyr Lys Thr Met Asp Leu Ser Phe Met Glu Ser Val Ile Trp Ala
 85 90 95

Phe Lys Glu Leu Tyr Asp Lys Gly Leu Ile Tyr Gln Gly Phe Arg Val
 100 105 110

Leu Pro Tyr Ser Trp Ala Glu His Thr Pro Leu Ser Asn Gln Glu Thr
 115 120 125

Arg Leu Asp Asp Ser Tyr Lys Leu Arg Gln Asp Pro Thr Leu Thr Val

130				135				140							
Thr	Phe	Pro	Val	Thr	Gly	Val	Val	Glu	Gly	Ser	Ser	Ala	Asn	Ala	Gly
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Leu	Val	Gly	Ala	Leu	Ala	Leu	Ala	Trp	Thr	Thr	Thr	Pro	Trp	Thr	Leu
				165					170						175
Pro	Ser	Asn	Leu	Ala	Leu	Ala	Val	Asn	Pro	Ala	Val	Thr	Tyr	Ala	Leu
			180					185					190		
Val	Glu	Val	Ala	Glu	Asp	Gly	Glu	Ala	Glu	Phe	Val	Gly	Lys	Arg	Val
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Leu	Leu	Ala	Lys	Asp	Leu	Val	Gly	Ser	Tyr	Ala	Lys	Glu	Leu	Gly	Ala
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Glu	Ala	Val	Ile	Val	Ser	Glu	His	Pro	Gly	Ser	Glu	Leu	Val	Gly	Leu
225					230					235					240
Thr	Tyr	Glu	Pro	Ile	Phe	Gly	Tyr	Phe	Arg	Asp	His	Ala	Asn	Gly	Phe
				245					250					255	
Gln	Ile	Leu	Gly	Ala	Glu	Tyr	Val	Thr	Thr	Glu	Asp	Gly	Thr	Gly	Ile
			260					265					270		
Val	His	Gln	Ala	Pro	Ala	Phe	Gly	Glu	Asp	Asp	Met	Asn	Thr	Cys	Asn
		275					280					285			
Ala	Ala	Gly	Ile	Glu	Pro	Val	Ile	Pro	Val	Asp	Ile	Asp	Gly	Lys	Phe
	290					295					300				
Thr	Gly	Leu	Val	Pro	Glu	Tyr	Gln	Gly	Gln	Leu	Val	Phe	Asp	Ala	Asn
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Lys	Asp	Ile	Ile	Lys	Asp	Leu	Lys	Ala	Ala	Gly	Arg	Val	Val	Arg	His
				325					330					335	
Gln	Thr	Ile	Glu	His	Ser	Tyr	Pro	His	Ser	Trp	Arg	Ser	Gly	Glu	Pro
			340					345					350		
Leu	Ile	Tyr	Met	Ala	Leu	Pro	Ser	Trp	Phe	Val	Asn	Val	Thr	Glu	Ile
	355						360					365			
Arg	Asp	Arg	Met	Val	Glu	Val	Asn	Gln	Asp	Ile	Glu	Trp	Met	Pro	Ala
	370					375					380				
His	Ile	Arg	Asp	Gly	Gln	Phe	Gly	Lys	Trp	Leu	Glu	Gly	Ala	Arg	Asp
385					390					395					400
Trp	Asn	Ile	Ser	Arg	Ser	Arg	Tyr	Trp	Gly	Ser	Pro	Ile	Pro	Ala	Trp
				405					410					415	
Val	Ser	Asp	Asn	Asp	Glu	Tyr	Pro	Arg	Val	Asp	Val	Tyr	Gly	Ser	Leu
			420					425					430		
Asp	Glu	Leu	Glu	Ala	Asp	Phe	Gly	Val	Arg	Pro	Lys	Ser	Leu	His	Arg
		435					440					445			
Pro	Asp	Ile	Asp	Glu	Leu	Thr	Arg	Pro	Asn	Pro	Asp	Asp	Pro	Thr	Gly
	450					455					460				

Lys Ser Thr Met Arg Arg Val Thr Asp Val Leu Asp Val Trp Phe Asp
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 Ser Gly Ser Met Pro Phe Ala Gln Val His Tyr Pro Phe Glu Asn Lys
 485 490 495
 Glu Trp Phe Asp Thr His Ala Pro Ala Asp Phe Ile Val Glu Tyr Ile
 500 505 510
 Gly Gln Thr Arg Gly Trp Phe Tyr Leu Leu His Val Leu Ser Thr Ala
 515 520 525
 Leu Phe Asp Arg Pro Ala Phe Lys Lys Val Val Ala His Gly Ile Val
 530 535 540
 Leu Gly Asp Asp Gly Leu Lys Met Ser Lys Ser Lys Gly Asn Tyr Pro
 545 550 555 560
 Asn Val Asn Glu Val Phe Asp Arg Asp Gly Ser Asp Ala Met Arg Trp
 565 570 575
 Phe Leu Met Ser Ser Pro Ile Leu Arg Gly Gly Asn Leu Ile Val Thr
 580 585 590
 Glu Lys Gly Ile Arg Glu Gly Val Arg Gln Ala Gln Leu Pro Met Trp
 595 600 605
 Asn Ala Tyr Ser Phe Leu Gln Leu Tyr Thr Ser Lys Asn Ala Thr Trp
 610 615 620
 Ser Val Asp Ser Thr Asp Val Leu Asp Arg Tyr Ile Leu Ala Lys Leu
 625 630 635 640
 His Asp Leu Val Ala Glu Thr Gln Ala Ala Leu Asp Gly Thr Asp Ile
 645 650 655
 Ala Lys Ala Cys Asp Leu Val Arg Asn Phe Cys Asp Ala Leu Thr Asn
 660 665 670
 Trp Tyr Val Arg Arg Ser Arg Asp Arg Phe Trp Ala Gly Asp Glu Ala
 675 680 685
 His Pro Glu Ala Phe Asn Thr Leu Tyr Thr Val Leu Glu Thr Leu Thr
 690 695 700
 Arg Val Ala Ala Pro Leu Leu Pro Met Thr Thr Glu Val Ile Trp Arg
 705 710 715 720
 Gly Leu Thr Gly Glu Arg Ser Val His Leu Thr Asp Phe Pro Ser Ala
 725 730 735
 Glu Ser Phe Pro Ala Asp Ala Asp Leu Val Arg Thr Met Asp Glu Ile
 740 745 750
 Arg Gly Val Cys Ser Ala Ala Ser Ser Val Arg Lys Ala His Lys Leu
 755 760 765
 Arg Asn Arg Leu Pro Leu Pro Gly Leu Thr Val Ala Leu Pro Asp Ser
 770 775 780

Ala Arg Leu Ala Asp Phe Ala Ser Ile Ile Arg Asp Glu Val Asn Val
 785 790 795 800
 Lys Asn Val Asp Leu Thr Ser Asp Val Asp Ser Val Gly Thr Phe Glu
 805 810 815
 Val Val Val Asn Ala Lys Val Ala Gly Pro Arg Leu Gly Lys Asp Val
 820 825 830
 Gln Arg Val Ile Lys Ala Val Lys Ala Gly Asn Tyr Thr Arg Glu Gly
 835 840 845
 Asp Val Val Val Ala Asp Gly Ile Glu Leu Asn Glu Gly Glu Phe Thr
 850 855 860
 Glu Arg Leu Val Ala Ala Asn Pro Asp Ser Thr Ala Gln Ile Asp Gly
 865 870 875 880
 Val Asp Gly Leu Val Val Leu Asp Met Glu Val Thr Glu Glu Leu Glu
 885 890 895
 Ala Glu Gly Trp Ala Ala Asp Ala Ile Arg Gly Leu Gln Asp Ala Arg
 900 905 910
 Lys Asn Ser Gly Phe Glu Val Ser Asp Arg Ile Ser Val Val Val Ser
 915 920 925
 Val Pro Glu Asp Lys Lys Glu Trp Ile Thr Thr His Ala Asp His Ile
 930 935 940
 Ala Ala Glu Val Leu Ala Thr Ser Phe Glu Ile Val Thr Asp Ala Leu
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 Asp Gly Glu Thr His Asp Ile Val Ala Gly Val Thr Ala Lys Val Thr
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 Lys Asn

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 Met Thr Asn Pro Ser
 1 5
 gaa ggc acc act ccc ctg gcg ttc cgt tat acc ccg gaa ctc gcc aac 163
 Glu Gly Thr Thr Pro Leu Ala Phe Arg Tyr Thr Pro Glu Leu Ala Asn
 10 15 20

aag atc gaa ggt gag tgg cag aat tac tgg act gac aac ggc aca ttc 211
Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr Asp Asn Gly Thr Phe
25 30 35

aac gca ccc aac cca gtg ggt gat tta gcg cct gcg gac ggt aaa gca 259
Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro Ala Asp Gly Lys Ala
40 45 50

ctt cct gag gac aag ctc ttt gtc cag gat atg ttc ccg tac cca tcc 307
Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met Phe Pro Tyr Pro Ser
55 60 65

gga gct ggc ctg cac gta ggc cac cca ctc ggt tac atc gca acg gat 355
Gly Ala Gly Leu His Val Gly His Pro Leu Gly Tyr Ile Ala Thr Asp
70 75 80 85

gtt ttc gcc cgc tac aac cgc atg ctg ggc aag aac gtt ctg cac acc 403
Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys Asn Val Leu His Thr
90 95 100

ttg ggc tat gac gcc ttc gga ctg cca gca gag cag tac gcg atc caa 451
Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Gln
105 110 115

acc ggt aca cac cca cgc acc acc acc atg gcc aac att gag aac atg 499
Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala Asn Ile Glu Asn Met
120 125 130

aag cgc cag ctc ggt gcg ctg ggt ctt ggc cat gat tcc cgt cgt gcg 547
Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His Asp Ser Arg Arg Ala
135 140 145

gtg gcc acc acg gat cct gag ttc tac aag tgg act cag tgg atc ttc 595
Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp Thr Gln Trp Ile Phe
150 155 160 165

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Leu Gln Ile Phe Asn Ser Trp Phe Asp Ala Glu Gln Gln Lys Ala
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Pro Glu Leu Ala Asn Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr
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Asp Asn Gly Thr Phe Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro
35 40 45

Ala Asp Gly Lys Ala Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met
50 55 60

Phe Pro Tyr Pro Ser Gly Ala Gly Leu His Val Gly His Pro Leu Gly
65 70 75 80

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Met Thr Asn Pro Ser																	
1 5																	
gaa ggc acc act ccc ctg gcg ttc cgt tat acc ccg gaa ctc gcc aac																	163
Glu Gly Thr Thr Pro Leu Ala Phe Arg Tyr Thr Pro Glu Leu Ala Asn																	
10 15 20																	
aag atc gaa ggt gag tgg cag aat tac tgg act gac aac ggc aca ttc																	211
Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr Asp Asn Gly Thr Phe																	
25 30 35																	
aac gca ccc aac cca gtg ggt gat tta gcg cct gcg gac ggt aaa gca																	259
Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro Ala Asp Gly Lys Ala																	
40 45 50																	
ctt cct gag gac aag ctc ttt gtc cag gat atg ttc ccg tac cca tcc																	307
Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met Phe Pro Tyr Pro Ser																	
55 60 65																	
gga gct ggc ctg cac gta ggc cac cca ctc ggt tac atc gca acg gat																	355
Gly Ala Gly Leu His Val Gly His Pro Leu Gly Tyr Ile Ala Thr Asp																	
70 75 80 85																	
gtt ttc gcc cgc tac aac cgc atg ctg ggc aag aac gtt ctg cac acc																	403

Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys Asn Val Leu His Thr
 90 95 100

ttg ggc tat gac gcc ttc gga ctg cca gca gag cag tac gcg atc caa 451
 Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu Gln Tyr Ala Ile Gln
 105 110 115

acc ggt aca cac cca cgc acc acc acc atg gcc aac att gag aac atg 499
 Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala Asn Ile Glu Asn Met
 120 125 130

aag cgc cag ctc ggt gcg ctg ggt ctt ggc cat gat tcc cgt cgt gcg 547
 Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His Asp Ser Arg Arg Ala
 135 140 145

gtg gcc acc acg gat cct gag ttc tac aag tgg act cag tgg atc ttc 595
 Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp Thr Gln Trp Ile Phe
 150 155 160 165

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 Leu Gln Ile Phe Asn Ser Trp Phe Asp Ala Glu
 170 175

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<211> 176

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

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Pro Glu Leu Ala Asn Lys Ile Glu Gly Glu Trp Gln Asn Tyr Trp Thr
 20 25 30

Asp Asn Gly Thr Phe Asn Ala Pro Asn Pro Val Gly Asp Leu Ala Pro
 35 40 45

Ala Asp Gly Lys Ala Leu Pro Glu Asp Lys Leu Phe Val Gln Asp Met
 50 55 60

Phe Pro Tyr Pro Ser Gly Ala Gly Leu His Val Gly His Pro Leu Gly
 65 70 75 80

Tyr Ile Ala Thr Asp Val Phe Ala Arg Tyr Asn Arg Met Leu Gly Lys
 85 90 95

Asn Val Leu His Thr Leu Gly Tyr Asp Ala Phe Gly Leu Pro Ala Glu
 100 105 110

Gln Tyr Ala Ile Gln Thr Gly Thr His Pro Arg Thr Thr Thr Met Ala
 115 120 125

Asn Ile Glu Asn Met Lys Arg Gln Leu Gly Ala Leu Gly Leu Gly His
 130 135 140

Asp Ser Arg Arg Ala Val Ala Thr Thr Asp Pro Glu Phe Tyr Lys Trp
 145 150 155 160

Thr Gln Trp Ile Phe Leu Gln Ile Phe Asn Ser Trp Phe Asp Ala Glu

165

170

175

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 tgg acc ggc cca cgc cca gaa acc cac gga cca aac gat cca ggc ggc 96
 Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn Asp Pro Gly Gly
 20 25 30
 gta gac ctc tac gtc ggt ggc gtc gag cac gca gtt ctc cac ctg ctc 144
 Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val Leu His Leu Leu
 35 40 45
 tac gca cgt ttc tgg cac aag gtc ctc ttc gac ctg ggc cac gtc tcc 192
 Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu Gly His Val Ser
 50 55 60
 tcc aag gag cca tac cgt cgc ctg tac aac cag ggc tac atc cag gcc 240
 Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly Tyr Ile Gln Ala
 65 70 75 80
 ttc gcc tac acc gat tcc cgt ggc gtc tac gtg cct gcc gat gat gtc 288
 Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro Ala Asp Asp Val
 85 90 95
 gaa gag aag gac gga aag ttc ttc tac cag ggc gaa gaa gtc aac cag 336
 Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu Glu Val Asn Gln
 100 105 110
 gaa tac gga aag atg ggc aag tcc ctg aag aac gcc gtt gcc cca gac 384
 Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala Val Ala Pro Asp
 115 120 125
 gat atc tgc aac aac ttc ggt gct gac acc ctg cgc gtt tac gag atg 432
 Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg Val Tyr Glu Met
 130 135 140
 gcc atg gga cct ttg gac acc tcc cgt cca tgg gca acc aag gac gtc 480
 Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala Thr Lys Asp Val
 145 150 155 160
 gtc ggt gcg cag cgc ttc ctc cag cgt ctg tgg cgt ctc gtc gtc gat 528
 Val Gly Ala Gln Arg Phe Leu Gln Arg Leu Trp Arg Leu Val Val Asp
 165 170 175
 gaa aac acc ggc gaa gtg ctc act cgc gat gaa gtc ctc acc gac gat 576
 Glu Asn Thr Gly Glu Val Leu Thr Arg Asp Glu Val Leu Thr Asp Asp
 180 185 190

gac aac aag caa ctg cac cgc acc atc gca ggc gtc cgc gac gac tac 624
 Asp Asn Lys Gln Leu His Arg Thr Ile Ala Gly Val Arg Asp Asp Tyr
 195 200 205

 acc aac ttg cgc gtt aac acc gtg gtt gcc aag ctc atc gaa tac gtc 672
 Thr Asn Leu Arg Val Asn Thr Val Val Ala Lys Leu Ile Glu Tyr Val
 210 215 220

 aac tac ctg acc aaa aca tac cca gac acc atc cca gct ggc gca gtc 720
 Asn Tyr Leu Thr Lys Thr Tyr Pro Asp Thr Ile Pro Ala Gly Ala Val
 225 230 235 240

 ctg cca ctg atc gtc atg gtc tcc cct atc gca cca cac atc gcg gag 768
 Leu Pro Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile Ala Glu
 245 250 255

 gaa ctc tgg aag aag ctc ggc cac gac gac acc gtc acc tac gaa cca 816
 Glu Leu Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr Glu Pro
 260 265 270

 ttc ccc acc ttt gag gaa aaa tgg ctc acc gac gat gaa atc gaa ctg 864
 Phe Pro Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile Glu Leu
 275 280 285

 cca gtc cag gtc aac ggc aag gtc cgc ggt cgc atc acc gtt gca gcc 912
 Pro Val Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val Ala Ala
 290 295 300

 gac gcc agc cag gag cag gtc atc gag gca gcg ctt gcc gac gag aag 960
 Asp Ala Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp Glu Lys
 305 310 315 320

 gtg cag gag caa atc tcc ggc aag aac ctg atc aag cag atc gtt gtt 1008
 Val Gln Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile Val Val
 325 330 335

 cca gga cgc atg gtt aac ctt gtg gtg aag taatccccct cggttttagat tcc 1061
 Pro Gly Arg Met Val Asn Leu Val Val Lys
 340 345

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<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

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Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn Asp Pro Gly Gly
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Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val Leu His Leu Leu
 35 40 45

Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu Gly His Val Ser
 50 55 60

Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly Tyr Ile Gln Ala

65	70					75					80				
Phe	Ala	Tyr	Thr	Asp	Ser	Arg	Gly	Val	Tyr	Val	Pro	Ala	Asp	Asp	Val
				85					90					95	
Glu	Glu	Lys	Asp	Gly	Lys	Phe	Phe	Tyr	Gln	Gly	Glu	Glu	Val	Asn	Gln
			100					105					110		
Glu	Tyr	Gly	Lys	Met	Gly	Lys	Ser	Leu	Lys	Asn	Ala	Val	Ala	Pro	Asp
		115					120					125			
Asp	Ile	Cys	Asn	Asn	Phe	Gly	Ala	Asp	Thr	Leu	Arg	Val	Tyr	Glu	Met
	130					135					140				
Ala	Met	Gly	Pro	Leu	Asp	Thr	Ser	Arg	Pro	Trp	Ala	Thr	Lys	Asp	Val
145					150					155					160
Val	Gly	Ala	Gln	Arg	Phe	Leu	Gln	Arg	Leu	Trp	Arg	Leu	Val	Val	Asp
				165					170					175	
Glu	Asn	Thr	Gly	Glu	Val	Leu	Thr	Arg	Asp	Glu	Val	Leu	Thr	Asp	Asp
			180					185					190		
Asp	Asn	Lys	Gln	Leu	His	Arg	Thr	Ile	Ala	Gly	Val	Arg	Asp	Asp	Tyr
		195					200					205			
Thr	Asn	Leu	Arg	Val	Asn	Thr	Val	Val	Ala	Lys	Leu	Ile	Glu	Tyr	Val
	210					215					220				
Asn	Tyr	Leu	Thr	Lys	Thr	Tyr	Pro	Asp	Thr	Ile	Pro	Ala	Gly	Ala	Val
225					230					235					240
Leu	Pro	Leu	Ile	Val	Met	Val	Ser	Pro	Ile	Ala	Pro	His	Ile	Ala	Glu
				245					250					255	
Glu	Leu	Trp	Lys	Lys	Leu	Gly	His	Asp	Asp	Thr	Val	Thr	Tyr	Glu	Pro
			260					265					270		
Phe	Pro	Thr	Phe	Glu	Glu	Lys	Trp	Leu	Thr	Asp	Asp	Glu	Ile	Glu	Leu
		275					280					285			
Pro	Val	Gln	Val	Asn	Gly	Lys	Val	Arg	Gly	Arg	Ile	Thr	Val	Ala	Ala
	290					295					300				
Asp	Ala	Ser	Gln	Glu	Gln	Val	Ile	Glu	Ala	Ala	Leu	Ala	Asp	Glu	Lys
305					310					315					320
Val	Gln	Glu	Gln	Ile	Ser	Gly	Lys	Asn	Leu	Ile	Lys	Gln	Ile	Val	Val
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Pro	Gly	Arg	Met	Val	Asn	Leu	Val	Val	Lys						
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<211> 471

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> FRXA01864

<400> 307

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Asn Glu Arg Tyr Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn
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gat cca ggc ggc gta gac ctc tac gtc ggt ggc gtc gag cac gca gtt 96
Asp Pro Gly Gly Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val
             20             25             30

ctc cac ctg ctc tac gca cgt ttc tgg cac aag gtc ctc ttc gac ctg 144
Leu His Leu Leu Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu
             35             40             45

ggc cac gtc tcc tcc aag gag cca tac cgt cgc ctg tac aac cag ggc 192
Gly His Val Ser Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly
             50             55             60

tac atc cag gcc ttc gcc tac acc gat tcc cgt ggc gtc tac gtg cct 240
Tyr Ile Gln Ala Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro
             65             70             75             80

gcc gat gat gtc gaa gag aag gac gga aag ttc ttc tac cag ggc gaa 288
Ala Asp Asp Val Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu
             85             90             95

gaa gtc aac cag gaa tac gga aag atg ggc aag tcc ctg aag aac gcc 336
Glu Val Asn Gln Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala
             100             105             110

gtt gcc cca gac gat atc tgc aac aac ttc ggt gct gac acc ctg cgc 384
Val Ala Pro Asp Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg
             115             120             125

gtt tac gag atg gcc atg gga cct ttg gac acc tcc cgt cca tgg gca 432
Val Tyr Glu Met Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala
             130             135             140

acc aag gac gtc gtc ggt gcg cag cgc ttc ctc agc gtc 471
Thr Lys Asp Val Val Gly Ala Gln Arg Phe Leu Ser Val
145             150             155

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<210> 308

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 308

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Asn Glu Arg Tyr Trp Thr Gly Pro Arg Pro Glu Thr His Gly Pro Asn
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Asp Pro Gly Gly Val Asp Leu Tyr Val Gly Gly Val Glu His Ala Val
             20             25             30

Leu His Leu Leu Tyr Ala Arg Phe Trp His Lys Val Leu Phe Asp Leu
             35             40             45

Gly His Val Ser Ser Lys Glu Pro Tyr Arg Arg Leu Tyr Asn Gln Gly

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50	55	60	
Tyr Ile Gln Ala Phe Ala Tyr Thr Asp Ser Arg Gly Val Tyr Val Pro			
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Ala Asp Asp Val Glu Glu Lys Asp Gly Lys Phe Phe Tyr Gln Gly Glu			
	85	90	95
Glu Val Asn Gln Glu Tyr Gly Lys Met Gly Lys Ser Leu Lys Asn Ala			
	100	105	110
Val Ala Pro Asp Asp Ile Cys Asn Asn Phe Gly Ala Asp Thr Leu Arg			
	115	120	125
Val Tyr Glu Met Ala Met Gly Pro Leu Asp Thr Ser Arg Pro Trp Ala			
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Thr Lys Asp Val Val Gly Ala Gln Arg Phe Leu Ser Val			
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	Leu Arg Val Asn Thr Val Val Ala Lys Leu Ile Glu		
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tac gtc aac tac ctg acc aaa aca tac cca gac acc atc cca gct ggc			158
Tyr Val Asn Tyr Leu Thr Lys Thr Tyr Pro Asp Thr Ile Pro Ala Gly			
	15	20	25
gca gtc ctg cca ctg atc gtc atg gtc tcc cct atc gca cca cac atc			206
Ala Val Leu Pro Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile			
	30	35	40
gcg gag gaa ctc tgg aag aag ctc ggc cac gac gac acc gtc acc tac			254
Ala Glu Glu Leu Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr			
	45	50	55
gaa cca ttc ccc acc ttt gag gaa aaa tgg ctc acc gac gat gaa atc			302
Glu Pro Phe Pro Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile			
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gaa ctg cca gtc cag gtc aac ggc aag gtc cgc ggt cgc atc acc gtt			350
Glu Leu Pro Val Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val			
	80	85	90
gca gcc gac gcc agc cag gag cag gtc atc gag gca gcg ctt gcc gac			398
Ala Ala Asp Ala Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp			
	95	100	105

gag aag gtg cag gag caa atc tcc ggc aag aac ctg atc aag cag atc 446
 Glu Lys Val Gln Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile
 110 115 120

gtt gtt cca gga cgc atg gtt aac ctt gtg gtg aag taatccccct 492
 Val Val Pro Gly Arg Met Val Asn Leu Val Val Lys
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cggtttagat tcc 505

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 310
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 Leu Ile Val Met Val Ser Pro Ile Ala Pro His Ile Ala Glu Glu Leu
 35 40 45
 Trp Lys Lys Leu Gly His Asp Asp Thr Val Thr Tyr Glu Pro Phe Pro
 50 55 60
 Thr Phe Glu Glu Lys Trp Leu Thr Asp Asp Glu Ile Glu Leu Pro Val
 65 70 75 80
 Gln Val Asn Gly Lys Val Arg Gly Arg Ile Thr Val Ala Ala Asp Ala
 85 90 95
 Ser Gln Glu Gln Val Ile Glu Ala Ala Leu Ala Asp Glu Lys Val Gln
 100 105 110
 Glu Gln Ile Ser Gly Lys Asn Leu Ile Lys Gln Ile Val Val Pro Gly
 115 120 125
 Arg Met Val Asn Leu Val Val Lys
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 <223> RXA00968

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atg cag cgt aac tgg att ggc cgt tcc cgc ggc gct gaa gtt gat ttc	96
Met Gln Arg Asn Trp Ile Gly Arg Ser Arg Gly Ala Glu Val Asp Phe	
20 25 30	
agt gca gag ggc gaa acc gtc acc gtg ttt acc acc cgc cca gat act	144
Ser Ala Glu Gly Glu Thr Val Thr Val Phe Thr Thr Arg Pro Asp Thr	
35 40 45	
ctg ttc ggc gcg acc tac atg gtt ctt gca cct gag cat gag ctg gtc	192
Leu Phe Gly Ala Thr Tyr Met Val Leu Ala Pro Glu His Glu Leu Val	
50 55 60	
gac gtg ctg ctg gag aag gct ggt tcc tac gag ggc gtt gat gcc cgt	240
Asp Val Leu Leu Glu Lys Ala Gly Ser Tyr Glu Gly Val Asp Ala Arg	
65 70 75 80	
tgg acc aat ggc cag gcg agc cct gcg gaa gct gtc gct gca tac cgc	288
Trp Thr Asn Gly Gln Ala Ser Pro Ala Glu Ala Val Ala Ala Tyr Arg	
85 90 95	
gcc tcc atc gcc gcg aag tcc gac ctg gag cgt cag gaa aac aag gaa	336
Ala Ser Ile Ala Ala Lys Ser Asp Leu Glu Arg Gln Glu Asn Lys Glu	
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aag acc ggc gtc ttc ctg ggc gtt tac gcg acc aac cca gtc aac ggc	384
Lys Thr Gly Val Phe Leu Gly Val Tyr Ala Thr Asn Pro Val Asn Gly	
115 120 125	
gat cag atc aca gtg ttc atc gct gac tac gtt ctg acc ggc tac ggc	432
Asp Gln Ile Thr Val Phe Ile Ala Asp Tyr Val Leu Thr Gly Tyr Gly	
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acc ggc gcc atc atg gcg gtt cct gct cac gac gag cgc gac tac gaa	480
Thr Gly Ala Ile Met Ala Val Pro Ala His Asp Glu Arg Asp Tyr Glu	
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ttc gcc acc gtt ttg ggt ctg cct atc aag gaa gtt gtc gca ggt ggc	528
Phe Ala Thr Val Leu Gly Leu Pro Ile Lys Glu Val Val Ala Gly Gly	
165 170 175	
aac atc gaa gag gct gct ttc acc gaa tct ggc gaa gca gtc aac tct	576
Asn Ile Glu Glu Ala Ala Phe Thr Glu Ser Gly Glu Ala Val Asn Ser	
180 185 190	
gcg aac gac aac ggc ctg gat atc aac ggc ctt gcc aag gat gag gct	624
Ala Asn Asp Asn Gly Leu Asp Ile Asn Gly Leu Ala Lys Asp Glu Ala	
195 200 205	
att gcc aag acc atc gaa tgg ttg gaa gaa aag gaa ctt ggc cgc ggc	672
Ile Ala Lys Thr Ile Glu Trp Leu Glu Glu Lys Glu Leu Gly Arg Gly	
210 215 220	
acc atc cag tac aag ctg cgc gac tgg ctg ttc gct cgc cag cgt tac	720
Thr Ile Gln Tyr Lys Leu Arg Asp Trp Leu Phe Ala Arg Gln Arg Tyr	
225 230 235 240	
tgg ggc gag cct ttc cca atc gtc tac gac gaa aac ggc caa gca cat	768
Trp Gly Glu Pro Phe Pro Ile Val Tyr Asp Glu Asn Gly Gln Ala His	
245 250 255	
gct ctg cca gac tcc atg ctt cca gtc gag ctg cca gag gta gag gac	816

Ala	Leu	Pro	Asp	Ser	Met	Leu	Pro	Val	Glu	Leu	Pro	Glu	Val	Glu	Asp	
			260					265					270			
tac	aag	cct	gtc	tcc	ttc	gac	cct	gaa	gac	gca	gac	tcc	gag	cct	tcc	864
Tyr	Lys	Pro	Val	Ser	Phe	Asp	Pro	Glu	Asp	Ala	Asp	Ser	Glu	Pro	Ser	
		275					280					285				
cca	cca	ctg	gct	aag	gcc	cgc	gaa	tgg	gtt	gag	gtg	gaa	ctc	gat	ctc	912
Pro	Pro	Leu	Ala	Lys	Ala	Arg	Glu	Trp	Val	Glu	Val	Glu	Leu	Asp	Leu	
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ggc	gat	ggc	aag	aag	aag	tac	acc	cgc	gac	acc	aac	gtc	atg	cca	cag	960
Gly	Asp	Gly	Lys	Lys	Lys	Tyr	Thr	Arg	Asp	Thr	Asn	Val	Met	Pro	Gln	
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<211> 334

<212> PRT

<213> Corynebacterium glutamicum

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			20					25					30			
Ser	Ala	Glu	Gly	Glu	Thr	Val	Thr	Val	Phe	Thr	Thr	Arg	Pro	Asp	Thr	
		35				40						45				
Leu	Phe	Gly	Ala	Thr	Tyr	Met	Val	Leu	Ala	Pro	Glu	His	Glu	Leu	Val	
	50					55					60					
Asp	Val	Leu	Leu	Glu	Lys	Ala	Gly	Ser	Tyr	Glu	Gly	Val	Asp	Ala	Arg	
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Trp	Thr	Asn	Gly	Gln	Ala	Ser	Pro	Ala	Glu	Ala	Val	Ala	Ala	Tyr	Arg	
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Ala	Ser	Ile	Ala	Ala	Lys	Ser	Asp	Leu	Glu	Arg	Gln	Glu	Asn	Lys	Glu	
			100					105					110			
Lys	Thr	Gly	Val	Phe	Leu	Gly	Val	Tyr	Ala	Thr	Asn	Pro	Val	Asn	Gly	
		115				120						125				
Asp	Gln	Ile	Thr	Val	Phe	Ile	Ala	Asp	Tyr	Val	Leu	Thr	Gly	Tyr	Gly	
130						135					140					
Thr	Gly	Ala	Ile	Met	Ala	Val	Pro	Ala	His	Asp	Glu	Arg	Asp	Tyr	Glu	
145					150					155					160	
Phe	Ala	Thr	Val	Leu	Gly	Leu	Pro	Ile	Lys	Glu	Val	Val	Ala	Gly	Gly	
				165					170					175		
Asn	Ile	Glu	Glu	Ala	Ala	Phe	Thr	Glu	Ser	Gly	Glu	Ala	Val	Asn	Ser	
			180					185					190			

Ala Asn Asp Asn Gly Leu Asp Ile Asn Gly Leu Ala Lys Asp Glu Ala
 195 200 205

Ile Ala Lys Thr Ile Glu Trp Leu Glu Glu Lys Glu Leu Gly Arg Gly
 210 215 220

Thr Ile Gln Tyr Lys Leu Arg Asp Trp Leu Phe Ala Arg Gln Arg Tyr
 225 230 235 240

Trp Gly Glu Pro Phe Pro Ile Val Tyr Asp Glu Asn Gly Gln Ala His
 245 250 255

Ala Leu Pro Asp Ser Met Leu Pro Val Glu Leu Pro Glu Val Glu Asp
 260 265 270

Tyr Lys Pro Val Ser Phe Asp Pro Glu Asp Ala Asp Ser Glu Pro Ser
 275 280 285

Pro Pro Leu Ala Lys Ala Arg Glu Trp Val Glu Val Glu Leu Asp Leu
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Gly Asp Gly Lys Lys Lys Tyr Thr Arg Asp Thr Asn Val Met Pro Gln
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Trp Ala Gly Ser Ser Trp Tyr Gln Leu Arg Tyr Val Asp Pro
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<210> 313

<211> 1701

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1678)

<223> RXA01522

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 Val Thr Asn Ser Asn
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ccc act tcc aag aac aat tcc gcc gat ttg cct gag cag ctg cga att 163
 Pro Thr Ser Lys Asn Asn Ser Ala Asp Leu Pro Glu Gln Leu Arg Ile
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cgt cgc gaa aag cgc gag cgc att ctg gac agt gga ttg gac gcc tac 211
 Arg Arg Glu Lys Arg Glu Arg Ile Leu Asp Ser Gly Leu Asp Ala Tyr
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cca gtc gag gtt gat cgc acc atc tca atc tct gac ctg cgc tcc caa 259
 Pro Val Glu Val Asp Arg Thr Ile Ser Ile Ser Asp Leu Arg Ser Gln
 40 45 50

ttt gtt gtc att aca gaa gac ctc caa gag cgc gaa gaa ggc gta acc 307
 Phe Val Val Ile Thr Glu Asp Leu Gln Glu Arg Glu Glu Gly Val Thr
 55 60 65

tac	ctc	gaa	gta	ggc	gaa	gaa	acc	gac	gtt	gag	gtc	gca	atc	gct	ggc	355
Tyr	Leu	Glu	Val	Gly	Glu	Glu	Thr	Asp	Val	Glu	Val	Ala	Ile	Ala	Gly	
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cgc	gtc	atg	ttc	gtt	cgc	aac	acc	ggc	aag	ctc	tgc	ttc	gca	tcc	atc	403
Arg	Val	Met	Phe	Val	Arg	Asn	Thr	Gly	Lys	Leu	Cys	Phe	Ala	Ser	Ile	
				90					95					100		
caa	gaa	gga	aac	ggc	acc	acc	gtc	caa	gca	atg	ctg	tcc	ctg	gca	gca	451
Gln	Glu	Gly	Asn	Gly	Thr	Thr	Val	Gln	Ala	Met	Leu	Ser	Leu	Ala	Ala	
			105					110					115			
gtc	ggc	gaa	gaa	tcc	ctc	aag	gcc	tgg	aaa	gcc	gat	gtg	gac	atg	ggc	499
Val	Gly	Glu	Glu	Ser	Leu	Lys	Ala	Trp	Lys	Ala	Asp	Val	Asp	Met	Gly	
		120					125					130				
gac	atc	gtt	tcc	gtc	cgc	ggc	aaa	gta	atc	tcc	tcc	aag	cgt	ggc	gaa	547
Asp	Ile	Val	Ser	Val	Arg	Gly	Lys	Val	Ile	Ser	Ser	Lys	Arg	Gly	Glu	
	135					140						145				
ctc	tcc	gtg	atg	gct	gac	tcc	tgg	cac	atg	gcc	tcc	aag	tcc	ctg	cgc	595
Leu	Ser	Val	Met	Ala	Asp	Ser	Trp	His	Met	Ala	Ser	Lys	Ser	Leu	Arg	
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cca	ctg	cca	gtc	gca	ttc	gcg	gac	ctc	agc	gaa	gac	acc	cgc	gtc	cgc	643
Pro	Leu	Pro	Val	Ala	Phe	Ala	Asp	Leu	Ser	Glu	Asp	Thr	Arg	Val	Arg	
				170					175					180		
cac	cgc	tac	acc	gac	ctc	atc	atg	cgc	gaa	caa	gcc	cgc	acc	aac	gcg	691
His	Arg	Tyr	Thr	Asp	Leu	Ile	Met	Arg	Glu	Gln	Ala	Arg	Thr	Asn	Ala	
			185					190					195			
ctc	acc	cgc	atc	aag	gtc	atg	cgt	gca	ctc	cgc	cac	tac	ctc	gaa	gac	739
Leu	Thr	Arg	Ile	Lys	Val	Met	Arg	Ala	Leu	Arg	His	Tyr	Leu	Glu	Asp	
		200					205					210				
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Gln	Asp	Phe	Leu	Glu	Val	Glu	Thr	Pro	Met	Leu	Gln	Thr	Leu	His	Gly	
	215					220					225					
ggc	gca	gca	gca	cga	cca	ttc	gaa	acc	cac	tcc	aac	gcc	ctc	gac	att	835
Gly	Ala	Ala	Ala	Arg	Pro	Phe	Glu	Thr	His	Ser	Asn	Ala	Leu	Asp	Ile	
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Asp	Leu	Tyr	Leu	Arg	Ile	Ala	Pro	Glu	Leu	Tyr	Leu	Lys	Arg	Cys	Val	
				250					255					260		
gtc	ggc	ggc	atc	gag	cgc	gtc	ttc	gaa	gtc	aac	cgc	aac	ttc	cgc	aac	931
Val	Gly	Gly	Ile	Glu	Arg	Val	Phe	Glu	Val	Asn	Arg	Asn	Phe	Arg	Asn	
			265					270					275			
gaa	ggc	gtc	gac	tcc	tcc	cac	tcc	cca	gaa	ttc	gcc	atg	ctc	gaa	acc	979
Glu	Gly	Val	Asp	Ser	Ser	His	Ser	Pro	Glu	Phe	Ala	Met	Leu	Glu	Thr	
		280					285					290				
tac	gaa	gcc	tgg	gga	acc	tac	gaa	acc	ggc	gcg	aaa	ctg	atc	aag	ggc	1027
Tyr	Glu	Ala	Trp	Gly	Thr	Tyr	Glu	Thr	Gly	Ala	Lys	Leu	Ile	Lys	Gly	
	295					300					305					

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 Leu Val Gln Ser Val Ala Gln Glu Val Phe Gly Thr Thr Leu Val Thr
 310 315 320 325

ctc gca gac ggc acc gaa tac gac ctc ggc ggc gag tgg aaa gtc atc 1123
 Leu Ala Asp Gly Thr Glu Tyr Asp Leu Gly Gly Glu Trp Lys Val Ile
 330 335 340

gag atg tac cct tcc ctc aac gaa gcc ctc gca cgc aaa ttc cca gga 1171
 Glu Met Tyr Pro Ser Leu Asn Glu Ala Leu Ala Arg Lys Phe Pro Gly
 345 350 355

caa cca gaa gta acc atc gac tcc acc gtc gaa gaa ctc cgc gaa atc 1219
 Gln Pro Glu Val Thr Ile Asp Ser Thr Val Glu Glu Leu Arg Glu Ile
 360 365 370

gcc aag gta atc ggc ctc tcc gtc ccc gaa aac ggc ggc tgg gga cac 1267
 Ala Lys Val Ile Gly Leu Ser Val Pro Glu Asn Gly Gly Trp Gly His
 375 380 385

ggc aaa ctc gtc gaa gaa atc tgg gaa ctc ctc tgc gaa gac caa ctc 1315
 Gly Lys Leu Val Glu Glu Ile Trp Glu Leu Leu Cys Glu Asp Gln Leu
 390 395 400 405

tac gga cca atc ttt gtc aaa gac ttc cca gta gaa acc ttc cca ctc 1363
 Tyr Gly Pro Ile Phe Val Lys Asp Phe Pro Val Glu Thr Phe Pro Leu
 410 415 420

aca cgc caa cac cgc acc aag cca ggc gtc acc gaa aag tgg gac ctc 1411
 Thr Arg Gln His Arg Thr Lys Pro Gly Val Thr Glu Lys Trp Asp Leu
 425 430 435

tac gtc cgc gga ttt gaa cta gca acc gga tac tcc gaa ctc atc gac 1459
 Tyr Val Arg Gly Phe Glu Leu Ala Thr Gly Tyr Ser Glu Leu Ile Asp
 440 445 450

cca gtc att caa cgc gaa cgc ttc gaa ggc caa gcc cgc ctc gcc gcc 1507
 Pro Val Ile Gln Arg Glu Arg Phe Glu Gly Gln Ala Arg Leu Ala Ala
 455 460 465

gac gga gac gac gaa gcc atg gtc ctc gac gaa gac ttc ctc acc gca 1555
 Asp Gly Asp Asp Glu Ala Met Val Leu Asp Glu Asp Phe Leu Thr Ala
 470 475 480 485

atg gaa caa ggc atg cca cca acc tcc ggc aac ggc atg gga atc gac 1603
 Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn Gly Met Gly Ile Asp
 490 495 500

cgc ctc ctc atg gcc ctc acc ggc ctc gga atc cgc gaa acc gta ctc 1651
 Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile Arg Glu Thr Val Leu
 505 510 515

ttc cca atg gtg aaa cca gaa caa aag taggtttttg ctctttgtgc ttg 1701
 Phe Pro Met Val Lys Pro Glu Gln Lys
 520 525

<210> 314

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

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			20					25					30		
Gly	Leu	Asp	Ala	Tyr	Pro	Val	Glu	Val	Asp	Arg	Thr	Ile	Ser	Ile	Ser
		35					40					45			
Asp	Leu	Arg	Ser	Gln	Phe	Val	Val	Ile	Thr	Glu	Asp	Leu	Gln	Glu	Arg
	50					55					60				
Glu	Glu	Gly	Val	Thr	Tyr	Leu	Glu	Val	Gly	Glu	Glu	Thr	Asp	Val	Glu
65					70					75					80
Val	Ala	Ile	Ala	Gly	Arg	Val	Met	Phe	Val	Arg	Asn	Thr	Gly	Lys	Leu
				85					90					95	
Cys	Phe	Ala	Ser	Ile	Gln	Glu	Gly	Asn	Gly	Thr	Thr	Val	Gln	Ala	Met
			100					105					110		
Leu	Ser	Leu	Ala	Ala	Val	Gly	Glu	Glu	Ser	Leu	Lys	Ala	Trp	Lys	Ala
		115					120					125			
Asp	Val	Asp	Met	Gly	Asp	Ile	Val	Ser	Val	Arg	Gly	Lys	Val	Ile	Ser
	130					135					140				
Ser	Lys	Arg	Gly	Glu	Leu	Ser	Val	Met	Ala	Asp	Ser	Trp	His	Met	Ala
145					150					155					160
Ser	Lys	Ser	Leu	Arg	Pro	Leu	Pro	Val	Ala	Phe	Ala	Asp	Leu	Ser	Glu
				165					170					175	
Asp	Thr	Arg	Val	Arg	His	Arg	Tyr	Thr	Asp	Leu	Ile	Met	Arg	Glu	Gln
			180					185					190		
Ala	Arg	Thr	Asn	Ala	Leu	Thr	Arg	Ile	Lys	Val	Met	Arg	Ala	Leu	Arg
		195					200					205			
His	Tyr	Leu	Glu	Asp	Gln	Asp	Phe	Leu	Glu	Val	Glu	Thr	Pro	Met	Leu
	210					215					220				
Gln	Thr	Leu	His	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Phe	Glu	Thr	His	Ser
225					230					235					240
Asn	Ala	Leu	Asp	Ile	Asp	Leu	Tyr	Leu	Arg	Ile	Ala	Pro	Glu	Leu	Tyr
				245					250					255	
Leu	Lys	Arg	Cys	Val	Val	Gly	Gly	Ile	Glu	Arg	Val	Phe	Glu	Val	Asn
			260					265					270		
Arg	Asn	Phe	Arg	Asn	Glu	Gly	Val	Asp	Ser	Ser	His	Ser	Pro	Glu	Phe
		275					280					285			
Ala	Met	Leu	Glu	Thr	Tyr	Glu	Ala	Trp	Gly	Thr	Tyr	Glu	Thr	Gly	Ala
	290					295					300				
Lys	Leu	Ile	Lys	Gly	Leu	Val	Gln	Ser	Val	Ala	Gln	Glu	Val	Phe	Gly
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Thr Thr Leu Val Thr Leu Ala Asp Gly Thr Glu Tyr Asp Leu Gly Gly
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 Glu Trp Lys Val Ile Glu Met Tyr Pro Ser Leu Asn Glu Ala Leu Ala
 340 345 350
 Arg Lys Phe Pro Gly Gln Pro Glu Val Thr Ile Asp Ser Thr Val Glu
 355 360 365
 Glu Leu Arg Glu Ile Ala Lys Val Ile Gly Leu Ser Val Pro Glu Asn
 370 375 380
 Gly Gly Trp Gly His Gly Lys Leu Val Glu Glu Ile Trp Glu Leu Leu
 385 390 395 400
 Cys Glu Asp Gln Leu Tyr Gly Pro Ile Phe Val Lys Asp Phe Pro Val
 405 410 415
 Glu Thr Phe Pro Leu Thr Arg Gln His Arg Thr Lys Pro Gly Val Thr
 420 425 430
 Glu Lys Trp Asp Leu Tyr Val Arg Gly Phe Glu Leu Ala Thr Gly Tyr
 435 440 445
 Ser Glu Leu Ile Asp Pro Val Ile Gln Arg Glu Arg Phe Glu Gly Gln
 450 455 460
 Ala Arg Leu Ala Ala Asp Gly Asp Asp Glu Ala Met Val Leu Asp Glu
 465 470 475 480
 Asp Phe Leu Thr Ala Met Glu Gln Gly Met Pro Pro Thr Ser Gly Asn
 485 490 495
 Gly Met Gly Ile Asp Arg Leu Leu Met Ala Leu Thr Gly Leu Gly Ile
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<211> 619

<212> DNA

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<220>

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 Val Leu Lys Phe Ser
 1 5

ctc aac ctg ctg gac gat atc cgc cca cgc gca atg tcg cgc gat atc 163
 Leu Asn Leu Leu Asp Asp Ile Arg Pro Arg Ala Met Ser Arg Asp Ile
 10 15 20

gac tgg ggc atc cca atc cca gtt gaa gga tgg caa gac aac aac gcc 211
 Asp Trp Gly Ile Pro Ile Pro Val Glu Gly Trp Gln Asp Asn Asn Ala
 25 30 35

aag aag ctc tac gtc tgg ttc gac gct gtc gtg ggc tac ttg tcc gca 259
 Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val Gly Tyr Leu Ser Ala
 40 45 50

tcc atc gaa tgg gcc tac cgc tcc ggc gac cca gaa gca tgg cgc acc 307
 Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro Glu Ala Trp Arg Thr
 55 60 65

ttc tgg aat gat cca gaa acc aag tcc tac tac ttc atg ggc aaa gac 355
 Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Tyr Phe Met Gly Lys Asp
 70 75 80 85

aac atc acc ttc cac tcc cag atc tgg cca gcg gag ctt ctc ggc tac 403
 Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala Glu Leu Leu Gly Tyr
 90 95 100

gca ggc aag ggc tcc cgc ggt gga gaa atc ggt gac ctg ggt gtt ctg 451
 Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly Asp Leu Gly Val Leu
 105 110 115

aac ctg cct act gag gtt gtt tcc tct gag ttc ctg act atg tct gga 499
 Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe Leu Thr Met Ser Gly
 120 125 130

tcc aag ttc tcc tca tcc aag ggc gtt gtc atc tac gtg aag gac ttc 547
 Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile Tyr Val Lys Asp Phe
 135 140 145

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Gln Asp Asn Asn Ala Lys Lys Leu Tyr Val Trp Phe Asp Ala Val Val
 35 40 45

Gly Tyr Leu Ser Ala Ser Ile Glu Trp Ala Tyr Arg Ser Gly Asp Pro
 50 55 60

Glu Ala Trp Arg Thr Phe Trp Asn Asp Pro Glu Thr Lys Ser Tyr Tyr

65	70	75	80
Phe Met Gly Lys Asp Asn Ile Thr Phe His Ser Gln Ile Trp Pro Ala	85	90	95
Glu Leu Leu Gly Tyr Ala Gly Lys Gly Ser Arg Gly Gly Glu Ile Gly	100	105	110
Asp Leu Gly Val Leu Asn Leu Pro Thr Glu Val Val Ser Ser Glu Phe	115	120	125
Leu Thr Met Ser Gly Ser Lys Phe Ser Ser Ser Lys Gly Val Val Ile	130	135	140
Tyr Val Lys Asp Phe Leu Lys Glu Phe Gly Pro Asp Ala Leu Arg Tyr	145	150	155
Phe Ile Ala Ala Arg Pro Arg Asn Asn Asp Thr Asp Phe	165	170	
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Met Ala Gly Leu Val 5			
gac tta aca ata aac atg agg gaa ggg ctg gac tac acg gtg tcc gaa 163			
Asp Leu Thr Ile Asn Met Arg Glu Gly Leu Asp Tyr Thr Val Ser Glu 20			
att cag ttg acc gaa gcc agt ttg aac gag gcg gcc gac gcc gcg atc 211			
Ile Gln Leu Thr Glu Ala Ser Leu Asn Glu Ala Ala Asp Ala Ala Ile 35			
aag gct ttc gac ggt gca caa aac cta gat gaa ctc gca gca cta cgc 259			
Lys Ala Phe Asp Gly Ala Gln Asn Leu Asp Glu Leu Ala Ala Leu Arg 50			
cgc gat cac ttg ggt gat gcc gca cct att ccg cag gca cga cgc tca 307			
Arg Asp His Leu Gly Asp Ala Ala Pro Ile Pro Gln Ala Arg Arg Ser 65			
ttg gga act att cct aaa gat cag cgc aag gat gcg ggc cgc ttt gtc 355			
Leu Gly Thr Ile Pro Lys Asp Gln Arg Lys Asp Ala Gly Arg Phe Val 85			
aac atg gca ctt ggt cgc gca gaa aag cac ttt gct cag gtc aag gtt 403			
Asn Met Ala Leu Gly Arg Ala Glu Lys His Phe Ala Gln Val Lys Val 100			

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Val Leu Glu Glu Lys Arg Asn Ala Glu Val Leu Glu Leu Glu Arg Val	
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gac gtc acc gtt cca acc acc cgc gag cag gtt ggt gcg ctg cac ccc	499
Asp Val Thr Val Pro Thr Thr Arg Glu Gln Val Gly Ala Leu His Pro	
120 125 130	
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Ile Thr Ile Leu Asn Glu Gln Ile Ala Asp Ile Phe Val Gly Met Gly	
135 140 145	
tgg gaa atc gcc gag ggc cca gag gtg gaa gca gaa tac ttc aac ttc	595
Trp Glu Ile Ala Glu Gly Pro Glu Val Glu Ala Glu Tyr Phe Asn Phe	
150 155 160 165	
gac gca ctg aac ttc ctg cct gat cac cca gct cgt aca ctg cag gac	643
Asp Ala Leu Asn Phe Leu Pro Asp His Pro Ala Arg Thr Leu Gln Asp	
170 175 180	
acc ttc cac att gcg ccg gaa ggc tcc cgc cag gtg ctg cgt acc cac	691
Thr Phe His Ile Ala Pro Glu Gly Ser Arg Gln Val Leu Arg Thr His	
185 190 195	
acc tca cca gtt cag gtg cgc acc atg ctc aac cgt gaa gtt ccg atc	739
Thr Ser Pro Val Gln Val Arg Thr Met Leu Asn Arg Glu Val Pro Ile	
200 205 210	
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Tyr Ile Ala Cys Pro Gly Arg Val Phe Arg Thr Asp Glu Leu Asp Ala	
215 220 225	
aca cac acc cct gtg ttc cac cag atc gaa ggc ctt gca gtt gat aag	835
Thr His Thr Pro Val Phe His Gln Ile Glu Gly Leu Ala Val Asp Lys	
230 235 240 245	
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Gly Leu Thr Met Ala His Leu Arg Gly Thr Leu Asp His Leu Ala Lys	
250 255 260	
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Glu Leu Phe Gly Pro Glu Thr Lys Thr Arg Met Arg Ser Asn Tyr Phe	
265 270 275	
cca ttc acc gag cct tcc gct gag gtt gat gtg tgg ttc cct aac aag	979
Pro Phe Thr Glu Pro Ser Ala Glu Val Asp Val Trp Phe Pro Asn Lys	
280 285 290	
aag ggt ggt gca ggc tgg atc gag tgg ggt ggc tgt ggc atg gtc aac	1027
Lys Gly Gly Ala Gly Trp Ile Glu Trp Gly Gly Cys Gly Met Val Asn	
295 300 305	
cca aac gtg ctt cgt gcc gtg ggt gtt gac cca gag gag tac acc gga	1075
Pro Asn Val Leu Arg Ala Val Gly Val Asp Pro Glu Glu Tyr Thr Gly	
310 315 320 325	
ttc gcg ttc ggc atg ggc att gaa cgt acc ctg cag ttc cgc aac ggc	1123
Phe Ala Phe Gly Met Gly Ile Glu Arg Thr Leu Gln Phe Arg Asn Gly	
330 335 340	

ctg agc gat atg cgc gac atg gtt gag ggc gat att cgc ttc acc ctc 1171
 Leu Ser Asp Met Arg Asp Met Val Glu Gly Asp Ile Arg Phe Thr Leu
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 Pro Phe Gly Ile Gln Ala
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<212> PRT

<213> Corynebacterium glutamicum

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Tyr Thr Val Ser Glu Ile Gln Leu Thr Glu Ala Ser Leu Asn Glu Ala
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 35 40 45

Leu Ala Ala Leu Arg Arg Asp His Leu Gly Asp Ala Ala Pro Ile Pro
 50 55 60

Gln Ala Arg Arg Ser Leu Gly Thr Ile Pro Lys Asp Gln Arg Lys Asp
 65 70 75 80

Ala Gly Arg Phe Val Asn Met Ala Leu Gly Arg Ala Glu Lys His Phe
 85 90 95

Ala Gln Val Lys Val Val Leu Glu Glu Lys Arg Asn Ala Glu Val Leu
 100 105 110

Glu Leu Glu Arg Val Asp Val Thr Val Pro Thr Thr Arg Glu Gln Val
 115 120 125

Gly Ala Leu His Pro Ile Thr Ile Leu Asn Glu Gln Ile Ala Asp Ile
 130 135 140

Phe Val Gly Met Gly Trp Glu Ile Ala Glu Gly Pro Glu Val Glu Ala
 145 150 155 160

Glu Tyr Phe Asn Phe Asp Ala Leu Asn Phe Leu Pro Asp His Pro Ala
 165 170 175

Arg Thr Leu Gln Asp Thr Phe His Ile Ala Pro Glu Gly Ser Arg Gln
 180 185 190

Val Leu Arg Thr His Thr Ser Pro Val Gln Val Arg Thr Met Leu Asn
 195 200 205

Arg Glu Val Pro Ile Tyr Ile Ala Cys Pro Gly Arg Val Phe Arg Thr
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Asp Glu Leu Asp Ala Thr His Thr Pro Val Phe His Gln Ile Glu Gly
 225 230 235 240

Leu Ala Val Asp Lys Gly Leu Thr Met Ala His Leu Arg Gly Thr Leu

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												Val	Glu	Thr	Ile	Glu	
												1				5	
gag ctc acc gag ttc aag aag ccc atc cgc cac tgc cac gtc aat gtt																163	
Glu	Leu	Thr	Glu	Phe	Lys	Lys	Pro	Ile	Arg	His	Cys	His	Val	Asn	Val		
				10					15					20			
ggc gac gcc aac gga acc ggc gaa ctg cag tcc atc gtt tgt ggc gcc																211	
Gly	Asp	Ala	Asn	Gly	Thr	Gly	Glu	Leu	Gln	Ser	Ile	Val	Cys	Gly	Ala		
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cgc aac ttc aag gaa ggc gac acc gtt gtc gtg tcc ctt cct ggc gct																259	
Arg	Asn	Phe	Lys	Glu	Gly	Asp	Thr	Val	Val	Val	Ser	Leu	Pro	Gly	Ala		
				40					45					50			
gtg ctg cct ggc gat ttc gcg atc tct gct cgt gaa act tac gga cgc																307	
Val	Leu	Pro	Gly	Asp	Phe	Ala	Ile	Ser	Ala	Arg	Glu	Thr	Tyr	Gly	Arg		
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atg tct gca ggc atg atc tgt tct gcc tct gag ctg ggt ctt gct gat																355	
Met	Ser	Ala	Gly	Met	Ile	Cys	Ser	Ala	Ser	Glu	Leu	Gly	Leu	Ala	Asp		
				70					75					80	85		

aag cag aac tcc ggc atc atc acc ctg gat cct tct tac ggc gag cct	403
Lys Gln Asn Ser Gly Ile Ile Thr Leu Asp Pro Ser Tyr Gly Glu Pro	
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ggc gaa gac gca cgt caa gca ctg gga ctt gaa gat acc gtt ttc gat	451
Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu Asp Thr Val Phe Asp	
105 110 115	
gtc aac gtc acc cca gac cgc ggt tac gca ctg tct gct cgt ggc ctg	499
Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu Ser Ala Arg Gly Leu	
120 125 130	
acc cgc gaa ctg gca tcg gct ttc agc ctg acc ttc acc gac cct gcg	547
Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr Phe Thr Asp Pro Ala	
135 140 145	
atc gag cca gct gta gca ggc att gag gtc aag gtc cca gca gtt gaa	595
Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys Val Pro Ala Val Glu	
150 155 160 165	
ggt tcc ttg att aac gtg gag ctg cgt gaa gag acc aag gca atc cgt	643
Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu Thr Lys Ala Ile Arg	
170 175 180	
ttc ggt ctg cgt aaa gtc tct ggc att gat cca gca gca gaa tcc cca	691
Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro Ala Ala Glu Ser Pro	
185 190 195	
ttc tgg atg cag cgt gaa ctc atg ctc tct ggt cag cga cca gtc aac	739
Phe Trp Met Gln Arg Glu Leu Met Leu Ser Gly Gln Arg Pro Val Asn	
200 205 210	
gcc gcc acc gac gtc acc aac tac gtc atg ttg ctg ctc ggc cag ccg	787
Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu Leu Leu Gly Gln Pro	
215 220 225	
atg cat gct ttc gac gca gcc aag gtt act ggc gat ctt gtt gtc cgc	835
Met His Ala Phe Asp Ala Ala Lys Val Thr Gly Asp Leu Val Val Arg	
230 235 240 245	
aac gca act gca ggc gag aag ttc gaa acc ctc gat cac gtc aag cgc	883
Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu Asp His Val Lys Arg	
250 255 260	
acc ctc aat gag gaa gac gtt gtg atc acc gat gac aac ggc att cag	931
Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp Asp Asn Gly Ile Gln	
265 270 275	
tct ttg gct ggc gtt atg ggt ggt ctc acc tcc gag atc tct gac acc	979
Ser Leu Ala Gly Val Met Gly Gly Leu Thr Ser Glu Ile Ser Asp Thr	
280 285 290	
acc acc gat gtc tac ttc gag gcc gca acc tgg gac acc atc acc gtt	1027
Thr Thr Asp Val Tyr Phe Glu Ala Ala Thr Trp Asp Thr Ile Thr Val	
295 300 305	
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Ala Arg Thr Ser Arg Arg His Lys Leu Ser Ser Glu Ala Ser Arg Arg	
310 315 320 325	
ttc gag cgt ggc gtt gac cct gcg atc gtg gaa atc gcc ctc gat atc	1123

Phe	Glu	Arg	Gly	Val	Asp	Pro	Ala	Ile	Val	Glu	Ile	Ala	Leu	Asp	Ile	
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gca	gca	acc	ctt	ctc	gtg	gag	atc	gca	ggc	ggc	acc	gtc	gat	gcg	ggt	1171
Ala	Ala	Thr	Leu	Leu	Val	Glu	Ile	Ala	Gly	Gly	Thr	Val	Asp	Ala	Gly	
			345					350					355			
cgc	acc	ctc	gtt	ggt	gat	gtc	cct	gcc	atg	caa	ccc	atc	acc	atg	aag	1219
Arg	Thr	Leu	Val	Gly	Asp	Val	Pro	Ala	Met	Gln	Pro	Ile	Thr	Met	Lys	
		360					365					370				
gtc	act	cga	cct	tcc	gag	ctc	gca	ggc	gtg	gat	tat	tcc	gca	gaa	act	1267
Val	Thr	Arg	Pro	Ser	Glu	Leu	Ala	Gly	Val	Asp	Tyr	Ser	Ala	Glu	Thr	
	375					380				385						
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Val	Ile	Ala	Arg	Leu	Glu	Glu	Val	Gly	Cys	Thr	Val	Ala	Val	Ser	Gly	
390					395				400						405	
gac	acc	ttg	gaa	gta	acc	cct	cca	acc	tgg	cgc	ggt	gac	ctc	acc	atg	1363
Asp	Thr	Leu	Glu	Val	Thr	Pro	Pro	Thr	Trp	Arg	Gly	Asp	Leu	Thr	Met	
			410					415					420			
tcc	gct	gac	ctc	gtg	gaa	gaa	gta	ctc	cgc	ctc	gaa	ggt	ttg	gaa	gca	1411
Ser	Ala	Asp	Leu	Val	Glu	Glu	Val	Leu	Arg	Leu	Glu	Gly	Leu	Glu	Ala	
			425				430						435			
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Ile	Pro	Thr	Ile	Ile	Pro	Thr	Ala	Pro	Ala	Gly	Arg	Gly	Leu	Thr	Asp	
		440					445					450				
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Ala	Gln	Lys	Arg	Arg	Arg	Ala	Val	Gly	His	Ala	Leu	Ala	Tyr	Ala	Gly	
	455					460					465					
tac	gcc	gaa	atc	atc	cca	agc	cca	ttc	atg	gac	cca	gag	gtc	ttc	gat	1555
Tyr	Ala	Glu	Ile	Ile	Pro	Ser	Pro	Phe	Met	Asp	Pro	Glu	Val	Phe	Asp	
470					475					480					485	
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Val	Trp	Gly	Leu	Ala	Ala	Asp	Asp	Glu	Arg	Arg	Lys	Thr	Val	Ser	Val	
			490					495						500		
ctc	aac	cca	ctt	gag	gca	gaa	cgc	aac	gtc	ctg	agc	acc	tcc	ttg	ctg	1651
Leu	Asn	Pro	Leu	Glu	Ala	Glu	Arg	Asn	Val	Leu	Ser	Thr	Ser	Leu	Leu	
			505					510					515			
ccc	tcc	atg	ctc	gat	gct	gtc	aag	cgc	aac	gtt	gca	cgt	gga	cac	aac	1699
Pro	Ser	Met	Leu	Asp	Ala	Val	Lys	Arg	Asn	Val	Ala	Arg	Gly	His	Asn	
		520					525					530				
gat	ttc	tcc	ctg	ttc	ggc	ctg	cag	cag	gtc	gcc	ttc	gag	cac	gga	tcc	1747
Asp	Phe	Ser	Leu	Phe	Gly	Leu	Gln	Gln	Val	Ala	Phe	Glu	His	Gly	Ser	
	535					540					545					
ggc	gtt	tcc	cca	atg	cca	tct	gtt	gct	tca	cgc	cct	gaa	gag	tct	gtc	1795
Gly	Val	Ser	Pro	Met	Pro	Ser	Val	Ala	Ser	Arg	Pro	Glu	Glu	Ser	Val	
550					555					560					565	
gtg	gca	gaa	ctg	gtg	gat	tca	ctg	cca	aac	cag	cca	ctg	cat	gtc	gca	1843
Val	Ala	Glu	Leu	Val	Asp	Ser	Leu	Pro	Asn	Gln	Pro	Leu	His	Val	Ala	

570										575					580					
acc	gtg	ggc	acc	ggc	aac	atc	gag	ttc	gaa	ggc	cca	tg	ggc	aag	ggc	1891				
Thr	Val	Gly	Thr	Gly	Asn	Ile	Glu	Phe	Glu	Gly	Pro	Trp	Gly	Lys	Gly					
			585					590					595							
cgc	gcc	tac	acc	ttc	ggc	gac	gcg	att	gaa	tcc	gcg	cgc	gca	gtc	gcc	1939				
Arg	Ala	Tyr	Thr	Phe	Ala	Asp	Ala	Ile	Glu	Ser	Ala	Arg	Ala	Val	Ala					
		600					605					610								
cgc	gct	gct	ggc	gtc	acc	ttg	gag	ctg	gcc	aac	gcc	gac	gcg	ctt	cct	1987				
Arg	Ala	Ala	Gly	Val	Thr	Leu	Glu	Leu	Ala	Asn	Ala	Asp	Ala	Leu	Pro					
	615					620					625									
tg	cac	cca	ggt	cgt	tgc	gcc	gca	ttg	ctt	atc	gac	ggt	acc	ccc	gtc	2035				
Trp	His	Pro	Gly	Arg	Cys	Ala	Ala	Leu	Leu	Ile	Asp	Gly	Thr	Pro	Val					
630					635					640					645					
ggt	tac	gct	ggc	gaa	ctt	cac	cca	cag	atc	ctg	gaa	aag	gcc	ggt	cta	2083				
Gly	Tyr	Ala	Gly	Glu	Leu	His	Pro	Gln	Ile	Leu	Glu	Lys	Ala	Gly	Leu					
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cca	gca	cgc	acc	tgt	gca	atg	gaa	ctg	gat	ctc	agc	gca	ctg	cca	ctg	2131				
Pro	Ala	Arg	Thr	Cys	Ala	Met	Glu	Leu	Asp	Leu	Ser	Ala	Leu	Pro	Leu					
			665					670					675							
gta	gaa	aac	ctc	cca	gcg	cca	gtc	ctg	tcc	tcc	ttc	cca	gca	ctg	cac	2179				
Val	Glu	Asn	Leu	Pro	Ala	Pro	Val	Leu	Ser	Ser	Phe	Pro	Ala	Leu	His					
		680					685					690								
caa	gac	atc	gcc	cta	gtt	gtg	gat	gag	acc	atc	ccg	gcc	gaa	gat	gtc	2227				
Gln	Asp	Ile	Ala	Leu	Val	Val	Asp	Glu	Thr	Ile	Pro	Ala	Glu	Asp	Val					
	695					700					705									
cgc	gca	gtt	gtc	gaa	ggc	ggc	ggc	gaa	ctg	atc	gaa	acg	gtc	gag		2275				
Arg	Ala	Val	Val	Glu	Ala	Gly	Ala	Gly	Glu	Leu	Ile	Glu	Thr	Val	Glu					
710					715				720					725						
ctt	ttc	cac	gtc	ttc	cgc	tcc	gaa	cag	cgc	ggc	gag	aac	aag	aaa	tcc	2323				
Leu	Phe	His	Val	Phe	Arg	Ser	Glu	Gln	Arg	Gly	Glu	Asn	Lys	Lys	Ser					
			730						735					740						
ctc	gcg	ttc	tcc	ctg	cgt	ttc	cgc	gca	gcc	ggc	cgc	acc	ctc	acc	gat	2371				
Leu	Ala	Phe	Ser	Leu	Arg	Phe	Arg	Ala	Ala	Gly	Arg	Thr	Leu	Thr	Asp					
			745					750					755							
gag	gaa	gcc	aac	gaa	gca	cga	ctt	cag	gca	gca	gag	cta	gca	aag	gag	2419				
Glu	Glu	Ala	Asn	Glu	Ala	Arg	Leu	Gln	Ala	Ala	Glu	Leu	Ala	Lys	Glu					
		760					765					770								
aaa	ttc	aac	gct	gaa	atg	cgt	ggc	tagtttcaca	taggttctat	agg						2466				
Lys	Phe	Asn	Ala	Glu	Met	Arg	Gly													
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<211> 781

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

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Ile	Val	Cys	Gly	Ala	Arg	Asn	Phe	Lys	Glu	Gly	Asp	Thr	Val	Val	Val	
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Ser	Leu	Pro	Gly	Ala	Val	Leu	Pro	Gly	Asp	Phe	Ala	Ile	Ser	Ala	Arg	
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Glu	Thr	Tyr	Gly	Arg	Met	Ser	Ala	Gly	Met	Ile	Cys	Ser	Ala	Ser	Glu	
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Leu	Gly	Leu	Ala	Asp	Lys	Gln	Asn	Ser	Gly	Ile	Ile	Thr	Leu	Asp	Pro	
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Ser	Tyr	Gly	Glu	Pro	Gly	Glu	Asp	Ala	Arg	Gln	Ala	Leu	Gly	Leu	Glu	
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Asp	Thr	Val	Phe	Asp	Val	Asn	Val	Thr	Pro	Asp	Arg	Gly	Tyr	Ala	Leu	
		115					120					125				
Ser	Ala	Arg	Gly	Leu	Thr	Arg	Glu	Leu	Ala	Ser	Ala	Phe	Ser	Leu	Thr	
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Phe	Thr	Asp	Pro	Ala	Ile	Glu	Pro	Ala	Val	Ala	Gly	Ile	Glu	Val	Lys	
145					150					155					160	
Val	Pro	Ala	Val	Glu	Gly	Ser	Leu	Ile	Asn	Val	Glu	Leu	Arg	Glu	Glu	
				165					170					175		
Thr	Lys	Ala	Ile	Arg	Phe	Gly	Leu	Arg	Lys	Val	Ser	Gly	Ile	Asp	Pro	
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Ala	Ala	Glu	Ser	Pro	Phe	Trp	Met	Gln	Arg	Glu	Leu	Met	Leu	Ser	Gly	
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Gln	Arg	Pro	Val	Asn	Ala	Ala	Thr	Asp	Val	Thr	Asn	Tyr	Val	Met	Leu	
	210				215						220					
Leu	Leu	Gly	Gln	Pro	Met	His	Ala	Phe	Asp	Ala	Ala	Lys	Val	Thr	Gly	
225					230					235					240	
Asp	Leu	Val	Val	Arg	Asn	Ala	Thr	Ala	Gly	Glu	Lys	Phe	Glu	Thr	Leu	
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Asp	His	Val	Lys	Arg	Thr	Leu	Asn	Glu	Glu	Asp	Val	Val	Ile	Thr	Asp	
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Asp	Asn	Gly	Ile	Gln	Ser	Leu	Ala	Gly	Val	Met	Gly	Gly	Leu	Thr	Ser	
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Glu	Ile	Ser	Asp	Thr	Thr	Thr	Asp	Val	Tyr	Phe	Glu	Ala	Ala	Thr	Trp	
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Asp	Thr	Ile	Thr	Val	Ala	Arg	Thr	Ser	Arg	Arg	His	Lys	Leu	Ser	Ser	
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Glu	Ala	Ser	Arg	Arg	Phe	Glu	Arg	Gly	Val	Asp	Pro	Ala	Ile	Val	Glu	

325										330					335				
Ile	Ala	Leu	Asp	Ile	Ala	Ala	Thr	Leu	Leu	Val	Glu	Ile	Ala	Gly	Gly				
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Thr	Val	Asp	Ala	Gly	Arg	Thr	Leu	Val	Gly	Asp	Val	Pro	Ala	Met	Gln				
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Pro	Ile	Thr	Met	Lys	Val	Thr	Arg	Pro	Ser	Glu	Leu	Ala	Gly	Val	Asp				
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Tyr	Ser	Ala	Glu	Thr	Val	Ile	Ala	Arg	Leu	Glu	Glu	Val	Gly	Cys	Thr				
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Val	Ala	Val	Ser	Gly	Asp	Thr	Leu	Glu	Val	Thr	Pro	Pro	Thr	Trp	Arg				
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Gly	Asp	Leu	Thr	Met	Ser	Ala	Asp	Leu	Val	Glu	Glu	Val	Leu	Arg	Leu				
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Glu	Gly	Leu	Glu	Ala	Ile	Pro	Thr	Ile	Ile	Pro	Thr	Ala	Pro	Ala	Gly				
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Arg	Gly	Leu	Thr	Asp	Ala	Gln	Lys	Arg	Arg	Arg	Ala	Val	Gly	His	Ala				
	450					455					460								
Leu	Ala	Tyr	Ala	Gly	Tyr	Ala	Glu	Ile	Ile	Pro	Ser	Pro	Phe	Met	Asp				
465					470					475					480				
Pro	Glu	Val	Phe	Asp	Val	Trp	Gly	Leu	Ala	Ala	Asp	Asp	Glu	Arg	Arg				
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Lys	Thr	Val	Ser	Val	Leu	Asn	Pro	Leu	Glu	Ala	Glu	Arg	Asn	Val	Leu				
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Ser	Thr	Ser	Leu	Leu	Pro	Ser	Met	Leu	Asp	Ala	Val	Lys	Arg	Asn	Val				
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Ala	Arg	Gly	His	Asn	Asp	Phe	Ser	Leu	Phe	Gly	Leu	Gln	Gln	Val	Ala				
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Phe	Glu	His	Gly	Ser	Gly	Val	Ser	Pro	Met	Pro	Ser	Val	Ala	Ser	Arg				
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Pro	Leu	His	Val	Ala	Thr	Val	Gly	Thr	Gly	Asn	Ile	Glu	Phe	Glu	Gly				
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Pro	Trp	Gly	Lys	Gly	Arg	Ala	Tyr	Thr	Phe	Ala	Asp	Ala	Ile	Glu	Ser				
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Ala	Asp	Ala	Leu	Pro	Trp	His	Pro	Gly	Arg	Cys	Ala	Ala	Leu	Leu	Ile				
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Asp	Gly	Thr	Pro	Val	Gly	Tyr	Ala	Gly	Glu	Leu	His	Pro	Gln	Ile	Leu				
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Glu Lys Ala Gly Leu Pro Ala Arg Thr Cys Ala Met Glu Leu Asp Leu
 660 665 670
 Ser Ala Leu Pro Leu Val Glu Asn Leu Pro Ala Pro Val Leu Ser Ser
 675 680 685
 Phe Pro Ala Leu His Gln Asp Ile Ala Leu Val Val Asp Glu Thr Ile
 690 695 700
 Pro Ala Glu Asp Val Arg Ala Val Val Glu Ala Gly Ala Gly Glu Leu
 705 710 715 720
 Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg Gly
 725 730 735
 Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala Gly
 740 745 750
 Arg Thr Leu Thr Asp Glu Glu Ala Asn Glu Ala Arg Leu Gln Ala Ala
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA01583

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 Val Glu Thr Ile Glu 5
 1
 gag ctc acc gag ttc aag aag ccc atc cgc cac tgc cac gtc aat gtt 163
 Glu Leu Thr Glu Phe Lys Lys Pro Ile Arg His Cys His Val Asn Val 20
 10 15
 ggc gac gcc aac gga acc ggc gaa ctg cag tcc atc gtt tgt ggc gcc 211
 Gly Asp Ala Asn Gly Thr Gly Glu Leu Gln Ser Ile Val Cys Gly Ala 35
 25 30
 cgc aac ttc aag gaa ggc gac acc gtt gtc gtg tcc ctt cct ggc gct 259
 Arg Asn Phe Lys Glu Gly Asp Thr Val Val Val Ser Leu Pro Gly Ala 50
 40 45
 gtg ctg cct ggc gat ttc gcg atc tct gct cgt gaa act tac gga cgc 307
 Val Leu Pro Gly Asp Phe Ala Ile Ser Ala Arg Glu Thr Tyr Gly Arg 65
 55 60
 atg tct gca ggc atg atc tgt tct gcc tct gag ctg ggt ctt gct gat 355
 Met Ser Ala Gly Met Ile Cys Ser Ala Ser Glu Leu Gly Leu Ala Asp

70	75	80	85	
aag cag aac tcc ggc atc atc acc ctg gat cct tct tac ggc gag cct				403
Lys Gln Asn Ser Gly Ile Ile Thr Leu Asp Pro Ser Tyr Gly Glu Pro	90	95	100	
ggc gaa gac gca cgt caa gca ctg gga ctt gaa gat acc gtt ttc gat				451
Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu Asp Thr Val Phe Asp	105	110	115	
gtc aac gtc acc cca gac cgc ggt tac gca ctg tct gct cgt ggc ctg				499
Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu Ser Ala Arg Gly Leu	120	125	130	
acc cgc gaa ctg gca tcg gct ttc agc ctg acc ttc acc gac cct gcg				547
Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr Phe Thr Asp Pro Ala	135	140	145	
atc gag cca gct gta gca ggc att gag gtc aag gtc cca gca gtt gaa				595
Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys Val Pro Ala Val Glu	150	155	160	165
ggt tcc ttg att aac gtg gag ctg cgt gaa gag acc aag gca atc cgt				643
Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu Thr Lys Ala Ile Arg	170	175	180	
ttc ggt ctg cgt aaa gtc tct ggc att gat cca gca gca gaa tcc cca				691
Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro Ala Ala Glu Ser Pro	185	190	195	
ttc tgg atg cag cgt gaa ctc atg ctc tct ggt cag cga cca gtc aac				739
Phe Trp Met Gln Arg Glu Leu Met Leu Ser Gly Gln Arg Pro Val Asn	200	205	210	
gcc gcc acc gac gtc acc aac tac gtc atg ttg ctg ctc ggc cag ccg				787
Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu Leu Leu Gly Gln Pro	215	220	225	
atg cat gct ttc gac gca gcc aag gtt act ggc gat ctt gtt gtc cgc				835
Met His Ala Phe Asp Ala Ala Lys Val Thr Gly Asp Leu Val Val Arg	230	235	240	245
aac gca act gca ggc gag aag ttc gaa acc ctc gat cac gtc aag cgc				883
Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu Asp His Val Lys Arg	250	255	260	
acc ctc aat gag gaa gac gtt gtg atc acc gat gac aac ggc att cag				931
Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp Asp Asn Gly Ile Gln	265	270	275	
tct ttg gct ggc gtt atg ggt ggt ctc acc tcc gag atc tct gac acc				979
Ser Leu Ala Gly Val Met Gly Gly Leu Thr Ser Glu Ile Ser Asp Thr	280	285	290	
acc acc gat gtc tac ttc gag gcc gca acc tgg gac acc atc acc gtt				1027
Thr Thr Asp Val Tyr Phe Glu Ala Ala Thr Trp Asp Thr Ile Thr Val	295	300	305	
gcg cgc acc tca cgt cgc cac aag ttg agc tcc gaa gct tct cga cgt				1075
Ala Arg Thr Ser Arg Arg His Lys Leu Ser Ser Glu Ala Ser Arg Arg	310	315	320	325

ttc gag cgt ggc gtt gac cct gcg atc gtg gaa atc gcc ctc gat atc	1123
Phe Glu Arg Gly Val Asp Pro Ala Ile Val Glu Ile Ala Leu Asp Ile	
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gca gca acc ctt ctc gtg gag atc gca ggc ggc acc gtc gat gcg ggt	1171
Ala Ala Thr Leu Leu Val Glu Ile Ala Gly Gly Thr Val Asp Ala Gly	
345 350 355	
cgc acc ctc gtt ggt gat gtc cct gcc atg caa ccc atc acc atg aag	1219
Arg Thr Leu Val Gly Asp Val Pro Ala Met Gln Pro Ile Thr Met Lys	
360 365 370	
gtc act cga cct tcc gag ctc gca ggc gtg gat tat tcc gca gaa act	1267
Val Thr Arg Pro Ser Glu Leu Ala Gly Val Asp Tyr Ser Ala Glu Thr	
375 380 385	
gtg atc gct cgt ctg gaa gag gtc gga tgc acc gtc gct gtt tcc ggc	1315
Val Ile Ala Arg Leu Glu Glu Val Gly Cys Thr Val Ala Val Ser Gly	
390 395 400 405	
gac acc ttg gaa gta acc cct cca acc tgg cgc ggt gac ctc acc atg	1363
Asp Thr Leu Glu Val Thr Pro Pro Thr Trp Arg Gly Asp Leu Thr Met	
410 415 420	
tcc gct gac ctc gtg gaa gaa gta ctc cgc ctc gaa ggt ttg gaa gca	1411
Ser Ala Asp Leu Val Glu Glu Val Leu Arg Leu Glu Gly Leu Glu Ala	
425 430 435	
att cca acc atc atc cca acc gca cca gca ggc cgt gga cta acc gat	1459
Ile Pro Thr Ile Ile Pro Thr Ala Pro Ala Gly Arg Gly Leu Thr Asp	
440 445 450	
gca cag aag cgc cgc cgc gcc gtt ggc cac gct ttg gct tac gct ggc	1507
Ala Gln Lys Arg Arg Arg Ala Val Gly His Ala Leu Ala Tyr Ala Gly	
455 460 465	
tac gcc gaa atc atc cca agc cca ttc atg gac cca gag gtc ttc gat	1555
Tyr Ala Glu Ile Ile Pro Ser Pro Phe Met Asp Pro Glu Val Phe Asp	
470 475 480 485	
gta tgg gga ctc gca gca gac gac gag cgc cgc aag acc gtt tcc gtt	1603
Val Trp Gly Leu Ala Ala Asp Asp Glu Arg Arg Lys Thr Val Ser Val	
490 495 500	
ctc aac cca ctt gag gca gaa cgc aac gtc ctg agc acc tcc ttg ctg	1651
Leu Asn Pro Leu Glu Ala Glu Arg Asn Val Leu Ser Thr Ser Leu Leu	
505 510 515	
ccc tcc atg ctc gat gct gtc aag cgc aac gtt gca cgt gga cac aac	1699
Pro Ser Met Leu Asp Ala Val Lys Arg Asn Val Ala Arg Gly His Asn	
520 525 530	
gat ttc tcc ctg ttc ggc ctg cag cag gtc gcc ttc gag cac gga tcc	1747
Asp Phe Ser Leu Phe Gly Leu Gln Gln Val Ala Phe Glu His Gly Ser	
535 540 545	
ggc gtt tcc cca atg cca tct gtt gct tca cgc cct gaa gag tct gtc	1795
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 Val Ala Glu Leu Val Asp Ser
 570

1816

<210> 322
 <211> 572
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 322
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 20 25 30
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 35 40 45
 Ser Leu Pro Gly Ala Val Leu Pro Gly Asp Phe Ala Ile Ser Ala Arg
 50 55 60
 Glu Thr Tyr Gly Arg Met Ser Ala Gly Met Ile Cys Ser Ala Ser Glu
 65 70 75 80
 Leu Gly Leu Ala Asp Lys Gln Asn Ser Gly Ile Ile Thr Leu Asp Pro
 85 90 95
 Ser Tyr Gly Glu Pro Gly Glu Asp Ala Arg Gln Ala Leu Gly Leu Glu
 100 105 110
 Asp Thr Val Phe Asp Val Asn Val Thr Pro Asp Arg Gly Tyr Ala Leu
 115 120 125
 Ser Ala Arg Gly Leu Thr Arg Glu Leu Ala Ser Ala Phe Ser Leu Thr
 130 135 140
 Phe Thr Asp Pro Ala Ile Glu Pro Ala Val Ala Gly Ile Glu Val Lys
 145 150 155 160
 Val Pro Ala Val Glu Gly Ser Leu Ile Asn Val Glu Leu Arg Glu Glu
 165 170 175
 Thr Lys Ala Ile Arg Phe Gly Leu Arg Lys Val Ser Gly Ile Asp Pro
 180 185 190
 Ala Ala Glu Ser Pro Phe Trp Met Gln Arg Glu Leu Met Leu Ser Gly
 195 200 205
 Gln Arg Pro Val Asn Ala Ala Thr Asp Val Thr Asn Tyr Val Met Leu
 210 215 220
 Leu Leu Gly Gln Pro Met His Ala Phe Asp Ala Ala Lys Val Thr Gly
 225 230 235 240
 Asp Leu Val Val Arg Asn Ala Thr Ala Gly Glu Lys Phe Glu Thr Leu
 245 250 255
 Asp His Val Lys Arg Thr Leu Asn Glu Glu Asp Val Val Ile Thr Asp
 260 265 270

Asp Asn Gly Ile Gln Ser Leu Ala Gly Val Met Gly Gly Leu Thr Ser
 275 280 285
 Glu Ile Ser Asp Thr Thr Thr Asp Val Tyr Phe Glu Ala Ala Thr Trp
 290 295 300
 Asp Thr Ile Thr Val Ala Arg Thr Ser Arg Arg His Lys Leu Ser Ser
 305 310 315 320
 Glu Ala Ser Arg Arg Phe Glu Arg Gly Val Asp Pro Ala Ile Val Glu
 325 330 335
 Ile Ala Leu Asp Ile Ala Ala Thr Leu Leu Val Glu Ile Ala Gly Gly
 340 345 350
 Thr Val Asp Ala Gly Arg Thr Leu Val Gly Asp Val Pro Ala Met Gln
 355 360 365
 Pro Ile Thr Met Lys Val Thr Arg Pro Ser Glu Leu Ala Gly Val Asp
 370 375 380
 Tyr Ser Ala Glu Thr Val Ile Ala Arg Leu Glu Glu Val Gly Cys Thr
 385 390 395 400
 Val Ala Val Ser Gly Asp Thr Leu Glu Val Thr Pro Pro Thr Trp Arg
 405 410 415
 Gly Asp Leu Thr Met Ser Ala Asp Leu Val Glu Glu Val Leu Arg Leu
 420 425 430
 Glu Gly Leu Glu Ala Ile Pro Thr Ile Ile Pro Thr Ala Pro Ala Gly
 435 440 445
 Arg Gly Leu Thr Asp Ala Gln Lys Arg Arg Arg Ala Val Gly His Ala
 450 455 460
 Leu Ala Tyr Ala Gly Tyr Ala Glu Ile Ile Pro Ser Pro Phe Met Asp
 465 470 475 480
 Pro Glu Val Phe Asp Val Trp Gly Leu Ala Ala Asp Asp Glu Arg Arg
 485 490 495
 Lys Thr Val Ser Val Leu Asn Pro Leu Glu Ala Glu Arg Asn Val Leu
 500 505 510
 Ser Thr Ser Leu Leu Pro Ser Met Leu Asp Ala Val Lys Arg Asn Val
 515 520 525
 Ala Arg Gly His Asn Asp Phe Ser Leu Phe Gly Leu Gln Gln Val Ala
 530 535 540
 Phe Glu His Gly Ser Gly Val Ser Pro Met Pro Ser Val Ala Ser Arg
 545 550 555 560
 Pro Glu Glu Ser Val Val Ala Glu Leu Val Asp Ser
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<211> 305

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (1)..(282)

<223> FRXA01717

<400> 323

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atc ccg gcg gaa gat gtc cgc gca gtt gtc aaa gcc ggc gcc ggc gaa 96
Ile Pro Ala Glu Asp Val Arg Ala Val Val Lys Ala Gly Ala Gly Glu
             20             25             30

ctg atc gaa acg gtc gag ctt ttc cac gtc ttc cgc tcc gaa cag cgc 144
Leu Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg
             35             40             45

ggc gag aac aag aaa tcc ctc gcg ttc tcc ctg cgt ttc cgc gca gcc 192
Gly Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala
             50             55             60

ggc cgc acc ctc acc gat gag gaa gcc aac gaa gca cga ctt cag gca 240
Gly Arg Thr Leu Thr Asp Glu Glu Ala Asn Glu Ala Arg Leu Gln Ala
             65             70             75             80

gca gag cta gca aag gag aaa ttc aac gct gaa atg cgt ggc 282
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<210> 324

<211> 94

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 324

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Leu Ile Glu Thr Val Glu Leu Phe His Val Phe Arg Ser Glu Gln Arg
             35             40             45

Gly Glu Asn Lys Lys Ser Leu Ala Phe Ser Leu Arg Phe Arg Ala Ala
             50             55             60

Gly Arg Thr Leu Thr Asp Glu Glu Ala Asn Glu Ala Arg Leu Gln Ala
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Ala Glu Leu Ala Lys Glu Lys Phe Asn Ala Glu Met Arg Gly
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<223> RXN01938
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Met Ile Thr Arg Leu																5
1																
tcc acg ctg ttt ttg cgc acc ctg cgc gaa gac cct gca gat gca gaa																163
Ser Thr Leu Phe Leu Arg Thr Leu Arg Glu Asp Pro Ala Asp Ala Glu																20
10 15																
gtt cca agc cac aag ctg ctt gtc cgt gca gga tat atc cgc cga gtt																211
Val Pro Ser His Lys Leu Leu Val Arg Ala Gly Tyr Ile Arg Arg Val																35
25 30																
gcc cca ggt atc tac tcc tgg ttg cca ctg ggt ttg cgc gca gtg cgc																259
Ala Pro Gly Ile Tyr Ser Trp Leu Pro Leu Gly Leu Arg Ala Val Arg																50
40 45																
aac att gaa gct gtc gta cgc gag gaa atg gat gcg atc gga gga cag																307
Asn Ile Glu Ala Val Val Arg Glu Glu Met Asp Ala Ile Gly Gly Gln																65
55 60																
gag ctg ctc ttc cca aca ctc ctg cca cgt gag cct tat gaa acc aca																355
Glu Leu Leu Phe Pro Thr Leu Leu Pro Arg Glu Pro Tyr Glu Thr Thr																85
70 75																
cag cgt tgg aca gaa tac ggc gat tcg ctg ttc cgt ctg aag gac cgc																403
Gln Arg Trp Thr Glu Tyr Gly Asp Ser Leu Phe Arg Leu Lys Asp Arg																100
90 95																
aag ggt gcc gac tac ctg ctc gga cca acc cac gag gaa atg ttc gcc																451
Lys Gly Ala Asp Tyr Leu Leu Gly Pro Thr His Glu Glu Met Phe Ala																115
105 110																
gcc acg gtg aag gat ctg tac aac tcc tac aag gac ttc cca gtc acc																499
Ala Thr Val Lys Asp Leu Tyr Asn Ser Tyr Lys Asp Phe Pro Val Thr																130
120 125																
ttg tac cag atc cag acc aag tac cgc gat gag gaa cgc cca cgc gca																547
Leu Tyr Gln Ile Gln Thr Lys Tyr Arg Asp Glu Glu Arg Pro Arg Ala																145
135 140																
ggc gtg ctc cgc gga cgc gaa ttt gtg atg aag gat tct tac tcc ttc																595
Gly Val Leu Arg Gly Arg Glu Phe Val Met Lys Asp Ser Tyr Ser Phe																165
150 155																
gac atc tcg gat gct ggt ttg gac gag tcc tac gca aag cac cgc gca																643
Asp Ile Ser Asp Ala Gly Leu Asp Glu Ser Tyr Ala Lys His Arg Ala																180
170 175																

gcg tat cag cgc atc ttt gac cgc ctt ggc ttg gaa tac gcc atc tgc	691
Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr Ala Ile Cys	
185 190 195	
cag gca acc tct ggt gcc atg ggc gga tcc gct tcc gag gaa ttc ctt	739
Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu Glu Phe Leu	
200 205 210	
gca gta tct gaa aac ggc gaa gat acc ttc gtg cgc tct acc tcc ggc	787
Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val Arg Ser Thr Ser Gly	
215 220 225	
aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca ggc gtt gag	835
Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro Gly Val Glu	
230 235 240 245	
cgt gac atc gaa ggc ctg cca gaa cca gtc acc tac gaa act cct gtt	883
Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu Thr Pro Val	
250 255 260	
tct gaa acc atc gat gct ttg gtt gat tgg gct aac tcc atc gac gtg	931
Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser Ile Asp Val	
265 270 275	
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Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp Thr Leu Lys Cys Ile	
280 285 290	
gtg gtg aag gtc cgc gag cca ggt gcc gaa gaa gca gaa ctc act gga	1027
Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu Ala Glu Leu Thr Gly	
295 300 305	
atc ttg ctt cca ggt gac cgc gaa gta gac atg aag cgc ctc gag gca	1075
Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met Lys Arg Leu Glu Ala	
310 315 320 325	
tca ctt gag cca gca gaa gtt gaa ctc gca gtg gaa tcc gac ttt gcc	1123
Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val Glu Ser Asp Phe Ala	
330 335 340	
gac aac cca ttc ctg gtc aag ggc tac gtc gga cca gtt ggc ctg gcc	1171
Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly Pro Val Gly Leu Ala	
345 350 355	
aag aac ggc gtg aag gtc ctt gcc gat cct cgc gtt gtc acc ggt acc	1219
Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg Val Val Thr Gly Thr	
360 365 370	
tcc tgg atc acc ggc gcc gat gaa aag gaa cgc cac gtc gta ggc ctc	1267
Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg His Val Val Gly Leu	
375 380 385	
gtc gcc gga cgc gat ttc acc cca gac ggc ttc atc gaa gct gca gaa	1315
Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe Ile Glu Ala Ala Glu	
390 395 400 405	
atc aag gaa ggc gac cca gcg cca gca ggc gag ggc acc ctc acc ctt	1363
Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu Gly Thr Leu Thr Leu	
410 415 420	
gct cgc ggc atc gaa att ggc ata tct tcc agc tcg gcc gca agt aca	1411

Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser Ser Ser Ala Ala Ser Thr
 425 430 435

ccg aag cct tcg acg tcc aaa tcc tgg acg aaa acg gca agc gcg cca 1459
 Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys Thr Ala Ser Ala Pro
 440 445 450

tcc caa cca tgg gct cta cgg gct cgg tgt cac ccg cct gct cgc cgt 1507
 Ser Gln Pro Trp Ala Leu Arg Ala Arg Cys His Pro Pro Ala Arg Arg
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cct ggc aga aca gcg cca cga tgacgctggc ctcaactggt ccg 1551
 Pro Gly Arg Thr Ala Pro Arg
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<210> 326

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

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Pro Ala Asp Ala Glu Val Pro Ser His Lys Leu Leu Val Arg Ala Gly
 20 25 30

Tyr Ile Arg Arg Val Ala Pro Gly Ile Tyr Ser Trp Leu Pro Leu Gly
 35 40 45

Leu Arg Ala Val Arg Asn Ile Glu Ala Val Val Arg Glu Glu Met Asp
 50 55 60

Ala Ile Gly Gly Gln Glu Leu Leu Phe Pro Thr Leu Leu Pro Arg Glu
 . 65 70 75 80

Pro Tyr Glu Thr Thr Gln Arg Trp Thr Glu Tyr Gly Asp Ser Leu Phe
 85 90 95

Arg Leu Lys Asp Arg Lys Gly Ala Asp Tyr Leu Leu Gly Pro Thr His
 100 105 110

Glu Glu Met Phe Ala Ala Thr Val Lys Asp Leu Tyr Asn Ser Tyr Lys
 115 120 125

Asp Phe Pro Val Thr Leu Tyr Gln Ile Gln Thr Lys Tyr Arg Asp Glu
 130 135 140

Glu Arg Pro Arg Ala Gly Val Leu Arg Gly Arg Glu Phe Val Met Lys
 145 150 155 160

Asp Ser Tyr Ser Phe Asp Ile Ser Asp Ala Gly Leu Asp Glu Ser Tyr
 165 170 175

Ala Lys His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu
 180 185 190

Glu Tyr Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala
 195 200 205

Ser Glu Glu Phe Leu Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val
 210 215 220
 Arg Ser Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr
 225 230 235 240
 Gln Pro Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr
 245 250 255
 Tyr Glu Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala
 260 265 270
 Asn Ser Ile Asp Val Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp
 275 280 285
 Thr Leu Lys Cys Ile Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu
 290 295 300
 Ala Glu Leu Thr Gly Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met
 305 310 315 320
 Lys Arg Leu Glu Ala Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val
 325 330 335
 Glu Ser Asp Phe Ala Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly
 340 345 350
 Pro Val Gly Leu Ala Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg
 355 360 365
 Val Val Thr Gly Thr Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg
 370 375 380
 His Val Val Gly Leu Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe
 385 390 395 400
 Ile Glu Ala Ala Glu Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu
 405 410 415
 Gly Thr Leu Thr Leu Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser Ser
 420 425 430
 Ser Ala Ala Ser Thr Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys
 435 440 445
 Thr Ala Ser Ala Pro Ser Gln Pro Trp Ala Leu Arg Ala Arg Cys His
 450 455 460
 Pro Pro Ala Arg Arg Pro Gly Arg Thr Ala Pro Arg
 465 470 475

<210> 327

<211> 1031

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (94)..(1008)

<223> FRXA01938

<400> 327

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attcttactc cttcgacatc tcgggatgct ggt ttg gac gag tcc tac gca aag 114
 Leu Asp Glu Ser Tyr Ala Lys
 1 5

cac cgc gca gcg tat cag cgc atc ttt gac cgc ctt ggc ttg gaa tac 162
 His Arg Ala Ala Tyr Gln Arg Ile Phe Asp Arg Leu Gly Leu Glu Tyr
 10 15 20

gcc atc tgc cag gca acc tct ggt gcc atg ggc gga tcc gct tcc gag 210
 Ala Ile Cys Gln Ala Thr Ser Gly Ala Met Gly Gly Ser Ala Ser Glu
 25 30 35

gaa ttc ctt gca gta tct gaa aac ggc gaa gat acc ttc gtg cgc tct 258
 Glu Phe Leu Ala Val Ser Glu Asn Gly Glu Asp Thr Phe Val Arg Ser
 40 45 50 55

acc tcc ggc aat tac gcc gca aac gtg gaa gct gtt gtt acc cag cca 306
 Thr Ser Gly Asn Tyr Ala Ala Asn Val Glu Ala Val Val Thr Gln Pro
 60 65 70

ggc gtt gag cgt gac atc gaa ggc ctg cca gaa cca gtc acc tac gaa 354
 Gly Val Glu Arg Asp Ile Glu Gly Leu Pro Glu Pro Val Thr Tyr Glu
 75 80 85

act cct gtt tct gaa acc atc gat gct ttg gtt gat tgg gct aac tcc 402
 Thr Pro Val Ser Glu Thr Ile Asp Ala Leu Val Asp Trp Ala Asn Ser
 90 95 100

atc gac gtg cag atc gag ggc cgc gag gtc acc gca gat gac acc ctc 450
 Ile Asp Val Gln Ile Glu Gly Arg Glu Val Thr Ala Asp Asp Thr Leu
 105 110 115

aag tgc att gtg gtg aag gtc cgc gag cca ggt gcc gaa gaa gca gaa 498
 Lys Cys Ile Val Val Lys Val Arg Glu Pro Gly Ala Glu Glu Ala Glu
 120 125 130 135

ctc act gga atc ttg ctt cca ggt gac cgc gaa gta gac atg aag cgc 546
 Leu Thr Gly Ile Leu Leu Pro Gly Asp Arg Glu Val Asp Met Lys Arg
 140 145 150

ctc gag gca tca ctt gag cca gca gaa gtt gaa ctc gca gtg gaa tcc 594
 Leu Glu Ala Ser Leu Glu Pro Ala Glu Val Glu Leu Ala Val Glu Ser
 155 160 165

gac ttt gcc gac aac cca ttc ctg gtc aag ggc tac gtc gga cca gtt 642
 Asp Phe Ala Asp Asn Pro Phe Leu Val Lys Gly Tyr Val Gly Pro Val
 170 175 180

ggc ctg gcc aag aac ggc gtg aag gtc ctt gcc gat cct cgc gtt gtc 690
 Gly Leu Ala Lys Asn Gly Val Lys Val Leu Ala Asp Pro Arg Val Val
 185 190 195

acc ggt acc tcc tgg atc acc ggc gcc gat gaa aag gaa cgc cac gtc 738
 Thr Gly Thr Ser Trp Ile Thr Gly Ala Asp Glu Lys Glu Arg His Val
 200 205 210 215

gta ggc ctc gtc gcc gga cgc gat ttc acc cca gac ggc ttc atc gaa 786

Val Gly Leu Val Ala Gly Arg Asp Phe Thr Pro Asp Gly Phe Ile Glu
 220 225 230

gct gca gaa atc aag gaa ggc gac cca gcg cca gca ggc gag ggc acc 834
 Ala Ala Glu Ile Lys Glu Gly Asp Pro Ala Pro Ala Gly Glu Gly Thr
 235 240 245

ctc acc ctt gct cgc ggc atc gaa att ggc ata tct tcc agc tcg gcc 882
 Leu Thr Leu Ala Arg Gly Ile Glu Ile Gly Ile Ser Ser Ser Ser Ala
 250 255 260

gca agt aca ccg aag cct tcg acg tcc aaa tcc tgg acg aaa acg gca 930
 Ala Ser Thr Pro Lys Pro Ser Thr Ser Lys Ser Trp Thr Lys Thr Ala
 265 270 275

agc gcg cca tcc caa cca tgg gct cta cgg gct cgg tgt cac ccg cct 978
 Ser Ala Pro Ser Gln Pro Trp Ala Leu Arg Ala Arg Cys His Pro Pro
 280 285 290 295

gct cgc cgt cct ggc aga aca gcg cca cga tgacgctggc ctcaactggt ccg 1031
 Ala Arg Arg Pro Gly Arg Thr Ala Pro Arg
 300 305

<210> 328

<211> 305

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 328

Leu Asp Glu Ser Tyr Ala Lys His Arg Ala Ala Tyr Gln Arg Ile Phe
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Asp Arg Leu Gly Leu Glu Tyr Ala Ile Cys Gln Ala Thr Ser Gly Ala
 20 25 30

Met Gly Gly Ser Ala Ser Glu Glu Phe Leu Ala Val Ser Glu Asn Gly
 35 40 45

Glu Asp Thr Phe Val Arg Ser Thr Ser Gly Asn Tyr Ala Ala Asn Val
 50 55 60

Glu Ala Val Val Thr Gln Pro Gly Val Glu Arg Asp Ile Glu Gly Leu
 65 70 75 80

Pro Glu Pro Val Thr Tyr Glu Thr Pro Val Ser Glu Thr Ile Asp Ala
 85 90 95

Leu Val Asp Trp Ala Asn Ser Ile Asp Val Gln Ile Glu Gly Arg Glu
 100 105 110

Val Thr Ala Asp Asp Thr Leu Lys Cys Ile Val Val Lys Val Arg Glu
 115 120 125

Pro Gly Ala Glu Glu Ala Glu Leu Thr Gly Ile Leu Leu Pro Gly Asp
 130 135 140

Arg Glu Val Asp Met Lys Arg Leu Glu Ala Ser Leu Glu Pro Ala Glu
 145 150 155 160

Val Glu Leu Ala Val Glu Ser Asp Phe Ala Asp Asn Pro Phe Leu Val

gct ttt gga aag aag atc gga cag gcc tct ccg gag gac cgc cct gca 307
Ala Phe Gly Lys Lys Ile Gly Gln Ala Ser Pro Glu Asp Arg Pro Ala

55					60					65						
ctt	ctg	gag	ggg	tcc	aac	gaa	ctc	aaa	gcc	aag	gtg	aag	gat	gct	gag	355
Leu	Leu	Glu	Gly	Ser	Asn	Glu	Leu	Lys	Ala	Lys	Val	Lys	Asp	Ala	Glu	
70					75					80					85	
gct	gca	cag	gaa	gct	gct	gag	gcg	aaa	gtc	aat	gag	ctg	cag	atg	aag	403
Ala	Ala	Gln	Glu	Ala	Ala	Glu	Ala	Lys	Val	Asn	Glu	Leu	Gln	Met	Lys	
				90					95					100		
ctc	tcc	aac	gtg	gtt	tcc	ggc	gcg	cct	gct	ggg	ggc	gaa	gat	gat	ttc	451
Leu	Ser	Asn	Val	Val	Ser	Gly	Ala	Pro	Ala	Gly	Gly	Glu	Asp	Asp	Phe	
			105					110					115			
gtc	gtc	ctg	gag	acc	atc	ggc	gag	cct	cgc	act	ttt	gat	ttc	gag	cca	499
Val	Val	Leu	Glu	Thr	Ile	Gly	Glu	Pro	Arg	Thr	Phe	Asp	Phe	Glu	Pro	
		120					125					130				
aag	gat	cac	ctg	gag	ctc	ggg	gaa	tcc	ctc	gga	ctt	atc	gat	atg	aag	547
Lys	Asp	His	Leu	Glu	Leu	Gly	Glu	Ser	Leu	Gly	Leu	Ile	Asp	Met	Lys	
	135					140					145					
cgc	ggc	acc	aag	gtt	tcc	ggg	gca	cgt	ttc	tac	tac	ctc	acc	ggg	gac	595
Arg	Gly	Thr	Lys	Val	Ser	Gly	Ala	Arg	Phe	Tyr	Tyr	Leu	Thr	Gly	Asp	
150					155				160					165		
ggc	gca	atg	ctg	cag	ttg	ggc	atg	ctc	atg	ttg	gct	gct	cag	aag	gcg	643
Gly	Ala	Met	Leu	Gln	Leu	Gly	Met	Leu	Met	Leu	Ala	Ala	Gln	Lys	Ala	
				170					175					180		
cgc	gaa	gct	gga	ttt	agc	atg	atg	atc	cct	cca	gtt	ttg	gtg	cgc	cct	691
Arg	Glu	Ala	Gly	Phe	Ser	Met	Met	Ile	Pro	Pro	Val	Leu	Val	Arg	Pro	
			185					190					195			
gaa	atc	atg	gcg	ggc	act	gga	ttc	ttg	ggg	gat	cac	tcc	gag	gag	atc	739
Glu	Ile	Met	Ala	Gly	Thr	Gly	Phe	Leu	Gly	Asp	His	Ser	Glu	Glu	Ile	
		200					205					210				
tac	tac	ctc	gaa	cgc	gat	gac	atg	tac	ttg	gtg	ggg	acc	tct	gag	gtg	787
Tyr	Tyr	Leu	Glu	Arg	Asp	Asp	Met	Tyr	Leu	Val	Gly	Thr	Ser	Glu	Val	
		215				220					225					
gct	ctt	gcg	ggg	tac	cac	aag	gac	gaa	atc	att	gat	ctc	aac	gaa	ggc	835
Ala	Leu	Ala	Gly	Tyr	His	Lys	Asp	Glu	Ile	Ile	Asp	Leu	Asn	Glu	Gly	
230					235					240					245	
cca	gtg	aag	tac	gcc	ggg	tgg	agc	tcc	tgc	ttc	cgc	cgt	gag	gct	ggg	883
Pro	Val	Lys	Tyr	Ala	Gly	Trp	Ser	Ser	Cys	Phe	Arg	Arg	Glu	Ala	Gly	
				250					255					260		
tcc	tac	ggc	aag	gac	acc	cga	ggc	att	ttg	cgt	gtg	cac	cag	ttc	gac	931
Ser	Tyr	Gly	Lys	Asp	Thr	Arg	Gly	Ile	Leu	Arg	Val	His	Gln	Phe	Asp	
			265					270					275			
aag	gtt	gag	atg	ttt	gtc	tac	tgc	aag	cct	gaa	gat	gct	gaa	gat	gta	979
Lys	Val	Glu	Met	Phe	Val	Tyr	Cys	Lys	Pro	Glu	Asp	Ala	Glu	Asp	Val	
		280					285					290				
cac	cag	cag	ctg	ctc	ggc	atg	gaa	aag	gaa	atg	ctc	gca	gcc	atc	gag	1027
His	Gln	Gln	Leu	Leu	Gly	Met	Glu	Lys	Glu	Met	Leu	Ala	Ala	Ile	Glu	
		295				300					305					

gtt cct tac cgc gtc atc gac gtt gcc ggt gga gac ttg ggt gca tct 1075
 Val Pro Tyr Arg Val Ile Asp Val Ala Gly Gly Asp Leu Gly Ala Ser
 310 315 320 325

 gct gcc cgc aag ttc gac acc gag gca tgg gtg cca acc cag gac acc 1123
 Ala Ala Arg Lys Phe Asp Thr Glu Ala Trp Val Pro Thr Gln Asp Thr
 330 335 340

 tac cgt gaa ctc acc tcg acc tct aac tgc acc act ttc cag gct cgt 1171
 Tyr Arg Glu Leu Thr Ser Thr Ser Asn Cys Thr Thr Phe Gln Ala Arg
 345 350 355

 cgc ctg cag act cgt tac cgc gat gaa aac ggc aag cca cag atc gcc 1219
 Arg Leu Gln Thr Arg Tyr Arg Asp Glu Asn Gly Lys Pro Gln Ile Ala
 360 365 370

 gca acc ctg aac ggt acg ttg gct acc act cgt tgg ctt gtc gcg atc 1267
 Ala Thr Leu Asn Gly Thr Leu Ala Thr Thr Arg Trp Leu Val Ala Ile
 375 380 385

 ctg gag aac aac cag cag gcc gat ggc tct gtt gtt gtt cct gag gcg 1315
 Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val Val Val Pro Glu Ala
 390 395 400 405

 ctt cgt cca ttc gtg ggc aaa gac gtg ctc aag cca gtg aaa caa gcc 1363
 Leu Arg Pro Phe Val Gly Lys Asp Val Leu Lys Pro Val Lys Gln Ala
 410 415 420

 ggt taattaagcg gaaagctcgt ggt 1389
 Gly

<210> 330

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

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 Ser Gln Ile Thr Arg Gly Glu Asp Pro Ala Leu Val Asp Glu Leu Ile
 20 25 30

 Ser Ala Asp Glu Ser Arg Arg Glu Ala Ile Lys Ala Ala Asp Asp Leu
 35 40 45

 Arg Ala Glu Gln Lys Ala Phe Gly Lys Lys Ile Gly Gln Ala Ser Pro
 50 55 60

 Glu Asp Arg Pro Ala Leu Leu Glu Gly Ser Asn Glu Leu Lys Ala Lys
 65 70 75 80

 Val Lys Asp Ala Glu Ala Ala Gln Glu Ala Ala Glu Ala Lys Val Asn
 85 90 95

 Glu Leu Gln Met Lys Leu Ser Asn Val Val Ser Gly Ala Pro Ala Gly
 100 105 110

Gly Glu Asp Asp Phe Val Val Leu Glu Thr Ile Gly Glu Pro Arg Thr
 115 120 125
 Phe Asp Phe Glu Pro Lys Asp His Leu Glu Leu Gly Glu Ser Leu Gly
 130 135 140
 Leu Ile Asp Met Lys Arg Gly Thr Lys Val Ser Gly Ala Arg Phe Tyr
 145 150 155 160
 Tyr Leu Thr Gly Asp Gly Ala Met Leu Gln Leu Gly Met Leu Met Leu
 165 170 175
 Ala Ala Gln Lys Ala Arg Glu Ala Gly Phe Ser Met Met Ile Pro Pro
 180 185 190
 Val Leu Val Arg Pro Glu Ile Met Ala Gly Thr Gly Phe Leu Gly Asp
 195 200 205
 His Ser Glu Glu Ile Tyr Tyr Leu Glu Arg Asp Asp Met Tyr Leu Val
 210 215 220
 Gly Thr Ser Glu Val Ala Leu Ala Gly Tyr His Lys Asp Glu Ile Ile
 225 230 235 240
 Asp Leu Asn Glu Gly Pro Val Lys Tyr Ala Gly Trp Ser Ser Cys Phe
 245 250 255
 Arg Arg Glu Ala Gly Ser Tyr Gly Lys Asp Thr Arg Gly Ile Leu Arg
 260 265 270
 Val His Gln Phe Asp Lys Val Glu Met Phe Val Tyr Cys Lys Pro Glu
 275 280 285
 Asp Ala Glu Asp Val His Gln Gln Leu Leu Gly Met Glu Lys Glu Met
 290 295 300
 Leu Ala Ala Ile Glu Val Pro Tyr Arg Val Ile Asp Val Ala Gly Gly
 305 310 315 320
 Asp Leu Gly Ala Ser Ala Ala Arg Lys Phe Asp Thr Glu Ala Trp Val
 325 330 335
 Pro Thr Gln Asp Thr Tyr Arg Glu Leu Thr Ser Thr Ser Asn Cys Thr
 340 345 350
 Thr Phe Gln Ala Arg Arg Leu Gln Thr Arg Tyr Arg Asp Glu Asn Gly
 355 360 365
 Lys Pro Gln Ile Ala Ala Thr Leu Asn Gly Thr Leu Ala Thr Thr Arg
 370 375 380
 Trp Leu Val Ala Ile Leu Glu Asn Asn Gln Gln Ala Asp Gly Ser Val
 385 390 395 400
 Val Val Pro Glu Ala Leu Arg Pro Phe Val Gly Lys Asp Val Leu Lys
 405 410 415
 Pro Val Lys Gln Ala Gly
 420

<400> 331																
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Met Asn Ile Ile Asp 5																
gaa ctc tcc tgg cgc gga ctc atc aac cag tcc acc gac ctt gag gcc 163																
Glu Leu Ser Trp Arg Gly Leu Ile Asn Gln Ser Thr Asp Leu Glu Ala 20																
ctt cgc gag gaa gct tca acc ccc atc acc ttg tac tgc gga ttc gac 211																
Leu Arg Glu Glu Ala Ser Thr Pro Ile Thr Leu Tyr Cys Gly Phe Asp 35																
cca acc ggt cca tcc ctc cac gca gga cac ctc gtt cca ctg ctc atg 259																
Pro Thr Gly Pro Ser Leu His Ala Gly His Leu Val Pro Leu Leu Met 50																
ctg cgc cgt ttc cag caa gca gga cac aac cca atc gtg ctc gca ggt 307																
Leu Arg Arg Phe Gln Gln Ala Gly His Asn Pro Ile Val Leu Ala Gly 65																
ggc gca acc ggc atg atc ggc gac ccc cgc gat gtc ggc gag cgc acc 355																
Gly Ala Thr Gly Met Ile Gly Asp Pro Arg Asp Val Gly Glu Arg Thr 85																
atg aac tcc gca gac acc gtc tct gat tgg gca gaa cgc atc tcc ggt 403																
Met Asn Ser Ala Asp Thr Val Ser Asp Trp Ala Glu Arg Ile Ser Gly 100																
cag ctc agc cgc ttc gtt gat ttc gac ggc gag cac gca gcc cgt ctg 451																
Gln Leu Ser Arg Phe Val Asp Phe Asp Gly Glu His Ala Ala Arg Leu 115																
gtc aac aac gcc gag tgg acc aac gaa atg tcc gta gtg acc ttc ctc 499																
Val Asn Asn Ala Glu Trp Thr Asn Glu Met Ser Val Val Thr Phe Leu 130																
cgt gat gta gga aag cac ttc tcc ctc aac acc atg ctc gcc cgc gac 547																
Arg Asp Val Gly Lys His Phe Ser Leu Asn Thr Met Leu Ala Arg Asp 145																
acc gtc aag cgt cgc ctc gag tcc gac ggc att tcc tac acc gag ttc 595																
Thr Val Lys Arg Arg Leu Glu Ser Asp Gly Ile Ser Tyr Thr Glu Phe 165																
tcc tac atg ctg cta cag gcc aac gac tac gtt gaa ctg aac aag cgc 643																
Ser Tyr Met Leu Leu Gln Ala Asn Asp Tyr Val Glu Leu Asn Lys Arg 180																

ttc ggc tgc acc ctg cag gta ggt ggc ggt gac cag tgg ggc aac atc	691
Phe Gly Cys Thr Leu Gln Val Gly Gly Gly Asp Gln Trp Gly Asn Ile	
185 190 195	
ggt tct ggc gtt gac ctc aac cgt cgc gtc aac ggc acc tct gtc cac	739
Val Ser Gly Val Asp Leu Asn Arg Arg Val Asn Gly Thr Ser Val His	
200 205 210	
gca gtg acc gta cct ttg gtt acc gat tcc gac ggc aag aag ttc ggc	787
Ala Val Thr Val Pro Leu Val Thr Asp Ser Asp Gly Lys Lys Phe Gly	
215 220 225	
aag tcc acc ggc ggc gga agc ctc tgg ttg gat ccg gaa atg acc agc	835
Lys Ser Thr Gly Gly Gly Ser Leu Trp Leu Asp Pro Glu Met Thr Ser	
230 235 240 245	
cca tac gct tgg tac cag tac ttc atc aac gca tcc gac gct gac gtg	883
Pro Tyr Ala Trp Tyr Gln Tyr Phe Ile Asn Ala Ser Asp Ala Asp Val	
250 255 260	
atc cgt tac ctc cgc tgg ttc acc ttc ctc acc cag gaa gaa ctt gct	931
Ile Arg Tyr Leu Arg Trp Phe Thr Phe Leu Thr Gln Glu Glu Leu Ala	
265 270 275	
gag ttg gaa gtt gaa gtt gca gag cgc cca ttc aag cgc gaa gca cag	979
Glu Leu Glu Val Glu Val Ala Glu Arg Pro Phe Lys Arg Glu Ala Gln	
280 285 290	
cgt cgt ctt gca cgc gaa atg acc aac ttg gtt cac gga acc gaa gca	1027
Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val His Gly Thr Glu Ala	
295 300 305	
acc gaa gca gtc gag ctt gct gct caa gca ctg ttc ggc cgc gca gaa	1075
Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu Phe Gly Arg Ala Glu	
310 315 320 325	
ctc cgc gac cta gac gaa aaa act ctc gct gca tcc gtt tct gaa act	1123
Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala Ser Val Ser Glu Thr	
330 335 340	
gca gtt gca gaa atc aag gca ggg gag cca cgc acc atc ata gat ctg	1171
Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg Thr Ile Ile Asp Leu	
345 350 355	
ctc gtg gcc agc gga ctt gct gat tcc aag ggc gca gca aag cgt gca	1219
Leu Val Ala Ser Gly Leu Ala Asp Ser Lys Gly Ala Ala Lys Arg Ala	
360 365 370	
gtc aag gaa ggc ggt gcg tac gta aac aac gaa cgc atc gaa tcg gat	1267
Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu Arg Ile Glu Ser Asp	
375 380 385	
gat tgg gag cct ttc gct gaa gat ctt ctt cac ggt tca tgg cta gta	1315
Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His Gly Ser Trp Leu Val	
390 395 400 405	
ctg cgc cgt ggc aag aag aac ttc gca gga gtt cag atc ctc ggc	1360
Leu Arg Arg Gly Lys Lys Asn Phe Ala Gly Val Gln Ile Leu Gly	
410 415 420	
taataatcgc tgaaatgatt gcg	1383

<210> 332

<211> 420

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Met	Asn	Ile	Ile	Asp	Glu	Leu	Ser	Trp	Arg	Gly	Leu	Ile	Asn	Gln	Ser
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Thr	Asp	Leu	Glu	Ala	Leu	Arg	Glu	Glu	Ala	Ser	Thr	Pro	Ile	Thr	Leu
		20					25						30		

Tyr	Cys	Gly	Phe	Asp	Pro	Thr	Gly	Pro	Ser	Leu	His	Ala	Gly	His	Leu
		35					40					45			

Val	Pro	Leu	Leu	Met	Leu	Arg	Arg	Phe	Gln	Gln	Ala	Gly	His	Asn	Pro
	50					55					60				

Ile	Val	Leu	Ala	Gly	Gly	Ala	Thr	Gly	Met	Ile	Gly	Asp	Pro	Arg	Asp
65					70					75					80

Val	Gly	Glu	Arg	Thr	Met	Asn	Ser	Ala	Asp	Thr	Val	Ser	Asp	Trp	Ala
			85						90					95	

Glu	Arg	Ile	Ser	Gly	Gln	Leu	Ser	Arg	Phe	Val	Asp	Phe	Asp	Gly	Glu
			100					105					110		

His	Ala	Ala	Arg	Leu	Val	Asn	Asn	Ala	Glu	Trp	Thr	Asn	Glu	Met	Ser
		115					120					125			

Val	Val	Thr	Phe	Leu	Arg	Asp	Val	Gly	Lys	His	Phe	Ser	Leu	Asn	Thr
	130					135					140				

Met	Leu	Ala	Arg	Asp	Thr	Val	Lys	Arg	Arg	Leu	Glu	Ser	Asp	Gly	Ile
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Ser	Tyr	Thr	Glu	Phe	Ser	Tyr	Met	Leu	Leu	Gln	Ala	Asn	Asp	Tyr	Val
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Glu	Leu	Asn	Lys	Arg	Phe	Gly	Cys	Thr	Leu	Gln	Val	Gly	Gly	Gly	Asp
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Gln	Trp	Gly	Asn	Ile	Val	Ser	Gly	Val	Asp	Leu	Asn	Arg	Arg	Val	Asn
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	210					215					220				

Gly	Lys	Lys	Phe	Gly	Lys	Ser	Thr	Gly	Gly	Gly	Ser	Leu	Trp	Leu	Asp
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Gln	Glu	Glu	Leu	Ala	Glu	Leu	Glu	Val	Glu	Val	Ala	Glu	Arg	Pro	Phe
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Lys Arg Glu Ala Gln Arg Arg Leu Ala Arg Glu Met Thr Asn Leu Val
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 His Gly Thr Glu Ala Thr Glu Ala Val Glu Leu Ala Ala Gln Ala Leu
 305 310 315 320
 Phe Gly Arg Ala Glu Leu Arg Asp Leu Asp Glu Lys Thr Leu Ala Ala
 325 330 335
 Ser Val Ser Glu Thr Ala Val Ala Glu Ile Lys Ala Gly Glu Pro Arg
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 Thr Ile Ile Asp Leu Leu Val Ala Ser Gly Leu Ala Asp Ser Lys Gly
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 Ala Ala Lys Arg Ala Val Lys Glu Gly Gly Ala Tyr Val Asn Asn Glu
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 Arg Ile Glu Ser Asp Asp Trp Glu Pro Phe Ala Glu Asp Leu Leu His
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 Glu Gly Gln Leu Lys Asp Leu Ser His Val Pro Glu Thr Thr Ala Thr
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 Phe Thr Ala Val Pro Ala Asn Thr Asp Asp Gly Arg Ala Val Ile Arg
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 His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro
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 Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr
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Glu	Lys	Arg	Met	Lys	Lys	Ile	Ile	Lys	Thr	Gly	Gln	Lys	Phe	Glu	Arg		
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Arg	Val	Tyr	Glu	Ser	Ala	Glu	Ala	Ala	Ala	Glu	Glu	Leu	Lys	Asn	Glu		
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Ser	Asp	Glu	Ala	Thr	Glu	Val	Gly	Ala	Gly	Glu	Leu	Thr	Ala	Tyr	Asp		
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Asn	Val	Asn	Pro	Arg	Thr	Ser	Glu	Val	Glu	Trp	Ser	Asp	Leu	Cys	Arg		
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			180					185					190				
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Arg	Ser	Ser	Ala	Ala	Tyr	Trp	Arg	Gly	Asp	Gln	Asp	Asn	Ala	Gly	Leu		
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Gln	Arg	Ile	Tyr	Gly	Thr	Ala	Trp	Glu	Asp	Lys	Glu	Ser	Leu	Asp	Ala		
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Thr	Pro	His	Ile	Thr	Lys	Gln	Asp	Leu	Phe	Glu	Arg	Ser	Gly	His	Leu		
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Phe	Asp	Glu	Asp	Gly	Asn	Val	Thr	Lys	Pro	Gly	Gln	Glu	Tyr	Tyr	Leu		

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Tyr	Arg	Tyr	Glu	Lys	Ser	Gly	Val	Ile	His	Gly	Leu	Thr	Arg	Ala	Arg					
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385					390					395					400					
gaa	gca	gag	ctc	acc	tct	gtg	ctg	gac	ttc	atc	ctg	tcg	ctg	ctg	cgc	1248				
Glu	Ala	Glu	Leu	Thr	Ser	Val	Leu	Asp	Phe	Ile	Leu	Ser	Leu	Leu	Arg					
			405						410					415						
gat	tac	ggt	ttg	gat	gat	ttc	tac	ctg	gag	ctc	tcc	acc	cgc	gat	cct	1296				
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Ala	Ile	Gly	Arg	Thr	Trp	Gln	Met	Ser	Thr	Val	Gln	Leu	Asp	Phe	Asn					
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Phe	Phe	Gly	Val	Leu	Leu	Glu	His	Tyr	Ala	Gly	Ala	Phe	Pro	Ala	Trp					
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ctg	gca	cct	cac	cag	gtc	atg	ggt	att	cca	gtt	gct	gat	gat	tgc	att	1680				
Leu	Ala	Pro	His	Gln	Val	Met	Gly	Ile	Pro	Val	Ala	Asp	Asp	Cys	Ile					
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cca	cac	ctg	gag	aca	atc	acc	gca	cag	ctg	cgt	gaa	aag	ggt	atc	cgc	1728				
Pro	His	Leu	Glu	Thr	Ile	Thr	Ala	Gln	Leu	Arg	Glu	Lys	Gly	Ile	Arg					
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 Ala Asp Val Asp Thr Ser Asp Asp Arg Met Gln Lys Lys Ile Arg Asn
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cac acc acc ggc aag gtt cca ttc atg ctg ctt gcc ggt gcc cgc gat 1824
 His Thr Thr Gly Lys Val Pro Phe Met Leu Leu Ala Gly Ala Arg Asp
 595 600 605

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 Val Glu Ala Asn Ala Val Ser Phe Arg Phe Leu Asp Gly Thr Gln Val
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aac ggc gtg ccc gtc gat gag gca atc gct gtg att tct tcc tgg att 1920
 Asn Gly Val Pro Val Asp Glu Ala Ile Ala Val Ile Ser Ser Trp Ile
 625 630 635 640

ggt gac cgc atc aat gat cag ccg agc gag gac tcc att gca gct cgc 1968
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 35 40 45

His Ser Cys Ala His Val Leu Ala Gln Ala Val Gln Ala Glu Phe Pro
 50 55 60

Gly Thr Lys Leu Gly Ile Gly Pro Ala Ile Glu Asn Gly Phe Tyr Tyr
 65 70 75 80

Asp Phe Asp Ala Ala Glu Pro Phe Thr Pro Glu Asp Leu Lys Thr Ile
 85 90 95

Glu Lys Arg Met Lys Lys Ile Ile Lys Thr Gly Gln Lys Phe Glu Arg
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Arg Val Tyr Glu Ser Ala Glu Ala Ala Ala Glu Glu Leu Lys Asn Glu
 115 120 125

Pro Tyr Lys Leu Glu Leu Ile Gln Asp Lys Gly Asn Val Asp Pro Asn
 130 135 140

Ser Asp Glu Ala Thr Glu Val Gly Ala Gly Glu Leu Thr Ala Tyr Asp
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Phe	Asp	Glu	Asp	Gly	Asn	Val	Thr	Lys	Pro	Gly	Gln	Glu	Tyr	Tyr	Leu	
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Glu	Ala	Glu	Leu	Thr	Ser	Val	Leu	Asp	Phe	Ile	Leu	Ser	Leu	Leu	Arg	
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Asp	Tyr	Gly	Leu	Asp	Asp	Phe	Tyr	Leu	Glu	Leu	Ser	Thr	Arg	Asp	Pro	
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Lys	Lys	Ser	Val	Gly	Ser	Asp	Glu	Ile	Trp	Glu	Arg	Ser	Thr	Glu	Ile	
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Leu	Asn	Arg	Val	Ala	Thr	Asn	Ser	Gly	Leu	Glu	Leu	Val	Pro	Asp	Pro	
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Glu	Gly	Ala	Ala	Phe	Tyr	Gly	Pro	Lys	Ile	Ser	Val	Gln	Ala	Arg	Asp	
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Met Pro Glu Arg Phe Asn Leu Glu Tyr Thr Ser Ser Asp Gly Ser Lys
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Gln Gln Pro Ile Met Ile His Arg Ala Leu Phe Gly Ser Ile Glu Arg
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Phe Phe Gly Val Leu Leu Glu His Tyr Ala Gly Ala Phe Pro Ala Trp
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Leu Ala Pro His Gln Val Met Gly Ile Pro Val Ala Asp Asp Cys Ile
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Pro His Leu Glu Thr Ile Thr Ala Gln Leu Arg Glu Lys Gly Ile Arg
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Ala Asp Val Asp Thr Ser Asp Asp Arg Met Gln Lys Lys Ile Arg Asn
580 585 590

His Thr Thr Gly Lys Val Pro Phe Met Leu Leu Ala Gly Ala Arg Asp
595 600 605

Val Glu Ala Asn Ala Val Ser Phe Arg Phe Leu Asp Gly Thr Gln Val
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Lys Gly Ile Ile Asn Leu Leu Asp Asp Pro Lys Val Ser Thr Lys Arg
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Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
35 40 45

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Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
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 Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
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 tac ggt gcg ttg aag ggt gac acc gcc gac gcg ctt gag gct ttc acc 288
 Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr
 85 90 95
 act cct ttg aag gca aag tac gac gag tac atg aat gac cgc ggc gag 336
 Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu
 100 105 110
 ctc gaa cga gtc ttg gct atc ggt gct gag cgc gcc acc gaa gtt gcc 384
 Leu Glu Arg Val Leu Ala Ile Gly Ala Glu Arg Ala Thr Glu Val Ala
 115 120 125
 aac gaa acc ttg gct gat gtg tac gac aag att ggt ttc ttg gcg tct 432
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 Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
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 Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
 50 55 60
 Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
 65 70 75 80
 Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr
 85 90 95
 Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu
 100 105 110
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Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
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Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
50 55 60
acg ggt acc tcc atc gat tgc ctt gtc gac ggc tac cag ggc gct ggc 240
Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
65 70 75 80
tac ggt gcg ttg aag ggt gac acc gcc gac gcg ctt gag gct ttc acc 288
Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr
85 90 95
act cct ttg aag gca aag tac gac gag tac atg aat gac cgc ggc gag 336
Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu
100 105 110
ctc gaa cga gtc ttg gct atc ggt gct gag cgc gcc acc gaa gtt gcc 384
Leu Glu Arg Val Leu Ala Ile Gly Ala Glu Arg Ala Thr Glu Val Ala
115 120 125
aac gaa acc ttg gct gat gtg tac gac aag att ggt ttc ttg gcg tct 432
Asn Glu Thr Leu Ala Asp Val Tyr Asp Lys Ile Gly Phe Leu Ala Ser
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Ile Lys Ser Ala Val Thr Asp Asn Asp Gly Val Ile Ala Tyr Asp Pro
 35 40 45

Glu Asn Lys Pro Gly Val Ser Asn Leu Leu Val Ile Gln Ser Ala Leu
 50 55 60

Thr Gly Thr Ser Ile Asp Ser Leu Val Asp Gly Tyr Gln Gly Ala Gly
 65 70 75 80

Tyr Gly Ala Leu Lys Gly Asp Thr Ala Asp Ala Leu Glu Ala Phe Thr
 85 90 95

Thr Pro Leu Lys Ala Lys Tyr Asp Glu Tyr Met Asn Asp Arg Gly Glu
 100 105 110

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 Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val Leu Ser Gly Ile Gln
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 Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr Leu Gly Ala Val Lys
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 Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala Phe Tyr Phe Ile Pro
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Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro Glu Glu Leu Arg Asn
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Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala Leu Gly Ile Asp Pro
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Glu Arg Ser Thr Leu Phe Val Gln Ser His Val Pro Ala His Ala Glu
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Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe Gly Glu Ala Ser Arg
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Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg Gly Ala Asp Arg Thr
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Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met Ala Ala Asp Ile Leu
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Phe Tyr Phe Ile Pro Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro
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Glu Glu Leu Arg Asn Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala
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Leu Gly Ile Asp Pro Glu Arg Ser Thr Leu Phe Val Gln Ser His Val
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Pro Ala His Ala Glu Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe
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Gly Glu Ala Ser Arg Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg
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 Lys Asp Leu Thr Ala Gln Thr Ala Ser Arg Val Leu Ser Gly Ile Gln
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 Pro Thr Ala Asp Ser Tyr His Leu Gly Asn Tyr Leu Gly Ala Val Lys
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 cag tgg att gac ctg caa gat tcc tac gat gcc ttc tac ttc att cca 259
 Gln Trp Ile Asp Leu Gln Asp Ser Tyr Asp Ala Phe Tyr Phe Ile Pro
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 Asp Leu His Ala Ile Thr Val Asp Gln Glu Pro Glu Glu Leu Arg Asn
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 Arg Thr Ile Ser Gly Ala Ala Gln Leu Leu Ala Leu Gly Ile Asp Pro
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 Glu Arg Ser Thr Leu Phe Val Gln Ser His Val Pro Ala His Ala Glu
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 Leu Ser Trp Val Leu Thr Cys Leu Thr Gly Phe Gly Glu Ala Ser Arg
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 atg acc cag ttc aag gac aag tcc tcc aag cgt ggc gcc gac cgt acc 499
 Met Thr Gln Phe Lys Asp Lys Ser Ser Lys Arg Gly Ala Asp Arg Thr
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 tca gct ggt ctg ttc acc tac ccg atg ctg atg gca gca gat att ttg 547
 Ser Ala Gly Leu Phe Thr Tyr Pro Met Leu Met Ala Ala Asp Ile Leu
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Phe	Tyr	Phe	Ile	Pro	Asp	Leu	His	Ala	Ile	Thr	Val	Asp	Gln	Glu	Pro
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Val	Asp	Ala	Gly 40	Tyr	Phe	Thr	Ala 45	Asp	Pro	Ala	Ser	Asp 50	Lys	Pro	Gly		
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Gly	His	Ala	Leu	Asp	His	Thr	Leu	Met	Asp	Ala	Leu	Ala	Arg	Arg	Lys 85		
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Trp	Glu	Trp	Lys	Gln	Glu	Tyr	Gly	Gly	Lys	Ile	Gly	Glu	Gln	Met	Arg		
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His	Val	Ile	Val	Ala	Thr	Thr	Arg	Val	Glu	Thr	Met	Leu	Gly	Asp	Val		
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Gln	Thr	Leu	Pro	His	Pro	Phe	Arg	Asp	Asp	Leu	Ser	Leu	Lys	Val	Val		

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Ala	Asp	Asp	Tyr	Val	Asp	Pro	Glu	Phe	Gly	Ser	Gly	Ala	Val	Lys	Ile			
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acc	cca	gca	cac	gac	cct	aat	gac	tac	gct	ctt	ggc	ctg	cgc	cac	aac	1027		
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Arg	Glu	Glu	Leu	Ala	Ala	Gln	Gly	Arg	Ile	Val	Lys	Glu	Ile	Arg	Pro			
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Tyr	Val	His	Ser	Val	Gly	His	Ser	Glu	Arg	Ser	Gly	Glu	Ala	Ile	Glu			
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cct	cgt	ctg	tct	ctg	cag	tgg	ttc	gtc	aag	gtc	gaa	gag	ctg	gcc	aag	1267		
Pro	Arg	Leu	Ser	Leu	Gln	Trp	Phe	Val	Lys	Val	Glu	Glu	Leu	Ala	Lys			
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Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu Val Arg Asp Glu His	
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Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu Glu Gln Val Arg Leu	
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Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys Asp Trp Tyr Leu Glu	
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Asn Thr Gln Lys Val Leu Gly His Val Leu Asp Ala Leu Leu Arg Leu	
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Leu His Pro Ala Met Pro Phe Val Thr Glu Val Leu Trp Gln Ala Leu	
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Thr Asn Gly Gly Val Ala Val Asp Ala Asp Ala Ala Arg Arg Ile Gly	
745 750 755	

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Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr
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 Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val
 485 490 495
 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Met Phe
 500 505 510
 Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys
 515 520 525
 Asp Gly Arg Pro Gln Val Pro Phe Thr Asp Leu Phe Leu His Gly Leu
 530 535 540
 Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly
 545 550 555 560
 Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg
 565 570 575
 Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly
 580 585 590
 Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn
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 Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro
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 Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu
 625 630 635 640
 Glu Gln Val Arg Leu Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe
 645 650 655
 Ala Lys Ala Asn Glu Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys
 660 665 670
 Asp Trp Tyr Leu Glu Ile Ala Lys Val Gln Ile Pro Arg Glu Gly Thr
 675 680 685
 Ser Ala Gln Gly Glu Asn Thr Gln Lys Val Leu Gly His Val Leu Asp
 690 695 700
 Ala Leu Leu Arg Leu Leu His Pro Ala Met Pro Phe Val Thr Glu Val
 705 710 715 720
 Leu Trp Gln Ala Leu Thr Asp Arg Thr Ser Ile Val Val Ala Ser Trp

725										730					735				
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			740					745					750						
Ala	Arg	Arg	Ile	Gly	Asp	Val	Glu	Lys	Leu	Val	Thr	Glu	Val	Arg	Arg				
		755					760					765							
Phe	Arg	Ala	Asp	Gln	Gly	Val	Lys	Pro	Ser	Gln	Lys	Val	Pro	Ala	Arg				
	770					775					780								
Leu	Asp	Phe	Val	Ala	Cys	Asp	Leu	Gln	Asp	Leu	Glu	Asp	Ser	Val	Arg				
785					790					795					800				
Ser	Leu	Val	Arg	Ile	Glu	Gln	Pro	Glu	Asp	Asp	Phe	Ala	Ala	Ser	Ala				
			805						810						815				
Ser	Leu	Glu	Ile	Arg	Leu	Ser	Gln	Ala	Thr	Ile	Thr	Val	Glu	Leu	Asp				
			820					825					830						
Thr	Ser	Gly	Thr	Val	Asp	Val	Ala	Ala	Glu	Arg	Lys	Arg	Leu	Glu	Lys				
		835					840					845							
Asp	Leu	Ala	Asn	Ala	Gln	Lys	Glu	Leu	Glu	Thr	Thr	Ala	Lys	Lys	Leu				
	850					855					860								
Gly	Asn	Glu	Ala	Phe	Leu	Ser	Lys	Ala	Pro	Asp	Ala	Val	Val	Asp	Lys				
865					870					875					880				
Ile	Arg	Gly	Arg	Ala	Gln	Ile	Ala	Gln	Glu	Glu	Val	Glu	Arg	Ile	Asn				
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (96)..(590)

<223> FRXA00985

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Val	Leu	Gly	His	Val	Leu	Asp
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gca ctg ctt cgt ctg ctg cac cca gct atg cct ttc gtc acc gaa gtt 164

Ala	Leu	Leu	Arg	Leu	Leu	His	Pro	Ala	Met	Pro	Phe	Val	Thr	Glu	Val
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ctg tgg cag gca ctt act gat cgc acc tcc atc gtg gtg gcc tcc tgg 212

Leu	Trp	Gln	Ala	Leu	Thr	Asp	Arg	Thr	Ser	Ile	Val	Val	Ala	Ser	Trp
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Pro Thr Ala Ala Asp Thr Asn Gly Gly Val Ala Val Asp Ala Asp Ala
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gct agg cgc att ggc gac gtc gag aag ctt gtt act gag gtt cgt cgt 308
Ala Arg Arg Ile Gly Asp Val Glu Lys Leu Val Thr Glu Val Arg Arg
60 65 70

ttc cgc gct gac cag ggt gtg aag cct tcc cag aag gtt cca gca cgc 356
Phe Arg Ala Asp Gln Gly Val Lys Pro Ser Gln Lys Val Pro Ala Arg
75 80 85

ctt gat ttc gtg gca tgt gac ctg cag gat ctg gaa gat tcc gtg cgc 404
Leu Asp Phe Val Ala Cys Asp Leu Gln Asp Leu Glu Asp Ser Val Arg
90 95 100

tcc ctg gtt cgc atc gag caa cca gaa gat gat ttc gca gct tct gcc 452
Ser Leu Val Arg Ile Glu Gln Pro Glu Asp Asp Phe Ala Ala Ser Ala
105 110 115

agc ctg gag atc cgc ctg agc caa gca acc atc acg gtg gag ctt gac 500
Ser Leu Glu Ile Arg Leu Ser Gln Ala Thr Ile Thr Val Glu Leu Asp
120 125 130 135

acc tct gga act gtt gac gtt gca gca gag cgc aag cgc ctg gaa aag 548
Thr Ser Gly Thr Val Asp Val Ala Ala Glu Arg Lys Arg Leu Glu Lys
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<210> 346

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<400> 346

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Ser Ile Val Val Ala Ser Trp Pro Thr Ala Ala Asp Thr Asn Gly Gly
35 40 45

Val Ala Val Asp Ala Asp Ala Ala Arg Arg Ile Gly Asp Val Glu Lys
50 55 60

Leu Val Thr Glu Val Arg Arg Phe Arg Ala Asp Gln Gly Val Lys Pro
65 70 75 80

Ser Gln Lys Val Pro Ala Arg Leu Asp Phe Val Ala Cys Asp Leu Gln
85 90 95

Asp Leu Glu Asp Ser Val Arg Ser Leu Val Arg Ile Glu Gln Pro Glu
100 105 110

Asp Asp Phe Ala Ala Ser Ala Ser Leu Glu Ile Arg Leu Ser Gln Ala

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Thr Ile Thr Val Glu Leu Asp Thr Ser Gly Thr Val Asp Val Ala Ala			
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	Met Val Cys Val Thr		
	1 5		
gac cag aat aat gag acc acc agc cag aac cgc gca gac aag ctg ccc	163		
Asp Gln Asn Asn Glu Thr Thr Ser Gln Asn Arg Ala Asp Lys Leu Pro			
10 15 20			
aag tcc tgg gat cct aaa gct gta gaa gct gat ttg tac cag ggc tgg	211		
Lys Ser Trp Asp Pro Lys Ala Val Glu Ala Asp Leu Tyr Gln Gly Trp			
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Val Asp Ala Gly Tyr Phe Thr Ala Asp Pro Ala Ser Asp Lys Pro Gly			
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ttc tcc att gtt ctg cct cca cca aac gtg acc ggc cag ctg cac atg	307		
Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr Gly Gln Leu His Met			
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gga cac gca ctt gac cac acc ctg atg gat gct ctt gca cgt cgc aag	355		
Gly His Ala Leu Asp His Thr Leu Met Asp Ala Leu Ala Arg Arg Lys			
70 75 80 85			
cgc atg cag ggc ttt gag gtt ttg tgg ctg cca ggt atg gac cac gcg	403		
Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro Gly Met Asp His Ala			
90 95 100			
ggt atc gcg acc cag acc aag gtc gag gag atg ctg aag gaa act gaa	451		
Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met Leu Lys Glu Thr Glu			
105 110 115			
ggc aaa act cgc tac gac tat gac cgc gaa gag ttc atc gcc aag gtc	499		
Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu Phe Ile Ala Lys Val			
120 125 130			

tgg gag tgg aag caa gaa tat ggt gga aag atc ggc gag cag atg cgc	547
Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile Gly Glu Gln Met Arg	
135 140 145	
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Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu Arg Phe Thr Leu Asp	
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gac ggc ttg tcc cgc gcc gtc caa acg att ttc aag aag ctt ttc gac	643
Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe Lys Lys Leu Phe Asp	
170 175 180	
gcc ggc ctc atc tat cag gcc aac cgc ctc gtc aac tgg tcg ccc gta	691
Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val Asn Trp Ser Pro Val	
185 190 195	
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Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile Tyr Lys Asp Val Glu	
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ggc gaa ctg gta tcc att cgc tat ggt tcc ctc aac gac gat gaa cca	787
Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu Asn Asp Asp Glu Pro	
215 220 225	
cat gtc att gtt gcc acc acc cgt gtg gaa acc atg ctc ggc gac gtc	835
His Val Ile Val Ala Thr Thr Arg Val Glu Thr Met Leu Gly Asp Val	
230 235 240 245	
gct gtt gcc gtg cac cca gac gat gag cgc tac aag gat ttg gtc gga	883
Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr Lys Asp Leu Val Gly	
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cag acc ctg cct cac cca ttc cgc gat gac ctg agc ctg aag gtt gtt	931
Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu Ser Leu Lys Val Val	
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Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser Gly Ala Val Lys Ile	
280 285 290	
acc cca gca cac gac cct aat gac tac gct ctt ggc ctg cgc cac aac	1027
Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu Gly Leu Arg His Asn	
295 300 305	
ctg gac atg cct acc atc atg gac aag acc gga cgc att gcc gat acc	1075
Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly Arg Ile Ala Asp Thr	
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gga acc cag ttt gat ggc ctg acc cgc gaa gaa gca cgc atc aag gtc	1123
Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu Ala Arg Ile Lys Val	
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Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val Lys Glu Ile Arg Pro	
345 350 355	
tac gtc cac tcc gtc gga cac tcc gag cgt tcc ggc gaa gct att gag	1219
Tyr Val His Ser Val Gly His Ser Glu Arg Ser Gly Glu Ala Ile Glu	
360 365 370	
cct cgt ctg tct ctg cag tgg ttc gtc aag gtc gaa gag ctg gcc aag	1267

Pro	Arg	Leu	Ser	Leu	Gln	Trp	Phe	Val	Lys	Val	Glu	Glu	Leu	Ala	Lys	
	375					380					385					
atg	tcc	ggc	gat	gcc	gtg	cgc	gaa	ggc	gac	acc	acc	atc	cac	ccg	aag	1315
Met	Ser	Gly	Asp	Ala	Val	Arg	Glu	Gly	Asp	Thr	Thr	Ile	His	Pro	Lys	
390					395				400						405	
tcc	ctg	gag	cct	cgc	tac	ttt	gac	tgg	gtt	gac	aac	atg	cat	gac	tgg	1363
Ser	Leu	Glu	Pro	Arg	Tyr	Phe	Asp	Trp	Val	Asp	Asn	Met	His	Asp	Trp	
				410					415					420		
acc	att	tcc	cgt	cag	ctg	tgg	tgg	gga	cac	cgc	atc	cca	att	tgg	tat	1411
Thr	Ile	Ser	Arg	Gln	Leu	Trp	Trp	Gly	His	Arg	Ile	Pro	Ile	Trp	Tyr	
			425					430					435			
gga	cca	aac	gat	gaa	atc	atc	tgc	gtt	ggg	cct	gat	gag	cag	gca	cct	1459
Gly	Pro	Asn	Asp	Glu	Ile	Ile	Cys	Val	Gly	Pro	Asp	Glu	Gln	Ala	Pro	
		440					445					450				
gag	ggc	tac	gtc	caa	gac	cca	gat	gtt	cta	gat	acc	tgg	ttc	tct	tct	1507
Glu	Gly	Tyr	Val	Gln	Asp	Pro	Asp	Val	Leu	Asp	Thr	Trp	Phe	Ser	Ser	
	455					460					465					
gcg	ctg	tgg	cca	ttt	tct	aca	atg	ggt	tgg	cca	gaa	aag	acc	cct	gag	1555
Ala	Leu	Trp	Pro	Phe	Ser	Thr	Met	Gly	Trp	Pro	Glu	Lys	Thr	Pro	Glu	
470					475					480					485	
ctg	gag	aag	ttc	tac	cca	acc	tcc	gtg	ctg	gtc	acc	gcc	tac	gac	atc	1603
Leu	Glu	Lys	Phe	Tyr	Pro	Thr	Ser	Val	Leu	Val	Thr	Ala	Tyr	Asp	Ile	
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ctg	ttc	ttc	tgg	gtt	gcc	cgc	atg	atg	atg	ttc	ggc	acc	ttt	gca	gcc	1651
Leu	Phe	Phe	Trp	Val	Ala	Arg	Met	Met	Met	Phe	Gly	Thr	Phe	Ala	Ala	
			505					510					515			
aag	gaa	acc	cca	gaa	ctt	ctg	ggc	gaa	ggc	aag	gat	gga	cgc	cca	cag	1699
Lys	Glu	Thr	Pro	Glu	Leu	Leu	Gly	Glu	Gly	Lys	Asp	Gly	Arg	Pro	Gln	
		520					525					530				
gtt	cca	ttc	acc	gac	ctc	ttc	ctg	cac	ggc	ctg	gtt	cgc	gat	gag	cac	1747
Val	Pro	Phe	Thr	Asp	Leu	Phe	Leu	His	Gly	Leu	Val	Arg	Asp	Glu	His	
	535					540					545					
ggc	cgc	aag	atg	tcc	aag	tct	ttg	ggc	aac	ggc	atc	gat	ccg	atg	gat	1795
Gly	Arg	Lys	Met	Ser	Lys	Ser	Leu	Gly	Asn	Gly	Ile	Asp	Pro	Met	Asp	
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tgg	gtg	gag	aac	tac	ggc	gcg	gat	gcg	ttg	cgc	ttc	acc	ctt	gcc	cgt	1843
Trp	Val	Glu	Asn	Tyr	Gly	Ala	Asp	Ala	Leu	Arg	Phe	Thr	Leu	Ala	Arg	
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ggc	gct	aac	cca	ggc	gtc	gac	ctg	cct	gtc	ggt	gaa	gac	tct	gca	cag	1891
Gly	Ala	Asn	Pro	Gly	Val	Asp	Leu	Pro	Val	Gly	Glu	Asp	Ser	Ala	Gln	
			585					590					595			
agc	tcc	cgt	aac	ttt	gcc	acc	aag	ctg	ttc	aac	gca	acc	aag	ttt	gcg	1939
Ser	Ser	Arg	Asn	Phe	Ala	Thr	Lys	Leu	Phe	Asn	Ala	Thr	Lys	Phe	Ala	
		600					605					610				
ctg	atg	aac	ggt	gca	gtg	tcc	gaa	ggc	ctg	cca	gca	cgt	gaa	gaa	ctc	1987
Leu	Met	Asn	Gly	Ala	Val	Ser	Glu	Gly	Leu	Pro	Ala	Arg	Glu	Glu	Leu	

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acc gac gct gac cgc tgg atc gtg gac ctc ctt gag cag gtt cgc ctc			2035
Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu Glu Gln Val Arg Leu			
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gac gtt gat gct tac ctg gac aac tac cag ttc gcg aag gcc aac gag			2083
Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe Ala Lys Ala Asn Glu			
	650	655	660
gag ctc tac cac ttt gcg tgg aac gag ttc tgt gac tgg tac ctg gaa			2131
Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys Asp Trp Tyr Leu Glu			
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atc gcg aag gtt cag atc			2149
Ile Ala Lys Val Gln Ile			
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<211> 683

<212> PRT

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35 40 45	
Ser Asp Lys Pro Gly Phe Ser Ile Val Leu Pro Pro Pro Asn Val Thr	
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Gly Gln Leu His Met Gly His Ala Leu Asp His Thr Leu Met Asp Ala	
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Leu Ala Arg Arg Lys Arg Met Gln Gly Phe Glu Val Leu Trp Leu Pro	
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Gly Met Asp His Ala Gly Ile Ala Thr Gln Thr Lys Val Glu Glu Met	
100 105 110	
Leu Lys Glu Thr Glu Gly Lys Thr Arg Tyr Asp Tyr Asp Arg Glu Glu	
115 120 125	
Phe Ile Ala Lys Val Trp Glu Trp Lys Gln Glu Tyr Gly Gly Lys Ile	
130 135 140	
Gly Glu Gln Met Arg Ala Ile Gly Asp Ser Val Asp Trp Ser Arg Glu	
145 150 155 160	
Arg Phe Thr Leu Asp Asp Gly Leu Ser Arg Ala Val Gln Thr Ile Phe	
165 170 175	
Lys Lys Leu Phe Asp Ala Gly Leu Ile Tyr Gln Ala Asn Arg Leu Val	
180 185 190	

Asn Trp Ser Pro Val Leu Glu Thr Ala Val Ser Asp Ile Glu Val Ile
 195 200 205
 Tyr Lys Asp Val Glu Gly Glu Leu Val Ser Ile Arg Tyr Gly Ser Leu
 210 215 220
 Asn Asp Asp Glu Pro His Val Ile Val Ala Thr Thr Arg Val Glu Thr
 225 230 235 240
 Met Leu Gly Asp Val Ala Val Ala Val His Pro Asp Asp Glu Arg Tyr
 245 250 255
 Lys Asp Leu Val Gly Gln Thr Leu Pro His Pro Phe Arg Asp Asp Leu
 260 265 270
 Ser Leu Lys Val Val Ala Asp Asp Tyr Val Asp Pro Glu Phe Gly Ser
 275 280 285
 Gly Ala Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Tyr Ala Leu
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 Gly Leu Arg His Asn Leu Asp Met Pro Thr Ile Met Asp Lys Thr Gly
 305 310 315 320
 Arg Ile Ala Asp Thr Gly Thr Gln Phe Asp Gly Leu Thr Arg Glu Glu
 325 330 335
 Ala Arg Ile Lys Val Arg Glu Glu Leu Ala Ala Gln Gly Arg Ile Val
 340 345 350
 Lys Glu Ile Arg Pro Tyr Val His Ser Val Gly His Ser Glu Arg Ser
 355 360 365
 Gly Glu Ala Ile Glu Pro Arg Leu Ser Leu Gln Trp Phe Val Lys Val
 370 375 380
 Glu Glu Leu Ala Lys Met Ser Gly Asp Ala Val Arg Glu Gly Asp Thr
 385 390 395 400
 Thr Ile His Pro Lys Ser Leu Glu Pro Arg Tyr Phe Asp Trp Val Asp
 405 410 415
 Asn Met His Asp Trp Thr Ile Ser Arg Gln Leu Trp Trp Gly His Arg
 420 425 430
 Ile Pro Ile Trp Tyr Gly Pro Asn Asp Glu Ile Ile Cys Val Gly Pro
 435 440 445
 Asp Glu Gln Ala Pro Glu Gly Tyr Val Gln Asp Pro Asp Val Leu Asp
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 Thr Trp Phe Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro
 465 470 475 480
 Glu Lys Thr Pro Glu Leu Glu Lys Phe Tyr Pro Thr Ser Val Leu Val
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 Thr Ala Tyr Asp Ile Leu Phe Phe Trp Val Ala Arg Met Met Met Phe
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 Gly Thr Phe Ala Ala Lys Glu Thr Pro Glu Leu Leu Gly Glu Gly Lys

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Val Arg Asp Glu His Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly		
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Ile Asp Pro Met Asp Trp Val Glu Asn Tyr Gly Ala Asp Ala Leu Arg		
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Phe Thr Leu Ala Arg Gly Ala Asn Pro Gly Val Asp Leu Pro Val Gly		
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Glu Asp Ser Ala Gln Ser Ser Arg Asn Phe Ala Thr Lys Leu Phe Asn		
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Ala Thr Lys Phe Ala Leu Met Asn Gly Ala Val Ser Glu Gly Leu Pro		
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Ala Arg Glu Glu Leu Thr Asp Ala Asp Arg Trp Ile Val Asp Leu Leu		
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Glu Gln Val Arg Leu Asp Val Asp Ala Tyr Leu Asp Asn Tyr Gln Phe		
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Ala Lys Ala Asn Glu Glu Leu Tyr His Phe Ala Trp Asn Glu Phe Cys		
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<223> RXN00454

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				Met Gly Gly Glu Ala	
				1	5

ggc tgc acg tta gac ttg gca cct atg tca gat ctt tca ttc acc ctc	163
Gly Cys Thr Leu Asp Leu Ala Pro Met Ser Asp Leu Ser Phe Thr Leu	
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	15
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aac aac aag ctt gcc gat gac gcc ccc ggc aag cat ggt cgt aca ggt	211
Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys His Gly Arg Thr Gly	
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gta atc cac aca cct cac ggt gat att gcc acc cct gct ttc att cct	259
Val Ile His Thr Pro His Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro	
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gtg gct acc aaa gcc acg gtg aaa acc ctt acc cct gag cag att cgg	307
Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr Pro Glu Gln Ile Arg	
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gag acc ggc gca cag gct att ttg tcc aac gcc tac cac ctg tat ctg	355
Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu	
70 75 80 85	
cag cct ggc ccc gac atc gtg gac gag gct ggc ggt gtg tct gcc ttt	403
Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly Gly Val Ser Ala Phe	
90 95 100	
gag aac tgg cac ggc ccc acc tac acc gac tcc ggc gga ttc cag gtc	451
Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val	
105 110 115	
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Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu Ala Met Asp Thr Thr	
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aac ttg acg cgc aac gat atc aag gcg gct aaa aaa gag cgc atg gcg	547
Asn Leu Thr Arg Asn Asp Ile Lys Ala Ala Lys Lys Glu Arg Met Ala	
135 140 145	
ctt gtc gac gaa gac ggc gtg gat ttc aaa tct gtt atc gat ggc tca	595
Leu Val Asp Glu Asp Gly Val Asp Phe Lys Ser Val Ile Asp Gly Ser	
150 155 160 165	
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Lys His Arg Phe Thr Pro Glu Val Ser Met Gln Ile Gln His Gln Leu	
170 175 180	
ggc gca gac atc atc ttt gct ttt gat gaa ctg acc acc ttg gtt gat	691
Gly Ala Asp Ile Ile Phe Ala Phe Asp Glu Leu Thr Thr Leu Val Asp	
185 190 195	
acc tat gac tac cag gtg gaa tct gtg gaa cgt acc cgc agg tgg gca	739
Thr Tyr Asp Tyr Gln Val Glu Ser Val Glu Arg Thr Arg Arg Trp Ala	
200 205 210	
cag cgc tgc ctc ctg gag cat gaa cgt ttg act cag gaa cgt gtg gat	787
Gln Arg Cys Leu Leu Glu His Glu Arg Leu Thr Gln Glu Arg Val Asp	
215 220 225	
aaa cca ctg caa tcc cta tgg gga gtg gtg cag ggc ggc cag ttc gag	835
Lys Pro Leu Gln Ser Leu Trp Gly Val Val Gln Gly Ala Gln Phe Glu	
230 235 240 245	
gat ttg cgt cga caa gca gta aaa ggc ctg ttg gac ctg gat cgc cag	883
Asp Leu Arg Arg Gln Ala Val Lys Gly Leu Leu Asp Leu Asp Arg Gln	
250 255 260	
gcc gcc gac gaa ggc cgt cgc ggc ttc ggc ggt ttc ggc atc ggt ggc	931
Ala Ala Asp Glu Gly Arg Arg Gly Phe Gly Gly Phe Gly Ile Gly Gly	
265 270 275	
gcc cta gag aag gaa aac ctg ggc acc atc gtg ggc tgg gtg tgc gat	979
Ala Leu Glu Lys Glu Asn Leu Gly Thr Ile Val Gly Trp Val Cys Asp	
280 285 290	

gag ctg ccc gag gac aag cca cgt cac ctg ctg ggc att tcc gag ccg 1027
 Glu Leu Pro Glu Asp Lys Pro Arg His Leu Leu Gly Ile Ser Glu Pro
 295 300 305

gac gat ctg ttc gtg gct gtc gaa gcc ggt gcg gac acc ttt gac tgc 1075
 Asp Asp Leu Phe Val Ala Val Glu Ala Gly Ala Asp Thr Phe Asp Cys
 310 315 320 325

gtg gcg ccg act cgt ttg ggt cga cgc ggc ggt gtc tac acg ctt gat 1123
 Val Ala Pro Thr Arg Leu Gly Arg Arg Gly Gly Val Tyr Thr Leu Asp
 330 335 340

gga cgc atg aat ttg acc ggt gcg cgt ttc aag cgt gac ttc aag gga 1171
 Gly Arg Met Asn Leu Thr Gly Ala Arg Phe Lys Arg Asp Phe Lys Gly
 345 350 355

atc gat gag gaa gtc ggc gga tac gcc agc gag aac tac tcc cgc gcg 1219
 Ile Asp Glu Glu Val Gly Gly Tyr Ala Ser Glu Asn Tyr Ser Arg Ala
 360 365 370

tac att cat cac ctg ctc aaa gcg aag gaa ttt ttg gcc ggc acg ctg 1267
 Tyr Ile His His Leu Leu Lys Ala Lys Glu Phe Leu Ala Gly Thr Leu
 375 380 385

tgc acc atg cac aat ctg cac ttc atg atc acc ttg gtg gat aag att 1315
 Cys Thr Met His Asn Leu His Phe Met Ile Thr Leu Val Asp Lys Ile
 390 395 400 405

cgt gcc agc atc gat gat ggc acg tac tac gaa ttc aag gaa gaa ttc 1363
 Arg Ala Ser Ile Asp Asp Gly Thr Tyr Tyr Glu Phe Lys Glu Glu Phe
 410 415 420

tta ggc cgg tac tac gcg tcg aag gtt tca taaccttcgc ggcgtttcac cca 1416
 Leu Gly Arg Tyr Tyr Ala Ser Lys Val Ser
 425 430

<210> 350

<211> 431

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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 1 5 10 15

Leu Ser Phe Thr Leu Asn Asn Lys Leu Ala Asp Asp Ala Pro Gly Lys
 20 25 30

His Gly Arg Thr Gly Val Ile His Thr Pro His Gly Asp Ile Ala Thr
 35 40 45

Pro Ala Phe Ile Pro Val Ala Thr Lys Ala Thr Val Lys Thr Leu Thr
 50 55 60

Pro Glu Gln Ile Arg Glu Thr Gly Ala Gln Ala Ile Leu Ser Asn Ala
 65 70 75 80

Tyr His Leu Tyr Leu Gln Pro Gly Pro Asp Ile Val Asp Glu Ala Gly
 85 90 95

Gly Val Ser Ala Phe Glu Asn Trp His Gly Pro Thr Tyr Thr Asp Ser
 100 105 110
 Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly Phe Lys Lys Val Leu
 115 120 125
 Ala Met Asp Thr Thr Asn Leu Thr Arg Asn Asp Ile Lys Ala Ala Lys
 130 135 140
 Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly Val Asp Phe Lys Ser
 145 150 155 160
 Val Ile Asp Gly Ser Lys His Arg Phe Thr Pro Glu Val Ser Met Gln
 165 170 175
 Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe Ala Phe Asp Glu Leu
 180 185 190
 Thr Thr Leu Val Asp Thr Tyr Asp Tyr Gln Val Glu Ser Val Glu Arg
 195 200 205
 Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu His Glu Arg Leu Thr
 210 215 220
 Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu Trp Gly Val Val Gln
 225 230 235 240
 Gly Ala Gln Phe Glu Asp Leu Arg Arg Gln Ala Val Lys Gly Leu Leu
 245 250 255
 Asp Leu Asp Arg Gln Ala Ala Asp Glu Gly Arg Arg Gly Phe Gly Gly
 260 265 270
 Phe Gly Ile Gly Gly Ala Leu Glu Lys Glu Asn Leu Gly Thr Ile Val
 275 280 285
 Gly Trp Val Cys Asp Glu Leu Pro Glu Asp Lys Pro Arg His Leu Leu
 290 295 300
 Gly Ile Ser Glu Pro Asp Asp Leu Phe Val Ala Val Glu Ala Gly Ala
 305 310 315 320
 Asp Thr Phe Asp Cys Val Ala Pro Thr Arg Leu Gly Arg Arg Gly Gly
 325 330 335
 Val Tyr Thr Leu Asp Gly Arg Met Asn Leu Thr Gly Ala Arg Phe Lys
 340 345 350
 Arg Asp Phe Lys Gly Ile Asp Glu Glu Val Gly Gly Tyr Ala Ser Glu
 355 360 365
 Asn Tyr Ser Arg Ala Tyr Ile His His Leu Leu Lys Ala Lys Glu Phe
 370 375 380
 Leu Ala Gly Thr Leu Cys Thr Met His Asn Leu His Phe Met Ile Thr
 385 390 395 400
 Leu Val Asp Lys Ile Arg Ala Ser Ile Asp Asp Gly Thr Tyr Tyr Glu
 405 410 415
 Phe Lys Glu Glu Phe Leu Gly Arg Tyr Tyr Ala Ser Lys Val Ser

420

425

430

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 <211> 864
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(864)
 <223> FRXA00454

<400> 351
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 Gly Asp Ile Ala Thr Pro Ala Phe Ile Pro Val Ala Thr Lys Ala Thr
 1 5 10 15

gtg aaa acc ctt acc cct gag cag att cgg gag acc ggc gca cag gct 96
 Val Lys Thr Leu Thr Pro Glu Gln Ile Arg Glu Thr Gly Ala Gln Ala
 20 25 30

att ttg tcc aac gcc tac cac ctg tat ctg cag cct ggc ccc gac atc 144
 Ile Leu Ser Asn Ala Tyr His Leu Tyr Leu Gln Pro Gly Pro Asp Ile
 35 40 45

gtg gac gag gct ggc ggt gtg tct gcc ttt gag aac tgg cac ggc ccc 192
 Val Asp Glu Ala Gly Gly Val Ser Ala Phe Glu Asn Trp His Gly Pro
 50 55 60

acc tac acc gac tcc ggc gga ttc cag gtc atg agc ctg ggc tcc ggc 240
 Thr Tyr Thr Asp Ser Gly Gly Phe Gln Val Met Ser Leu Gly Ser Gly
 65 70 75 80

ttt aaa aag gtg ctg gcc atg gac acc acc aac ttg acg cgc aac gat 288
 Phe Lys Lys Val Leu Ala Met Asp Thr Thr Asn Leu Thr Arg Asn Asp
 85 90 95

atc aag gcg gct aaa aaa gag cgc atg gcg ctt gtc gac gaa gac ggc 336
 Ile Lys Ala Ala Lys Lys Glu Arg Met Ala Leu Val Asp Glu Asp Gly
 100 105 110

gtg gat ttc aaa tct gtt atc gat ggc tca aag cac cga ttc acc cca 384
 Val Asp Phe Lys Ser Val Ile Asp Gly Ser Lys His Arg Phe Thr Pro
 115 120 125

gaa gtc tcc atg cag att cag cac caa ttg ggc gca gac atc atc ttt 432
 Glu Val Ser Met Gln Ile Gln His Gln Leu Gly Ala Asp Ile Ile Phe
 130 135 140

gct ttt gat gaa ctg acc acc ttg gtt gat acc tat gac tac cag gtg 480
 Ala Phe Asp Glu Leu Thr Thr Leu Val Asp Thr Tyr Asp Tyr Gln Val
 145 150 155 160

gaa tct gtg gaa cgt acc cgc agg tgg gca cag cgc tgc ctc ctg gag 528
 Glu Ser Val Glu Arg Thr Arg Arg Trp Ala Gln Arg Cys Leu Leu Glu
 165 170 175

cat gaa cgt ttg act cag gaa cgt gtg gat aaa cca ctg caa tcc cta 576
 His Glu Arg Leu Thr Gln Glu Arg Val Asp Lys Pro Leu Gln Ser Leu
 180 185 190

<400> 352															
Gly 1	Asp	Ile	Ala	Thr 5	Pro	Ala	Phe	Ile	Pro 10	Val	Ala	Thr	Lys	Ala 15	Thr
Val	Lys	Thr	Leu 20	Thr	Pro	Glu	Gln	Ile 25	Arg	Glu	Thr	Gly	Ala 30	Gln	Ala
Ile	Leu	Ser 35	Asn	Ala	Tyr	His	Leu 40	Tyr	Leu	Gln	Pro	Gly 45	Pro	Asp	Ile
Val	Asp 50	Glu	Ala	Gly	Gly	Val 55	Ser	Ala	Phe	Glu	Asn 60	Trp	His	Gly	Pro
Thr 65	Tyr	Thr	Asp	Ser	Gly 70	Gly	Phe	Gln	Val	Met 75	Ser	Leu	Gly	Ser	Gly 80
Phe	Lys	Lys	Val	Leu 85	Ala	Met	Asp	Thr	Thr 90	Asn	Leu	Thr	Arg	Asn 95	Asp
Ile	Lys	Ala	Ala 100	Lys	Lys	Glu	Arg	Met 105	Ala	Leu	Val	Asp	Glu 110	Asp	Gly
Val	Asp	Phe 115	Lys	Ser	Val	Ile	Asp 120	Gly	Ser	Lys	His	Arg 125	Phe	Thr	Pro
Glu 130	Val	Ser	Met	Gln	Ile	Gln 135	His	Gln	Leu	Gly	Ala 140	Asp	Ile	Ile	Phe
Ala 145	Phe	Asp	Glu	Leu 150	Thr	Thr	Leu	Val	Asp 155	Thr	Tyr	Asp	Tyr	Gln	Val 160

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<210> 353
<211> 1014
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(991)
<223> RXN01490
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aatatccact gtttttagact acggcataga ctcaacagac															115
Met Asn Ala Pro Ala															
1 5															
cct aaa cct gga ctc gtg atc gtc gac aag ccc gcc gga atg aca tcc															163
Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro Ala Gly Met Thr Ser															
10 15 20															
cat gac gtg gtg tcc aaa ttg cgc cgc gca ttt tcc acc cgc aaa gta															211
His Asp Val Val Ser Lys Leu Arg Arg Ala Phe Ser Thr Arg Lys Val															
25 30 35															
ggc cac gca ggc acc ctc gac ccc atg gca acc ggc gtg tta gtc gtc															259
Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr Gly Val Leu Val Val															
40 45 50															
gga att gag cgc gga acc cgc ttc ctg gca cac atg gtg gcc tcc acc															307
Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His Met Val Ala Ser Thr															
55 60 65															
aaa gcc tac gac gcc acc att cga ctc ggc gcc gcc acc agc acc gat															355
Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala Ala Thr Ser Thr Asp															

70	75	80	85	
gat gca gaa ggc gag gtt atc tcc aca aca gac gca tcc ggc ctc gac				403
Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp Ala Ser Gly Leu Asp	90	95	100	
cac agc acc atc ctt gct gaa atc gtc aac ctc acc ggc gac atc atg				451
His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu Thr Gly Asp Ile Met	105	110	115	
caa aaa ccc acc aaa gtc tcc gcc atc aaa atc gac ggc aaa cgc gcc				499
Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile Asp Gly Lys Arg Ala	120	125	130	
cac gaa cgc gtc cgc gac ggc gaa gaa gta gac att ccc gca cgt ccc				547
His Glu Arg Val Arg Asp Gly Glu Glu Val Asp Ile Pro Ala Arg Pro	135	140	145	
gtc acc gtc agc gtc ttt gac gtg ctc gac tac cac gtc gac ggt gaa				595
Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr His Val Asp Gly Glu	150	155	160	165
ttt tat gac tta gat gtg cgc gtc cac tgc tcc tcc ggc acc tac atc				643
Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser Ser Gly Thr Tyr Ile	170	175	180	
cgc gcg ctc gcc cgc gac ctc ggc aac gct ttg cag gtc ggc ggc cac				691
Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu Gln Val Gly Gly His	185	190	195	
ctg acc gcg ctt agg cgc aca gag gtc ggc cct ttt acg ctt aac gac				739
Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro Phe Thr Leu Asn Asp	200	205	210	
gcg acc ccc ctc tcc aaa ctc caa gag aat cca gaa ctc tcc ctc aac				787
Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro Glu Leu Ser Leu Asn	215	220	225	
ctc gac cag gca ctc acc cgc agt tac cca gtc ctt gac atc acc gaa				835
Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val Leu Asp Ile Thr Glu	230	235	240	245
gac gaa ggc gtt gac ctg tcc atg ggc aaa tgg ttg gaa cct cgc gga				883
Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp Leu Glu Pro Arg Gly	250	255	260	
ctg aaa ggc gtc cac gct gca gta aca cca tca gga aaa gcc gtg gcg				931
Leu Lys Gly Val His Ala Ala Val Thr Pro Ser Gly Lys Ala Val Ala	265	270	275	
ctc atc gaa gaa aag ggc aaa cgc ctg gcc acc gtg ttt gtt gct cac				979
Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr Val Phe Val Ala His	280	285	290	
ccc aac act ctt tagttggtct gccagaagcc gat				1014
Pro Asn Thr Leu	295			

<210> 354

<211> 297

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 354

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Met Asn Ala Pro Ala Pro Lys Pro Gly Leu Val Ile Val Asp Lys Pro
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Ala Gly Met Thr Ser His Asp Val Val Ser Lys Leu Arg Arg Ala Phe
      20              25              30

Ser Thr Arg Lys Val Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr
      35              40              45

Gly Val Leu Val Val Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His
 50              55              60

Met Val Ala Ser Thr Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala
 65              70              75              80

Ala Thr Ser Thr Asp Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp
      85              90              95

Ala Ser Gly Leu Asp His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu
      100              105              110

Thr Gly Asp Ile Met Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile
 115              120              125

Asp Gly Lys Arg Ala His Glu Arg Val Arg Asp Gly Glu Glu Val Asp
 130              135              140

Ile Pro Ala Arg Pro Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr
 145              150              155              160

His Val Asp Gly Glu Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser
      165              170              175

Ser Gly Thr Tyr Ile Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu
      180              185              190

Gln Val Gly Gly His Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro
 195              200              205

Phe Thr Leu Asn Asp Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro
 210              215              220

Glu Leu Ser Leu Asn Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val
 225              230              235              240

Leu Asp Ile Thr Glu Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp
      245              250              255

Leu Glu Pro Arg Gly Leu Lys Gly Val His Ala Ala Val Thr Pro Ser
      260              265              270

Gly Lys Ala Val Ala Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr
      275              280              285

Val Phe Val Ala His Pro Asn Thr Leu
 290              295

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<400> 355																
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aatatccact	gttttagact	acggcataga	ctcaacagac	atg	aat	gct	cct	gcc	115							
				Met	Asn	Ala	Pro	Ala	5							
				1												
cct	aaa	cct	gga	ctc	gtg	atc	gtc	gac	aag	ccc	gcc	gga	atg	aca	tcc	163
Pro	Lys	Pro	Gly	Leu	Val	Ile	Val	Asp	Lys	Pro	Ala	Gly	Met	Thr	Ser	
				10					15					20		
cat	gac	gtg	gtg	tcc	aaa	ttg	cgc	cgc	gca	ttt	tcc	acc	cgc	aaa	gta	211
His	Asp	Val	Val	Ser	Lys	Leu	Arg	Arg	Ala	Phe	Ser	Thr	Arg	Lys	Val	
				25				30					35			
ggc	cac	gca	ggc	acc	ctc	gac	ccc	atg	gca	acc	ggc	gtg	tta	gtc	gtc	259
Gly	His	Ala	Gly	Thr	Leu	Asp	Pro	Met	Ala	Thr	Gly	Val	Leu	Val	Val	
				40			45					50				
gga	att	gag	cgc	gga	acc	cgc	ttc	ctg	gca	cac	atg	gtg	gcc	tcc	acc	307
Gly	Ile	Glu	Arg	Gly	Thr	Arg	Phe	Leu	Ala	His	Met	Val	Ala	Ser	Thr	
	55					60					65					
aaa	gcc	tac	gac	gcc	acc	att	cga	ctc	ggc	gcc	gcc	acc	agc	acc	gat	355
Lys	Ala	Tyr	Asp	Ala	Thr	Ile	Arg	Leu	Gly	Ala	Ala	Thr	Ser	Thr	Asp	
	70				75					80					85	
gat	gca	gaa	ggc	gag	gtt	atc	tcc	aca	aca	gac	gca	tcc	ggc	ctc	gac	403
Asp	Ala	Glu	Gly	Glu	Val	Ile	Ser	Thr	Thr	Asp	Ala	Ser	Gly	Leu	Asp	
				90					95					100		
cac	agc	acc	atc	ctt	gct	gaa	atc	gtc	aac	ctc	acc	ggc	gac	atc	atg	451
His	Ser	Thr	Ile	Leu	Ala	Glu	Ile	Val	Asn	Leu	Thr	Gly	Asp	Ile	Met	
			105					110					115			
caa	aaa	ccc	acc	aaa	gtc	tcc	gcc	atc	aaa	atc	gac	ggc	aaa	cgc	gcc	499
Gln	Lys	Pro	Thr	Lys	Val	Ser	Ala	Ile	Lys	Ile	Asp	Gly	Lys	Arg	Ala	
			120				125					130				
cac	gaa	cgc	gtc	cgc	gac	ggc	gaa	gaa	gta	gac	att	ccc	gca	cgt	ccc	547
His	Glu	Arg	Val	Arg	Asp	Gly	Glu	Glu	Val	Asp	Ile	Pro	Ala	Arg	Pro	
	135					140					145					
gtc	acc	gtc	agc	gtc	ttt	gac	gtg	ctc	gac	tac	cac	gtc	gac	ggg	gaa	595
Val	Thr	Val	Ser	Val	Phe	Asp	Val	Leu	Asp	Tyr	His	Val	Asp	Gly	Glu	
	150				155				160						165	
ttt	tat	gac	tta	gat	gtg	cgc	gtc	cac	tgc	tcc	tcc	ggc	acc	tac	atc	643
Phe	Tyr	Asp	Leu	Asp	Val	Arg	Val	His	Cys	Ser	Ser	Gly	Thr	Tyr	Ile	
				170					175					180		

cgc gcg ctc gcc cgc gac ctc ggc aac gct ttg cag gtc ggc ggc cac 691
 Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu Gln Val Gly Gly His
 185 190 195

ctg acc gcg ctt agg cgc aca gag gtc ggc cct ttt acg ctt aac gac 739
 Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro Phe Thr Leu Asn Asp
 200 205 210

gcg acc ccc ctc tcc aaa ctc caa gag aat cca gaa ctc tcc ctc aac 787
 Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro Glu Leu Ser Leu Asn
 215 220 225

ctc gac cag gca ctc acc cgc agt tac cca gtc ctt gac atc acc gaa 835
 Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val Leu Asp Ile Thr Glu
 230 235 240 245

gac gaa ggc gtt gac ctg tcc atg ggc aaa tgg ttg gaa cct cgc gga 883
 Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp Leu Glu Pro Arg Gly
 250 255 260

ctg aaa ggc gtc cac gct gca gta aca cca tca gga aaa gcc gtg gcg 931
 Leu Lys Gly Val His Ala Ala Val Thr Pro Ser Gly Lys Ala Val Ala
 265 270 275

ctc atc gaa gaa aag ggc aaa cgc ctg gcc acc gtg ttt gtt gct cac 979
 Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr Val Phe Val Ala His
 280 285 290

ccc aac act ctt tagttggtct gccagaagcc gat 1014
 Pro Asn Thr Leu
 295

<210> 356

<211> 297

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

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 20 25 30

Ser Thr Arg Lys Val Gly His Ala Gly Thr Leu Asp Pro Met Ala Thr
 35 40 45

Gly Val Leu Val Val Gly Ile Glu Arg Gly Thr Arg Phe Leu Ala His
 50 55 60

Met Val Ala Ser Thr Lys Ala Tyr Asp Ala Thr Ile Arg Leu Gly Ala
 65 70 75 80

Ala Thr Ser Thr Asp Asp Ala Glu Gly Glu Val Ile Ser Thr Thr Asp
 85 90 95

Ala Ser Gly Leu Asp His Ser Thr Ile Leu Ala Glu Ile Val Asn Leu
 100 105 110

Thr Gly Asp Ile Met Gln Lys Pro Thr Lys Val Ser Ala Ile Lys Ile
 115 120 125
 Asp Gly Lys Arg Ala His Glu Arg Val Arg Asp Gly Glu Glu Val Asp
 130 135 140
 Ile Pro Ala Arg Pro Val Thr Val Ser Val Phe Asp Val Leu Asp Tyr
 145 150 155 160
 His Val Asp Gly Glu Phe Tyr Asp Leu Asp Val Arg Val His Cys Ser
 165 170 175
 Ser Gly Thr Tyr Ile Arg Ala Leu Ala Arg Asp Leu Gly Asn Ala Leu
 180 185 190
 Gln Val Gly Gly His Leu Thr Ala Leu Arg Arg Thr Glu Val Gly Pro
 195 200 205
 Phe Thr Leu Asn Asp Ala Thr Pro Leu Ser Lys Leu Gln Glu Asn Pro
 210 215 220
 Glu Leu Ser Leu Asn Leu Asp Gln Ala Leu Thr Arg Ser Tyr Pro Val
 225 230 235 240
 Leu Asp Ile Thr Glu Asp Glu Gly Val Asp Leu Ser Met Gly Lys Trp
 245 250 255
 Leu Glu Pro Arg Gly Leu Lys Gly Val His Ala Ala Val Thr Pro Ser
 260 265 270
 Gly Lys Ala Val Ala Leu Ile Glu Glu Lys Gly Lys Arg Leu Ala Thr
 275 280 285
 Val Phe Val Ala His Pro Asn Thr Leu
 290 295

<210> 357
 <211> 1563
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1540)
 <223> RXA01621

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 Val Asp Gln Glu Val 1 5
 gac cgc ctt gct tta atg gcg cgc gct cac cag gca att ggt gag ctt 163
 Asp Arg Leu Ala Leu Met Ala Arg Ala His Gln Ala Ile Gly Glu Leu 10 15 20
 tca gac atc ctt gtg ccc cta gcg gca gca ttt tcc agc aag gga cac 211
 Ser Asp Ile Leu Val Pro Leu Ala Ala Phe Ser Ser Lys Gly His 25 30 35

tcc cta tat ttg gtg ggc ggt tcc gtg agg gat gct ttc tta ggt gag	259
Ser Leu Tyr Leu Val Gly Gly Ser Val Arg Asp Ala Phe Leu Gly Glu	
40 45 50	
ttg ggg cat gac ctt gat ttc acc acg tcg gca cgc cct gag gag aca	307
Leu Gly His Asp Leu Asp Phe Thr Thr Ser Ala Arg Pro Glu Glu Thr	
55 60 65	
aag gcg atc ctg gat gat tac gcc gat gtg gtg tgg gat acc gga att	355
Lys Ala Ile Leu Asp Asp Tyr Ala Asp Val Val Trp Asp Thr Gly Ile	
70 75 80 85	
gcg ttt ggc acc ctt tct gca gaa aag cat ggt cag cag atc gaa atc	403
Ala Phe Gly Thr Leu Ser Ala Glu Lys His Gly Gln Gln Ile Glu Ile	
90 95 100	
acg aca ttc cgt tct gat ctc tat gac gga aac tcc cgc aac cct gaa	451
Thr Thr Phe Arg Ser Asp Leu Tyr Asp Gly Asn Ser Arg Asn Pro Glu	
105 110 115	
gtg acc ttc ggt gac acc ttg gaa ggc gat ctg att agg cgc gat ttc	499
Val Thr Phe Gly Asp Thr Leu Glu Gly Asp Leu Ile Arg Arg Asp Phe	
120 125 130	
aag gtc aac gcc atg gct gtg gag atc caa gcc gat ggt gaa tta act	547
Lys Val Asn Ala Met Ala Val Glu Ile Gln Ala Asp Gly Glu Leu Thr	
135 140 145	
ttc cac gat cca gtg ggt ggc ttg gaa gat cta ctt acc cac act ttg	595
Phe His Asp Pro Val Gly Gly Leu Glu Asp Leu Leu Thr His Thr Leu	
150 155 160 165	
gat acc cca gct act ccg gaa caa tca ttc aat gat gat cct ctg cga	643
Asp Thr Pro Ala Thr Pro Glu Gln Ser Phe Asn Asp Asp Pro Leu Arg	
170 175 180	
atg ctg cgc gct gcc cgc ttt gtt tcc caa ctg aat ttc acc ctt gca	691
Met Leu Arg Ala Ala Arg Phe Val Ser Gln Leu Asn Phe Thr Leu Ala	
185 190 195	
cca cga gtt att acc gcc atg act gaa atg gcg cag cag att act cgg	739
Pro Arg Val Ile Thr Ala Met Thr Glu Met Ala Gln Gln Ile Thr Arg	
200 205 210	
atc act gtg gaa cgc atg cag gtt gag ttg gac aaa atg atc ctt ggc	787
Ile Thr Val Glu Arg Met Gln Val Glu Leu Asp Lys Met Ile Leu Gly	
215 220 225	
aaa aac cct gag gct ggc att gac ctc atg gtg gag tcc ggt atc gcg	835
Lys Asn Pro Glu Ala Gly Ile Asp Leu Met Val Glu Ser Gly Ile Ala	
230 235 240 245	
cag att att tat ccg gag atc cct gcg atg cag atg act caa gat gaa	883
Gln Ile Ile Tyr Pro Glu Ile Pro Ala Met Gln Met Thr Gln Asp Glu	
250 255 260	
cac atg cag cac aag gat gtg tac gcg cac tcg ttg cag gtg atg cgc	931
His Met Gln His Lys Asp Val Tyr Ala His Ser Leu Gln Val Met Arg	
265 270 275	

caa gcg att gat cag gaa gaa gat ggc cct gac ctg gtg ctt cgt tgg	979
Gln Ala Ile Asp Gln Glu Glu Asp Gly Pro Asp Leu Val Leu Arg Trp	
280 285 290	
gct gct ctg ctt cat gat tgc ggt aag cca gat act cgt gac ttc aat	1027
Ala Ala Leu Leu His Asp Cys Gly Lys Pro Asp Thr Arg Asp Phe Asn	
295 300 305	
gag gaa ggc cgc gtg agc ttc cat cag cat gag gta gtt ggc gcc aag	1075
Glu Glu Gly Arg Val Ser Phe His Gln His Glu Val Val Gly Ala Lys	
310 315 320 325	
ctg gtg agg cga cgg atg cgc aag ctg aag tac tca aag caa atg gtc	1123
Leu Val Arg Arg Arg Met Arg Lys Leu Lys Tyr Ser Lys Gln Met Val	
330 335 340	
ggc gat gtc ggg cag ttg gtg ttc ctg cac atg cgt ttc cat ggt ttc	1171
Gly Asp Val Gly Gln Leu Val Phe Leu His Met Arg Phe His Gly Phe	
345 350 355	
agc gaa ggc cag tgg acg gat tct gca gtg cgt agg tat gcc gca gat	1219
Ser Glu Gly Gln Trp Thr Asp Ser Ala Val Arg Arg Tyr Ala Ala Asp	
360 365 370	
gcg ggt gaa ttg ctg cca cgt ttg cac aag tta gtg cgt gct gat tgc	1267
Ala Gly Glu Leu Leu Pro Arg Leu His Lys Leu Val Arg Ala Asp Cys	
375 380 385	
acc aca aga aat aaa agg aag gca gca cga ctg caa gcc acc tac gat	1315
Thr Thr Arg Asn Lys Arg Lys Ala Ala Arg Leu Gln Ala Thr Tyr Asp	
390 395 400 405	
cat ttg gaa gag cgc atc gcg gag atc gcc gca aag gaa gat ctt gcc	1363
His Leu Glu Glu Arg Ile Ala Glu Ile Ala Ala Lys Glu Asp Leu Ala	
410 415 420	
agg gtg cgc cca gat ttg gat ggc aat gag atc atg gag att ctg aac	1411
Arg Val Arg Pro Asp Leu Asp Gly Asn Glu Ile Met Glu Ile Leu Asn	
425 430 435	
atc caa gcc gga cct gaa gtg ggt aag gcg tgg gcg ttt ttg aag gag	1459
Ile Gln Ala Gly Pro Glu Val Gly Lys Ala Trp Ala Phe Leu Lys Glu	
440 445 450	
ctt cgt ttg gag cgc ggt cct ttg gat cgt gaa gtt gcc atc gca gag	1507
Leu Arg Leu Glu Arg Gly Pro Leu Asp Arg Glu Val Ala Ile Ala Glu	
455 460 465	
ctg aag agc tgg tgg gaa gga gaa aac aat gag tgatttttat gccgacaggt	1560
Leu Lys Ser Trp Trp Glu Gly Glu Asn Asn Glu	
470 475 480	
tgt	1563
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<213> Corynebacterium glutamicum	
<400> 358	

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Ala	Ile	Gly	Glu 20	Leu	Ser	Asp	Ile	Leu 25	Val	Pro	Leu	Ala	Ala 30	Ala	Phe
Ser	Ser	Lys 35	Gly	His	Ser	Leu	Tyr 40	Leu	Val	Gly	Gly 45	Ser	Val	Arg	Asp
Ala	Phe 50	Leu	Gly	Glu	Leu	Gly 55	His	Asp	Leu	Asp	Phe 60	Thr	Thr	Ser	Ala
Arg 65	Pro	Glu	Glu	Thr	Lys 70	Ala	Ile	Leu	Asp	Asp 75	Tyr	Ala	Asp	Val	Val 80
Trp	Asp	Thr	Gly	Ile 85	Ala	Phe	Gly	Thr 90	Leu	Ser	Ala	Glu	Lys	His 95	Gly
Gln	Gln	Ile	Glu 100	Ile	Thr	Thr	Phe	Arg 105	Ser	Asp	Leu	Tyr	Asp 110	Gly	Asn
Ser	Arg	Asn 115	Pro	Glu	Val	Thr	Phe 120	Gly	Asp	Thr	Leu	Glu	Gly 125	Asp	Leu
Ile 130	Arg	Arg	Asp	Phe	Lys	Val 135	Asn	Ala	Met	Ala	Val 140	Glu	Ile	Gln	Ala
Asp 145	Gly	Glu	Leu	Thr	Phe 150	His	Asp	Pro	Val	Gly 155	Gly	Leu	Glu	Asp	Leu 160
Leu	Thr	His	Thr	Leu 165	Asp	Thr	Pro	Ala	Thr 170	Pro	Glu	Gln	Ser	Phe 175	Asn
Asp	Asp	Pro	Leu 180	Arg	Met	Leu	Arg	Ala 185	Ala	Arg	Phe	Val	Ser 190	Gln	Leu
Asn	Phe	Thr 195	Leu	Ala	Pro	Arg	Val 200	Ile	Thr	Ala	Met	Thr 205	Glu	Met	Ala
Gln 210	Gln	Ile	Thr	Arg	Ile	Thr 215	Val	Glu	Arg	Met	Gln 220	Val	Glu	Leu	Asp
Lys 225	Met	Ile	Leu	Gly	Lys 230	Asn	Pro	Glu	Ala	Gly 235	Ile	Asp	Leu	Met	Val 240
Glu	Ser	Gly	Ile	Ala 245	Gln	Ile	Ile	Tyr	Pro 250	Glu	Ile	Pro	Ala	Met 255	Gln
Met	Thr	Gln 260	Asp	Glu	His	Met	Gln 265	His	Lys	Asp	Val	Tyr	Ala 270	His	Ser
Leu	Gln	Val 275	Met	Arg	Gln	Ala	Ile 280	Asp	Gln	Glu	Glu 285	Asp	Gly	Pro	Asp
Leu	Val	Leu	Arg	Trp	Ala	Ala 295	Leu	Leu	His	Asp	Cys 300	Gly	Lys	Pro	Asp
Thr 305	Arg	Asp	Phe	Asn 310	Glu	Gly	Arg	Val	Ser 315	Phe	His	Gln	His	Glu 320	
Val	Val	Gly	Ala	Lys	Leu	Val	Arg	Arg	Arg	Met	Arg	Lys	Leu	Lys	Tyr

				325						330						335
Ser	Lys	Gln	Met	Val	Gly	Asp	Val	Gly	Gln	Leu	Val	Phe	Leu	His	Met	
			340					345					350			
Arg	Phe	His	Gly	Phe	Ser	Glu	Gly	Gln	Trp	Thr	Asp	Ser	Ala	Val	Arg	
		355					360					365				
Arg	Tyr	Ala	Ala	Asp	Ala	Gly	Glu	Leu	Leu	Pro	Arg	Leu	His	Lys	Leu	
	370					375					380					
Val	Arg	Ala	Asp	Cys	Thr	Thr	Arg	Asn	Lys	Arg	Lys	Ala	Ala	Arg	Leu	
385					390					395					400	
Gln	Ala	Thr	Tyr	Asp	His	Leu	Glu	Glu	Arg	Ile	Ala	Glu	Ile	Ala	Ala	
				405					410					415		
Lys	Glu	Asp	Leu	Ala	Arg	Val	Arg	Pro	Asp	Leu	Asp	Gly	Asn	Glu	Ile	
			420					425					430			
Met	Glu	Ile	Leu	Asn	Ile	Gln	Ala	Gly	Pro	Glu	Val	Gly	Lys	Ala	Trp	
		435					440					445				
Ala	Phe	Leu	Lys	Glu	Leu	Arg	Leu	Glu	Arg	Gly	Pro	Leu	Asp	Arg	Glu	
	450					455					460					
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<211> 1100

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1077)

<223> RXN01704

<400> 359

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1				5					10					15		
gct	gat	cgt	gtc	gat	tcc	cgg	tgc	cca	gca	gcg	gca	gca	ggt	gct	ggt	96
Ala	Asp	Arg	Val	Asp	Ser	Arg	Cys	Pro	Ala	Ala	Ala	Ala	Gly	Ala	Gly	
			20					25					30			
tgc	tgt	gac	tat	gca	gaa	ctc	aac	cca	act	gtg	gag	ctt	gag	atc	aag	144
Cys	Cys	Asp	Tyr	Ala	Glu	Leu	Asn	Pro	Thr	Val	Glu	Leu	Glu	Ile	Lys	
		35				40						45				
tcc	cgc	gtg	ctt	cgt	gat	cag	ttg	gag	cgc	atc	ggt	gga	atc	gat	gag	192
Ser	Arg	Val	Leu	Arg	Asp	Gln	Leu	Glu	Arg	Ile	Gly	Gly	Ile	Asp	Glu	
	50					55					60					
ctt	cct	gaa	ttt	gag	ctt	caa	gat	ctg	gag	cca	aca	gct	ggt	tggt	cgt	240
Leu	Pro	Glu	Phe	Glu	Leu	Gln	Asp	Leu	Glu	Pro	Thr	Ala	Gly	Trp	Arg	
65					70					75					80	

acc cgc gtt cgc ctc ggc gtt gat gcg tct ggt cgt gcc ggg ttc cgc	288
Thr Arg Val Arg Leu Gly Val Asp Ala Ser Gly Arg Ala Gly Phe Arg	
85 90 95	
aag ctg aag tcc aat gag ttg gtt act gag gtt gcg tgt tct cag gtt	336
Lys Leu Lys Ser Asn Glu Leu Val Thr Glu Val Ala Cys Ser Gln Val	
100 105 110	
gtg cca gag ctt ctt gag ggc ctt gtg ggt gag ggc gct cgt cgt ttc	384
Val Pro Glu Leu Leu Glu Gly Leu Val Gly Glu Gly Ala Arg Arg Phe	
115 120 125	
acc cct ggc gtg gag atc att gca gct att gat gat gcg ggt cag cgc	432
Thr Pro Gly Val Glu Ile Ile Ala Ala Ile Asp Asp Ala Gly Gln Arg	
130 135 140	
cac gtt gtg gaa tcc cgt aag gct cct cgt ggt cgt cgt act gaa act	480
His Val Val Glu Ser Arg Lys Ala Pro Arg Gly Arg Arg Thr Glu Thr	
145 150 155 160	
gtg ttg aag gtg ctg gaa ggc act ggc gag gtg gag cag aag gta ggc	528
Val Leu Lys Val Leu Glu Gly Thr Gly Glu Val Glu Gln Lys Val Gly	
165 170 175	
gat tac acc tgg aag ttc cca gtt tct tcc ttc tgg cag gcg cac acc	576
Asp Tyr Thr Trp Lys Phe Pro Val Ser Ser Phe Trp Gln Ala His Thr	
180 185 190	
aag gcc cct gcg gcg tat tca gag ttc atc gcc gaa gcg tta acc gga	624
Lys Ala Pro Ala Ala Tyr Ser Glu Phe Ile Ala Glu Ala Leu Thr Gly	
195 200 205	
ttg gaa ctg gtt gac gtc gat aag cgt ggc cct gtt gcg tgg gac ctt	672
Leu Glu Leu Val Asp Val Asp Lys Arg Gly Pro Val Ala Trp Asp Leu	
210 215 220	
tat ggc ggc gtc ggc ctg ttc gcg ccg att atc acc agc aag ctg cag	720
Tyr Gly Gly Val Gly Leu Phe Ala Pro Ile Ile Thr Ser Lys Leu Gln	
225 230 235 240	
gca gct gtc cac tct gtg gag ctg tcc cca ggt tca gcg gag gct ggc	768
Ala Ala Val His Ser Val Glu Leu Ser Pro Gly Ser Ala Glu Ala Gly	
245 250 255	
gaa gag gcg ttg gct ggt ttg cct gtc act ttc cac act ggt cgg gta	816
Glu Glu Ala Leu Ala Gly Leu Pro Val Thr Phe His Thr Gly Arg Val	
260 265 270	
gag ggc atg gcg tcc cag ctg cct tcg cca aac gtg gtt gtt ttg gat	864
Glu Gly Met Ala Ser Gln Leu Pro Ser Pro Asn Val Val Val Leu Asp	
275 280 285	
cct cct cgc acc ggt gca ggc agt gac gtg ttg aag agc atc gcg gag	912
Pro Pro Arg Thr Gly Ala Gly Ser Asp Val Leu Lys Ser Ile Ala Glu	
290 295 300	
gct aag cct cag ctg gtt atc cac att ggt tgt gac ccg gcg act ttc	960
Ala Lys Pro Gln Leu Val Ile His Ile Gly Cys Asp Pro Ala Thr Phe	
305 310 315 320	
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Cys	Cys	Asp 35	Tyr	Ala	Glu	Leu	Asn 40	Pro	Thr	Val	Glu	Leu 45	Glu	Ile	Lys	
Ser	Arg 50	Val	Leu	Arg	Asp	Gln 55	Leu	Glu	Arg	Ile	Gly 60	Gly	Ile	Asp	Glu	
Leu 65	Pro	Glu	Phe	Glu	Leu 70	Gln	Asp	Leu	Glu	Pro 75	Thr	Ala	Gly	Trp	Arg 80	
Thr	Arg	Val	Arg	Leu 85	Gly	Val	Asp	Ala	Ser 90	Gly	Arg	Ala	Gly	Phe 95	Arg	
Lys	Leu	Lys	Ser 100	Asn	Glu	Leu	Val 105	Thr	Glu	Val	Ala	Cys 110	Ser	Gln	Val	
Val	Pro	Glu 115	Leu	Leu	Glu	Gly	Leu 120	Val	Gly	Glu	Gly	Ala 125	Arg	Arg	Phe	
Thr	Pro 130	Gly	Val	Glu	Ile	Ile 135	Ala	Ala	Ile	Asp	Asp 140	Ala	Gly	Gln	Arg	
His 145	Val	Val	Glu	Ser	Arg 150	Lys	Ala	Pro	Arg	Gly 155	Arg	Arg	Thr	Glu	Thr 160	
Val	Leu	Lys	Val	Leu 165	Glu	Gly	Thr	Gly	Glu 170	Val	Glu	Gln	Lys	Val 175	Gly	
Asp	Tyr	Thr	Trp 180	Lys	Phe	Pro	Val 185	Ser	Ser	Phe	Trp	Gln 190	Ala	His	Thr	
Lys	Ala	Pro 195	Ala	Ala	Tyr	Ser	Glu 200	Phe	Ile	Ala	Glu	Ala 205	Leu	Thr	Gly	
Leu	Glu 210	Leu	Val	Asp	Val	Asp 215	Lys	Arg	Gly	Pro	Val 220	Ala	Trp	Asp	Leu	
Tyr	Gly	Gly	Val	Gly	Leu	Phe	Ala	Pro	Ile	Ile	Thr	Ser	Lys	Leu	Gln	

225	230	235	240
Ala Ala Val His Ser	Val Glu Leu Ser	Pro Gly Ser Ala Glu	Ala Gly
245		250	255
Glu Glu Ala Leu Ala Gly	Leu Pro Val Thr Phe His Thr	Gly Arg Val	
260	265	270	
Glu Gly Met Ala Ser Gln Leu	Pro Ser Pro Asn Val Val	Val Leu Asp	
275	280	285	
Pro Pro Arg Thr Gly Ala Gly	Ser Asp Val Leu Lys Ser Ile Ala Glu		
290	295	300	
Ala Lys Pro Gln Leu Val Ile His Ile	Gly Cys Asp Pro Ala Thr Phe		
305	310	315	320
Ala Arg Asp Val Ala Asp Trp Lys Leu	Asn Gly Tyr Glu Met Asp Gln		
325	330	335	
Leu Ala Val Phe Asn Ala Phe Pro	Gly Thr His His Phe Glu Thr Ile		
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Gly Val Phe Val Arg Val Ser			
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<211> 839

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<213> Corynebacterium glutamicum

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<222> (1)..(816)

<223> FRXA01704

<400> 361

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ggt act gag gtt gcg tgt tct cag gtt gtg cca gag ctt ctt gag ggc	96
Val Thr Glu Val Ala Cys Ser Gln Val Val Pro Glu Leu Leu Glu Gly	
20 25 30	
ctt gtg ggt gag ggc gct cgt cgt ttc acc cct ggc gtg gag atc att	144
Leu Val Gly Glu Gly Ala Arg Arg Phe Thr Pro Gly Val Glu Ile Ile	
35 40 45	
gca gct att gat gat gcg ggt cag cgc cac gtt gtg gaa tcc cgt aag	192
Ala Ala Ile Asp Asp Ala Gly Gln Arg His Val Val Glu Ser Arg Lys	
50 55 60	
gct cct cgt ggt cgt cgt act gaa act gtg ttg aag gtg ctg gaa ggc	240
Ala Pro Arg Gly Arg Arg Thr Glu Thr Val Leu Lys Val Leu Glu Gly	
65 70 75 80	
act ggc gag gtg gag cag aag gta ggc gat tac acc tgg aag ttc cca	288
Thr Gly Glu Val Glu Gln Lys Val Gly Asp Tyr Thr Trp Lys Phe Pro	
85 90 95	

gtt tct tcc ttc tgg cag gcg cac acc aag gcc cct gcg gcg tat tca 336
 Val Ser Ser Phe Trp Gln Ala His Thr Lys Ala Pro Ala Ala Tyr Ser
 100 105 110

gag ttc atc gcc gaa gcg tta acc gga ttg gaa ctg gtt gac gtc gat 384
 Glu Phe Ile Ala Glu Ala Leu Thr Gly Leu Glu Leu Val Asp Val Asp
 115 120 125

aag cgt ggc cct gtt gcg tgg gac ctt tat ggc ggc gtc ggc ctg ttc 432
 Lys Arg Gly Pro Val Ala Trp Asp Leu Tyr Gly Gly Val Gly Leu Phe
 130 135 140

gcg ccg att atc acc agc aag ctg cag gca gct gtc cac tct gtg gag 480
 Ala Pro Ile Ile Thr Ser Lys Leu Gln Ala Ala Val His Ser Val Glu
 145 150 155 160

ctg tcc cca ggt tca gcg gag gct ggc gaa gag gcg ttg gct ggt ttg 528
 Leu Ser Pro Gly Ser Ala Glu Ala Gly Glu Glu Ala Leu Ala Gly Leu
 165 170 175

cct gtc act ttc cac act ggt cgg gta gag ggc atg gcg tcc cag ctg 576
 Pro Val Thr Phe His Thr Gly Arg Val Glu Gly Met Ala Ser Gln Leu
 180 185 190

cct tcg cca aac gtg gtt gtt ttg gat cct cct cgc acc ggt gca ggc 624
 Pro Ser Pro Asn Val Val Val Leu Asp Pro Pro Arg Thr Gly Ala Gly
 195 200 205

agt gac gtg ttg aag agc atc gcg gag gct aag cct cag ctg gtt atc 672
 Ser Asp Val Leu Lys Ser Ile Ala Glu Ala Lys Pro Gln Leu Val Ile
 210 215 220

cac att ggt tgt gac ccg gcg act ttc gct cgc gac gtt gcc gat tgg 720
 His Ile Gly Cys Asp Pro Ala Thr Phe Ala Arg Asp Val Ala Asp Trp
 225 230 235 240

aag ctc aac ggc tac gaa atg gat caa ttg gct gtt ttt aac gcg ttc 768
 Lys Leu Asn Gly Tyr Glu Met Asp Gln Leu Ala Val Phe Asn Ala Phe
 245 250 255

cct gga act cac cac ttt gag acg att ggt gta ttt gtc cgc gtt tcc 816
 Pro Gly Thr His His Phe Glu Thr Ile Gly Val Phe Val Arg Val Ser
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taaggcggat taagccttgg cta 839

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<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 362

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Val Thr Glu Val Ala Cys Ser Gln Val Val Pro Glu Leu Leu Glu Gly
 20 25 30

Leu Val Gly Glu Gly Ala Arg Arg Phe Thr Pro Gly Val Glu Ile Ile

35	40	45
Ala Ala Ile Asp Asp Ala Gly Gln Arg His Val Val Glu Ser Arg Lys 50 55 60		
Ala Pro Arg Gly Arg Arg Thr Glu Thr Val Leu Lys Val Leu Glu Gly 65 70 75 80		
Thr Gly Glu Val Glu Gln Lys Val Gly Asp Tyr Thr Trp Lys Phe Pro 85 90 95		
Val Ser Ser Phe Trp Gln Ala His Thr Lys Ala Pro Ala Ala Tyr Ser 100 105 110		
Glu Phe Ile Ala Glu Ala Leu Thr Gly Leu Glu Leu Val Asp Val Asp 115 120 125		
Lys Arg Gly Pro Val Ala Trp Asp Leu Tyr Gly Gly Val Gly Leu Phe 130 135 140		
Ala Pro Ile Ile Thr Ser Lys Leu Gln Ala Ala Val His Ser Val Glu 145 150 155 160		
Leu Ser Pro Gly Ser Ala Glu Ala Gly Glu Glu Ala Leu Ala Gly Leu 165 170 175		
Pro Val Thr Phe His Thr Gly Arg Val Glu Gly Met Ala Ser Gln Leu 180 185 190		
Pro Ser Pro Asn Val Val Val Leu Asp Pro Pro Arg Thr Gly Ala Gly 195 200 205		
Ser Asp Val Leu Lys Ser Ile Ala Glu Ala Lys Pro Gln Leu Val Ile 210 215 220		
His Ile Gly Cys Asp Pro Ala Thr Phe Ala Arg Asp Val Ala Asp Trp 225 230 235 240		
Lys Leu Asn Gly Tyr Glu Met Asp Gln Leu Ala Val Phe Asn Ala Phe 245 250 255		
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<211> 942

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(919)

<223> RXA02523

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ctccgaaaat	cttgattccc	accgtctgcg	gcttgatgtc	gtg	acc	att	ttc	ccc	115
				Val	Thr	Ile	Phe	Pro	
				1				5	

gaa tac ctg gat cct ctg cgc cat gcc ctg ctg ggt aag gcg att gag	163
Glu Tyr Leu Asp Pro Leu Arg His Ala Leu Leu Gly Lys Ala Ile Glu	
10 15 20	
gat ggc att ttg gaa gtc ggt gtt cat gat ctt cgg aat tgg gcg acc	211
Asp Gly Ile Leu Glu Val Gly Val His Asp Leu Arg Asn Trp Ala Thr	
25 30 35	
ggc gga cac aag gcc gtc gac gat acc ccg tat ggc ggt ggc ccg ggc	259
Gly Gly His Lys Ala Val Asp Asp Thr Pro Tyr Gly Gly Gly Pro Gly	
40 45 50	
atg gtg atg aag cca gag gtc tgg ggg cca gcg ctt gat gat gtc gcc	307
Met Val Met Lys Pro Glu Val Trp Gly Pro Ala Leu Asp Asp Val Ala	
55 60 65	
gca ggc cgg gtg agc ggt gcg gaa ctc gat tcg gcc tcg ctg cac ctg	355
Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser Ala Ser Leu His Leu	
70 75 80 85	
aaa aat gtg cgc cat gat gag ctg ggt ggc gtc gaa aag cgt gct tat	403
Lys Asn Val Arg His Asp Glu Leu Gly Gly Val Glu Lys Arg Ala Tyr	
90 95 100	
gtc gtg gaa gaa gac cgc gac ctg ccg ctg ttg ctg gtg ccc acc ccg	451
Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu Leu Val Pro Thr Pro	
105 110 115	
gct ggc aag ccg ttc acg cag gcg gat gcg cag gcg tgg tcc aac gag	499
Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln Ala Trp Ser Asn Glu	
120 125 130	
gag cac att gtg ttc gcg tgc ggg cgc tac gag ggc att gac cag cgc	547
Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu Gly Ile Asp Gln Arg	
135 140 145	
gtt att gat gat gcc gcc aac cgc tac cgc gtg cgc gag gta tcg atc	595
Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val Arg Glu Val Ser Ile	
150 155 160 165	
ggc gat tat gtg ctg atc ggc ggg gaa gtg gca gtc ctg gtc atc gcg	643
Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala Val Leu Val Ile Ala	
170 175 180	
gaa gcc gtc gtg cgc ctg atc cct ggc gtg ctc gga aac cgt cgt agc	691
Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu Gly Asn Arg Arg Ser	
185 190 195	
cac gaa gaa gac agc ttc tcc gat ggc ctg ctc gaa ggc ccg tcg tac	739
His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu Glu Gly Pro Ser Tyr	
200 205 210	
aca aag ccg cgc acc tgg cgc gga ctt gac gtc ccc gaa gta cta ttc	787
Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val Pro Glu Val Leu Phe	
215 220 225	
tcg ggc aac cac gcc aag gtc gat cgc tgg cga cgc gat cag gcg ctc	835
Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg Arg Asp Gln Ala Leu	
230 235 240 245	

cta cgc acc cag gca att agg cct gag ctt atc gac gca tcc ctc ctc 883
 Leu Arg Thr Gln Ala Ile Arg Pro Glu Leu Ile Asp Ala Ser Leu Leu
 250 255 260

gat tcc acc gac ctc aaa gta ttg gga ctg gac aaa tgacagagac 929
 Asp Ser Thr Asp Leu Lys Val Leu Gly Leu Asp Lys
 265 270

cacacctcaa ccc 942

<210> 364

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

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Gly Lys Ala Ile Glu Asp Gly Ile Leu Glu Val Gly Val His Asp Leu
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Arg Asn Trp Ala Thr Gly Gly His Lys Ala Val Asp Asp Thr Pro Tyr
 35 40 45

Gly Gly Gly Pro Gly Met Val Met Lys Pro Glu Val Trp Gly Pro Ala
 50 55 60

Leu Asp Asp Val Ala Ala Gly Arg Val Ser Gly Ala Glu Leu Asp Ser
 65 70 75 80

Ala Ser Leu His Leu Lys Asn Val Arg His Asp Glu Leu Gly Gly Val
 85 90 95

Glu Lys Arg Ala Tyr Val Val Glu Glu Asp Arg Asp Leu Pro Leu Leu
 100 105 110

Leu Val Pro Thr Pro Ala Gly Lys Pro Phe Thr Gln Ala Asp Ala Gln
 115 120 125

Ala Trp Ser Asn Glu Glu His Ile Val Phe Ala Cys Gly Arg Tyr Glu
 130 135 140

Gly Ile Asp Gln Arg Val Ile Asp Asp Ala Ala Asn Arg Tyr Arg Val
 145 150 155 160

Arg Glu Val Ser Ile Gly Asp Tyr Val Leu Ile Gly Gly Glu Val Ala
 165 170 175

Val Leu Val Ile Ala Glu Ala Val Val Arg Leu Ile Pro Gly Val Leu
 180 185 190

Gly Asn Arg Arg Ser His Glu Glu Asp Ser Phe Ser Asp Gly Leu Leu
 195 200 205

Glu Gly Pro Ser Tyr Thr Lys Pro Arg Thr Trp Arg Gly Leu Asp Val
 210 215 220

Pro Glu Val Leu Phe Ser Gly Asn His Ala Lys Val Asp Arg Trp Arg
 225 230 235 240

Lys

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<222> (101)..(1045)
<223> RXA02243
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Met Arg Leu Val Phe 5																
gcc gga act ccg gaa cct gca gtg gtg gca ctg caa aag ctc att gat 163																
Ala Gly Thr Pro Glu Pro Ala Val Val Ala Leu Gln Lys Leu Ile Asp 20																
tcc gat cat gag gtc gtc gct gtg ttg acg caa cca gat gca cgt cgc 211																
Ser Asp His Glu Val Val Ala Val Leu Thr Gln Pro Asp Ala Arg Arg 35																
ggc cgt ggt cgt acg ctg cat cct tca gct gtc gcg gag ctt gca cag 259																
Gly Arg Gly Arg Thr Leu His Pro Ser Ala Val Ala Glu Leu Ala Gln 50																
cag cac ggt att gag gtg tta aag ccc acc tcc ctg aag gct gat acg 307																
Gln His Gly Ile Glu Val Leu Lys Pro Thr Ser Leu Lys Ala Asp Thr 65																
gaa gat ggc caa gca atc cgt cag cgc ttg gct gag ctt gcc ccc gat 355																
Glu Asp Gly Gln Ala Ile Arg Gln Arg Leu Ala Glu Leu Ala Pro Asp 85																
tgc ttg ccg gtg gtg gca tac gga cag ctg atc acc aag gat ttg ctg 403																
Cys Leu Pro Val Val Ala Tyr Gly Gln Leu Ile Thr Lys Asp Leu Leu 100																
gat gtt gcg cca cac ggt tgg gtg aat ctg cac ttt tct ttg ctt cct 451																
Asp Val Ala Pro His Gly Trp Val Asn Leu His Phe Ser Leu Leu Pro 115																
gca tgg cgt ggg gcg gcg ccg gtt cag gcg tcg atc cgt gaa ggc gat 499																
Ala Trp Arg Gly Ala Ala Pro Val Gln Ala Ser Ile Arg Glu Gly Asp 130																
caq atc act ggt gcc acg acc ttc cgc att gat gag ggc ctg gat acc 547																

Gln Ile Thr Gly Ala Thr Thr Phe Arg Ile Asp Glu Gly Leu Asp Thr
 135 140 145
 ggc gtg att ttg tcc acc atc gag gac aca att cag ccc acc gat act 595
 Gly Val Ile Leu Ser Thr Ile Glu Asp Thr Ile Gln Pro Thr Asp Thr
 150 155 160 165
 gcg gat gat ctt ctt act cgc ctg gcg tat tca ggc ggt gac ctg ctg 643
 Ala Asp Asp Leu Leu Thr Arg Leu Ala Tyr Ser Gly Gly Asp Leu Leu
 170 175 180
 gtt gag acc atg act ggc ctg gag cag ggc aca atc acc ccg cgc gcc 691
 Val Glu Thr Met Thr Gly Leu Glu Gln Gly Thr Ile Thr Pro Arg Ala
 185 190 195
 cag gaa ggc gag gcc acg tac gcc tca aaa atc acc acc cag gac gcg 739
 Gln Glu Gly Glu Ala Thr Tyr Ala Ser Lys Ile Thr Thr Gln Asp Ala
 200 205 210
 cag att gat tgg tcg aag ccc gcc gag gtc atc gac cgc cac atc agg 787
 Gln Ile Asp Trp Ser Lys Pro Ala Glu Val Ile Asp Arg His Ile Arg
 215 220 225
 gca cat acc cca gga cct ggc gca tgg acc acg ctt gtc gac gcc cgc 835
 Ala His Thr Pro Gly Pro Gly Ala Trp Thr Thr Leu Val Asp Ala Arg
 230 235 240 245
 ctc aag gtc ggg ccc atc agc cac tca ggc gag gtc gaa gta gca gcg 883
 Leu Lys Val Gly Pro Ile Ser His Ser Gly Glu Val Glu Val Ala Ala
 250 255 260
 gac ttg gcg cct ggc gcc atc ctg gcg caa aag aac tcc gtg gtg gtc 931
 Asp Leu Ala Pro Gly Ala Ile Leu Ala Gln Lys Asn Ser Val Val Val
 265 270 275
 gga acg ggc acc aca cca att gtt ctg ggc aat atc caa ccc ccg gga 979
 Gly Thr Gly Thr Thr Pro Ile Val Leu Gly Asn Ile Gln Pro Pro Gly
 280 285 290
 aag aaa atg atg aat gca gca gac tgg gcg cgt ggt gtc caa ctt gat 1027
 Lys Lys Met Met Asn Ala Ala Asp Trp Ala Arg Gly Val Gln Leu Asp
 295 300 305
 cag gaa gcg aaa ttc caa tgagcctaga aaaatccggc gga 1068
 Gln Glu Ala Lys Phe Gln
 310 315

<210> 366

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met Arg Leu Val Phe Ala Gly Thr Pro Glu Pro Ala Val Val Ala Leu
 1 5 10 15

Gln Lys Leu Ile Asp Ser Asp His Glu Val Val Ala Val Leu Thr Gln
 20 25 30

Pro Asp Ala Arg Arg Gly Arg Gly Arg Thr Leu His Pro Ser Ala Val

35					40					45					
Ala	Glu	Leu	Ala	Gln	Gln	His	Gly	Ile	Glu	Val	Leu	Lys	Pro	Thr	Ser
50						55					60				
Leu	Lys	Ala	Asp	Thr	Glu	Asp	Gly	Gln	Ala	Ile	Arg	Gln	Arg	Leu	Ala
65					70					75					80
Glu	Leu	Ala	Pro	Asp	Cys	Leu	Pro	Val	Val	Ala	Tyr	Gly	Gln	Leu	Ile
				85					90					95	
Thr	Lys	Asp	Leu	Leu	Asp	Val	Ala	Pro	His	Gly	Trp	Val	Asn	Leu	His
			100					105					110		
Phe	Ser	Leu	Leu	Pro	Ala	Trp	Arg	Gly	Ala	Ala	Pro	Val	Gln	Ala	Ser
		115					120					125			
Ile	Arg	Glu	Gly	Asp	Gln	Ile	Thr	Gly	Ala	Thr	Thr	Phe	Arg	Ile	Asp
	130					135					140				
Glu	Gly	Leu	Asp	Thr	Gly	Val	Ile	Leu	Ser	Thr	Ile	Glu	Asp	Thr	Ile
145					150					155					160
Gln	Pro	Thr	Asp	Thr	Ala	Asp	Asp	Leu	Leu	Thr	Arg	Leu	Ala	Tyr	Ser
				165					170					175	
Gly	Gly	Asp	Leu	Leu	Val	Glu	Thr	Met	Thr	Gly	Leu	Glu	Gln	Gly	Thr
			180					185					190		
Ile	Thr	Pro	Arg	Ala	Gln	Glu	Gly	Glu	Ala	Thr	Tyr	Ala	Ser	Lys	Ile
		195					200					205			
Thr	Thr	Gln	Asp	Ala	Gln	Ile	Asp	Trp	Ser	Lys	Pro	Ala	Glu	Val	Ile
		210				215					220				
Asp	Arg	His	Ile	Arg	Ala	His	Thr	Pro	Gly	Pro	Gly	Ala	Trp	Thr	Thr
225					230					235					240
Leu	Val	Asp	Ala	Arg	Leu	Lys	Val	Gly	Pro	Ile	Ser	His	Ser	Gly	Glu
				245					250					255	
Val	Glu	Val	Ala	Ala	Asp	Leu	Ala	Pro	Gly	Ala	Ile	Leu	Ala	Gln	Lys
			260					265					270		
Asn	Ser	Val	Val	Val	Gly	Thr	Gly	Thr	Thr	Pro	Ile	Val	Leu	Gly	Asn
		275					280					285			
Ile	Gln	Pro	Pro	Gly	Lys	Lys	Met	Met	Asn	Ala	Ala	Asp	Trp	Ala	Arg
	290					295					300				
Gly	Val	Gln	Leu	Asp	Gln	Glu	Ala	Lys	Phe	Gln					
305					310					315					

<210> 367

<211> 1218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1195)

<223> RXA00217

<400> 367

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ttaagtaaac gtaggcagaa agctttgtag aggggagatc atg cgg gtt ctt gca 115
                                         Met Arg Val Leu Ala
                                         1                               5

gca atg agt gga ggc gtt gat tcc gcc gtc gcg gcg tca cgc gcg gtc 163
Ala Met Ser Gly Gly Val Asp Ser Ala Val Ala Ala Ser Arg Ala Val
                        10                               15                               20

gca gct ggt cat gaa gtg gtt ggc gtg cat ttg gcg ttg tcg caa gat 211
Ala Ala Gly His Glu Val Val Gly Val His Leu Ala Leu Ser Gln Asp
                        25                               30                               35

ccg caa acg gtg cgt gag tct tcg cgc ggt tgc tgc tct ctg gaa gat 259
Pro Gln Thr Val Arg Glu Ser Ser Arg Gly Cys Cys Ser Leu Glu Asp
                        40                               45                               50

tcc gct gat gct cgt cgc gtg tgt gac aag ttg ggt atc ccg ttt tat 307
Ser Ala Asp Ala Arg Arg Val Cys Asp Lys Leu Gly Ile Pro Phe Tyr
                        55                               60                               65

gtc tgg gat ttc tcg gat cgt ttc aag gaa gat gtg atc gac aac ttc 355
Val Trp Asp Phe Ser Asp Arg Phe Lys Glu Asp Val Ile Asp Asn Phe
                        70                               75                               80                               85

att gat tct tac gcg atc ggt gag act cca aac cct tgc ctg cgt tgt 403
Ile Asp Ser Tyr Ala Ile Gly Glu Thr Pro Asn Pro Cys Leu Arg Cys
                        90                               95                               100

aat gag aaa atc aag ttt gcc gcc ttg ctt gag cgt ggc atc gcg ctt 451
Asn Glu Lys Ile Lys Phe Ala Ala Leu Leu Glu Arg Gly Ile Ala Leu
                        105                               110                               115

ggt ttc gat gca gtg gtt acc ggc cac tac gcg cgc ttg acc cag cct 499
Gly Phe Asp Ala Val Val Thr Gly His Tyr Ala Arg Leu Thr Gln Pro
                        120                               125                               130

gct gat ggt ggc gat ggc tac ttg cgt cgc gga gtt gat ccc aac aag 547
Ala Asp Gly Gly Asp Gly Tyr Leu Arg Arg Gly Val Asp Pro Asn Lys
                        135                               140                               145

gat cag tct tac gtg ctt ggt gtg ctt ggc gct cat gag atc gag cac 595
Asp Gln Ser Tyr Val Leu Gly Val Leu Gly Ala His Glu Ile Glu His
                        150                               155                               160                               165

tgc atg ttc cca gtc ggc gat acc atc aag cct gaa atc cgt gaa gaa 643
Cys Met Phe Pro Val Gly Asp Thr Ile Lys Pro Glu Ile Arg Glu Glu
                        170                               175                               180

gcc agt gct gca ggt ttc tct gtg gca aag aag cca gac tcc tac gac 691
Ala Ser Ala Ala Gly Phe Ser Val Ala Lys Lys Pro Asp Ser Tyr Asp
                        185                               190                               195

att tgc ttc att ccg gat ggc aac acc cag gcg ttc ttg ggc aag cac 739
Ile Cys Phe Ile Pro Asp Gly Asn Thr Gln Ala Phe Leu Gly Lys His
                        200                               205                               210

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atc ggt atg cgt ccg ggc atg atc gtg gat cag gaa ggc acg cat ctc 787
 Ile Gly Met Arg Pro Gly Met Ile Val Asp Gln Glu Gly Thr His Leu
 215 220 225

 cgt gag cac gct ggt gtc cat gaa ttc acc att ggt cag cgc aag ggc 835
 Arg Glu His Ala Gly Val His Glu Phe Thr Ile Gly Gln Arg Lys Gly
 230 235 240 245

 ctt gac att aag gct cca gca gcc gat ggt cgt cca cgt tac gtc acc 883
 Leu Asp Ile Lys Ala Pro Ala Ala Asp Gly Arg Pro Arg Tyr Val Thr
 250 255 260

 gat att gat gcc aag acc ggc acc gtc acc gtt ggt act cgc gaa aac 931
 Asp Ile Asp Ala Lys Thr Gly Thr Val Thr Val Gly Thr Arg Glu Asn
 265 270 275

 cta aag atc agc acc atc cac gcc gat cgt ttg aag ttc ctc cat cca 979
 Leu Lys Ile Ser Thr Ile His Ala Asp Arg Leu Lys Phe Leu His Pro
 280 285 290

 gcg atg gac gga cag atc gat tgc gaa gtc cag gtc cgc gca cac ggt 1027
 Ala Met Asp Gly Gln Ile Asp Cys Glu Val Gln Val Arg Ala His Gly
 295 300 305

 gga gta gtt tcc tgc tct gcg acg att gat cgt gac gct gat ttc atg 1075
 Gly Val Val Ser Cys Ser Ala Thr Ile Asp Arg Asp Ala Asp Phe Met
 310 315 320 325

 gtg ctc aac ctc aat gaa cct ctt cag ggt gtt gct cgc ggc cag gca 1123
 Val Leu Asn Leu Asn Glu Pro Leu Gln Gly Val Ala Arg Gly Gln Ala
 330 335 340

 gca gtg ctg tac ctg cct gac gcg gat ggt gac atc gtt ctt gga tca 1171
 Ala Val Leu Tyr Leu Pro Asp Ala Asp Gly Asp Ile Val Leu Gly Ser
 345 350 355

 ggc acc atc tgc cac acg gag tct taagaaaatt gggcgcttat ggt 1218
 Gly Thr Ile Cys His Thr Glu Ser
 360 365

<210> 368

<211> 365

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 368

Met Arg Val Leu Ala Ala Met Ser Gly Gly Val Asp Ser Ala Val Ala
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 Ala Ser Arg Ala Val Ala Ala Gly His Glu Val Val Gly Val His Leu
 20 25 30

 Ala Leu Ser Gln Asp Pro Gln Thr Val Arg Glu Ser Ser Arg Gly Cys
 35 40 45

 Cys Ser Leu Glu Asp Ser Ala Asp Ala Arg Arg Val Cys Asp Lys Leu
 50 55 60

 Gly Ile Pro Phe Tyr Val Trp Asp Phe Ser Asp Arg Phe Lys Glu Asp

65						70						75						80
Val	Ile	Asp	Asn	Phe	Ile	Asp	Ser	Tyr	Ala	Ile	Gly	Glu	Thr	Pro	Asn			
				85					90					95				
Pro	Cys	Leu	Arg	Cys	Asn	Glu	Lys	Ile	Lys	Phe	Ala	Ala	Leu	Leu	Glu			
			100					105					110					
Arg	Gly	Ile	Ala	Leu	Gly	Phe	Asp	Ala	Val	Val	Thr	Gly	His	Tyr	Ala			
		115					120					125						
Arg	Leu	Thr	Gln	Pro	Ala	Asp	Gly	Gly	Asp	Gly	Tyr	Leu	Arg	Arg	Gly			
		130				135					140							
Val	Asp	Pro	Asn	Lys	Asp	Gln	Ser	Tyr	Val	Leu	Gly	Val	Leu	Gly	Ala			
145				150						155					160			
His	Glu	Ile	Glu	His	Cys	Met	Phe	Pro	Val	Gly	Asp	Thr	Ile	Lys	Pro			
				165					170					175				
Glu	Ile	Arg	Glu	Glu	Ala	Ser	Ala	Ala	Gly	Phe	Ser	Val	Ala	Lys	Lys			
			180					185					190					
Pro	Asp	Ser	Tyr	Asp	Ile	Cys	Phe	Ile	Pro	Asp	Gly	Asn	Thr	Gln	Ala			
		195					200					205						
Phe	Leu	Gly	Lys	His	Ile	Gly	Met	Arg	Pro	Gly	Met	Ile	Val	Asp	Gln			
	210					215					220							
Glu	Gly	Thr	His	Leu	Arg	Glu	His	Ala	Gly	Val	His	Glu	Phe	Thr	Ile			
225				230						235					240			
Gly	Gln	Arg	Lys	Gly	Leu	Asp	Ile	Lys	Ala	Pro	Ala	Ala	Asp	Gly	Arg			
			245						250					255				
Pro	Arg	Tyr	Val	Thr	Asp	Ile	Asp	Ala	Lys	Thr	Gly	Thr	Val	Thr	Val			
			260					265					270					
Gly	Thr	Arg	Glu	Asn	Leu	Lys	Ile	Ser	Thr	Ile	His	Ala	Asp	Arg	Leu			
		275					280					285						
Lys	Phe	Leu	His	Pro	Ala	Met	Asp	Gly	Gln	Ile	Asp	Cys	Glu	Val	Gln			
	290					295					300							
Val	Arg	Ala	His	Gly	Gly	Val	Val	Ser	Cys	Ser	Ala	Thr	Ile	Asp	Arg			
305				310						315					320			
Asp	Ala	Asp	Phe	Met	Val	Leu	Asn	Leu	Asn	Glu	Pro	Leu	Gln	Gly	Val			
			325						330					335				
Ala	Arg	Gly	Gln	Ala	Ala	Val	Leu	Tyr	Leu	Pro	Asp	Ala	Asp	Gly	Asp			
			340					345					350					
Ile	Val	Leu	Gly	Ser	Gly	Thr	Ile	Cys	His	Thr	Glu	Ser						
		355					360					365						

<210> 369

<211> 735

<212> DNA

<213> Corynebacterium glutamicum

<223> RXA01223

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gcc gcc gag gca gtg gat ttg ctg ctg gcc cag gga tta tct gct gcg 691
Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln Gly Leu Ser Ala Ala
185 190 195

caa aac gct atc cac agc cgc tagattgcta gagattcccg cac
 Gln Asn Ala Ile His Ser Arg
 200

735

<210> 370
 <211> 204
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 370
 Met Thr Ser Val Ser Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro
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 Lys Pro Glu Leu Pro Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn
 20 25 30
 Pro Gly Ala Lys Tyr Glu Ser Thr Arg His Asn Val Gly Tyr Met Cys
 35 40 45
 Gln Asp Met Leu Ile Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala
 50 55 60
 Thr Gly Tyr Lys Ala Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala
 65 70 75 80
 Val Arg Ser Thr Thr Phe Met Asn His Ser Gly Gln Gly Val Ala Pro
 85 90 95
 Ile Ala Ala Ala Leu Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His
 100 105 110
 Asp Glu Leu Asp Leu Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly
 115 120 125
 Asn Glu Asn Gly His Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly
 130 135 140
 Thr Arg Asp Tyr Leu Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala
 145 150 155 160
 Gly Met Ala Val Pro Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln
 165 170 175
 Pro Gly Ile Glu Leu Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln
 180 185 190
 Gly Leu Ser Ala Ala Gln Asn Ala Ile His Ser Arg
 195 200

<210> 371
 <211> 475
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (9)..(452)
 <223> RXA01226

<400> 371

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ttgaggtt gca gaa gaa cta gtg tcg cgc agc ttt gga tca ttt agt gtg 50
      Ala Glu Glu Leu Val Ser Arg Ser Phe Gly Ser Phe Ser Val
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cac aag cgc tcc aac acc gat atc gcg cag ctt cct ggg cta att gtg 98
His Lys Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val
  15              20              25              30

gcc aag ccg cgc agc ttt atg aac ctg tcg gga act ccg att cgg gcg 146
Ala Lys Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala
              35              40              45

ctg tgt gac ttc ttt aag att tcc cca gcc aat gtc atc gtg gtg cat 194
Leu Cys Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His
              50              55              60

gat gaa ttg gag ctt gat ttc ggc tca gtg aag cta cgt cag ggt ggc 242
Asp Glu Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly
      65              70              75

ggg gat cat ggg cac aat ggt ctg aaa tcc acg tcc aaa tct ttg gga 290
Gly Asp His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly
      80              85              90

act aag gac tat tgg aag ctc agc atg ggt atc ggt agg cca ccg ggt 338
Thr Lys Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly
      95              100              105              110

cgg atg gat ccg gca agt ttt gtg ttg aag cct ttt ggc aag caa gaa 386
Arg Met Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu
              115              120              125

ctg gcg gat att ccc atc atg gcg gct gac gct gca gat ctc gtc gaa 434
Leu Ala Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu
      130              135              140

aag cat ttg cag cag ggc tagctacttg cgccgcgcct ctt 475
Lys His Leu Gln Gln Gly
      145

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<210> 372

<211> 148

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

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Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys
      20              25              30

Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys
      35              40              45

Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His Asp Glu
      50              55              60

Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp

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65	70	75	80
His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys	85	90	95
Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met	100	105	110
Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala	115	120	125
Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His	130	135	140
Leu Gln Gln Gly			
145			
<210> 373			
<211> 1614			
<212> DNA			
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<221> CDS			
<222> (101)..(1591)			
<223> RXA00209			
<400> 373			
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		Met Thr Asn Lys Tyr	
		1 5	
ctg gtt gaa ggc tct gaa aac gag ctg acc aca aag acc gca gca gag			163
Leu Val Glu Gly Ser Glu Asn Glu Leu Thr Thr Lys Thr Ala Ala Glu	10	15	20
ctg gca ggt ctt att cat tcc cgc gag gta act tcc cgc gag gtt act			211
Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr Ser Arg Glu Val Thr	25	30	35
caa gcg cac cta gat cgc att gct gcg gtt gac ggc gat att cat gca			259
Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp Gly Asp Ile His Ala	40	45	50
ttt ctc cac gtt ggc cag gag gag gcc ctg aac gcg gcg gat gac gtc			307
Phe Leu His Val Gly Gln Glu Glu Ala Leu Asn Ala Ala Asp Asp Val	55	60	65
gat aag cgt cta gac gct gga gag gca cct gcc tcg gct ttg gct ggc			355
Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala Ser Ala Leu Ala Gly	70	75	80
			85
gtg ccg ctt gcg ctg aag gat gtc ttt acc acc act gat gcg ccg acc			403
Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr Thr Asp Ala Pro Thr	90	95	100
acg gcg gca tcg aag atg ctt gag ggc tac atg agc cct tat gac gcg			451
Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met Ser Pro Tyr Asp Ala			

105										110					115					
act	gtg	acc	cgc	aag	atc	cgt	gag	gct	ggc	atc	cca	att	ttg	ggt	aag	499				
Thr	Val	Thr	Arg	Lys	Ile	Arg	Glu	Ala	Gly	Ile	Pro	Ile	Leu	Gly	Lys					
		120					125					130								
acc	aac	atg	gat	gag	ttt	gcg	atg	ggt	tcc	tcc	act	gag	aac	tcc	gca	547				
Thr	Asn	Met	Asp	Glu	Phe	Ala	Met	Gly	Ser	Ser	Thr	Glu	Asn	Ser	Ala					
	135					140					145									
tac	ggc	cca	acc	cac	aat	ccg	tgg	gat	ctg	gag	cgc	acc	gca	ggt	ggt	595				
Tyr	Gly	Pro	Thr	His	Asn	Pro	Trp	Asp	Leu	Glu	Arg	Thr	Ala	Gly	Gly					
150					155					160					165					
tct	ggt	ggt	ggc	tct	tca	gct	gct	ctt	gct	gca	ggt	cag	gcg	cca	ctt	643				
Ser	Gly	Gly	Gly	Ser	Ser	Ala	Ala	Leu	Ala	Ala	Gly	Gln	Ala	Pro	Leu					
				170					175					180						
gcg	att	ggt	act	gac	act	ggt	gga	tcc	atc	cgt	cag	cca	gct	gcg	ctg	691				
Ala	Ile	Gly	Thr	Asp	Thr	Gly	Gly	Ser	Ile	Arg	Gln	Pro	Ala	Ala	Leu					
			185					190					195							
acc	aac	act	gtc	ggt	gtg	aag	cca	acc	tac	gga	acc	gta	tcc	cgt	tac	739				
Thr	Asn	Thr	Val	Gly	Val	Lys	Pro	Thr	Tyr	Gly	Thr	Val	Ser	Arg	Tyr					
		200					205					210								
ggt	ctg	att	gcg	tgt	gcg	tcc	tcc	ctg	gat	cag	ggt	ggc	cca	acc	gct	787				
Gly	Leu	Ile	Ala	Cys	Ala	Ser	Ser	Leu	Asp	Gln	Gly	Gly	Pro	Thr	Ala					
	215					220					225									
cgt	act	gtt	ctg	gat	acc	gcg	ctt	ttg	cac	gag	gtt	atc	gca	ggc	cac	835				
Arg	Thr	Val	Leu	Asp	Thr	Ala	Leu	Leu	His	Glu	Val	Ile	Ala	Gly	His					
230					235					240					245					
gac	gct	ttt	gat	gcg	acc	tcc	gtg	aat	cgt	ccg	gtt	gct	cct	gtt	gtg	883				
Asp	Ala	Phe	Asp	Ala	Thr	Ser	Val	Asn	Arg	Pro	Val	Ala	Pro	Val	Val					
				250					255					260						
cag	gct	gcc	cgt	gaa	ggc	gcg	aac	ggt	gac	ctg	aaa	ggc	gtg	aag	gtc	931				
Gln	Ala	Ala	Arg	Glu	Gly	Ala	Asn	Gly	Asp	Leu	Lys	Gly	Val	Lys	Val					
			265					270					275							
ggt	gtg	gtc	aag	cag	ttc	gac	cgc	gac	ggc	tac	cag	cct	ggc	gtg	ctt	979				
Gly	Val	Val	Lys	Gln	Phe	Asp	Arg	Asp	Gly	Tyr	Gln	Pro	Gly	Val	Leu					
		280					285					290								
gag	gca	ttc	cac	gct	tct	gtt	gag	cag	atg	cgc	tcc	cag	ggt	gcg	gaa	1027				
Glu	Ala	Phe	His	Ala	Ser	Val	Glu	Gln	Met	Arg	Ser	Gln	Gly	Ala	Glu					
		295				300					305									
atc	gtc	gag	gtt	gat	tgc	cct	cac	ttt	gat	gac	gct	ctt	ggc	gcg	tac	1075				
Ile	Val	Glu	Val	Asp	Cys	Pro	His	Phe	Asp	Asp	Ala	Leu	Gly	Ala	Tyr					
310					315					320					325					
tac	ctg	att	ctt	cct	tgt	gaa	gtt	tcc	tcc	aac	ctc	gcg	cgt	ttt	gac	1123				
Tyr	Leu	Ile	Leu	Pro	Cys	Glu	Val	Ser	Ser	Asn	Leu	Ala	Arg	Phe	Asp					
				330					335					340						
ggc	atg	cgt	tac	ggt	ttg	cgc	gct	ggt	gat	gac	gga	act	cgt	tcc	gcc	1171				
Gly	Met	Arg	Tyr	Gly	Leu	Arg	Ala	Gly	Asp	Asp	Gly	Thr	Arg	Ser	Ala					
			345					350					355							

gat gag gtc atg gcg tac acc cgt gcg cag gga ttc ggc cct gag gtt 1219
Asp Glu Val Met Ala Tyr Thr Arg Ala Gln Gly Phe Gly Pro Glu Val
360 365 370

aag cgc cgt atc atc ctc ggc act tac gcg ttg tct gtt ggt tac tac 1267
Lys Arg Arg Ile Ile Leu Gly Thr Tyr Ala Leu Ser Val Gly Tyr Tyr
375 380 385

gac gcg tac tac ctg cag gct cag cgc gtt cgt acc ctc att gca cag 1315
Asp Ala Tyr Tyr Leu Gln Ala Gln Arg Val Arg Thr Leu Ile Ala Gln
390 395 400 405

gac ttc gcc aag gct tac gag cag gtc gac atc ttg gtg tcc cca acc 1363
Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile Leu Val Ser Pro Thr
410 415 420

act cca acc acc gcg ttc aag ctg ggg gag aag gtc acc gat ccg ctg 1411
Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys Val Thr Asp Pro Leu
425 430 435

gag atg tac aac ttc gac ttg tgc acc ctg cca ctg aac ctg gct ggt 1459
Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro Leu Asn Leu Ala Gly
440 445 450

ctc gcg ggc atg tcc ctg cct tcc ggc ttg gca tca gat act ggt ctg 1507
Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala Ser Asp Thr Gly Leu
455 460 465

cct gtt ggt ttg cag ctg atg gct cct gct ttc cag gac gat cgt ctc 1555
Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe Gln Asp Asp Arg Leu
470 475 480 485

tac cgc gtc ggc gct gct ttt gaa gct gga cgc aag taggttctaa 1601
Tyr Arg Val Gly Ala Ala Phe Glu Ala Gly Arg Lys
490 495

acccttttta aga 1614

<210> 374

<211> 497

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

Met Thr Asn Lys Tyr Leu Val Glu Gly Ser Glu Asn Glu Leu Thr Thr
1 5 10 15

Lys Thr Ala Ala Glu Leu Ala Gly Leu Ile His Ser Arg Glu Val Thr
20 25 30

Ser Arg Glu Val Thr Gln Ala His Leu Asp Arg Ile Ala Ala Val Asp
35 40 45

Gly Asp Ile His Ala Phe Leu His Val Gly Gln Glu Glu Ala Leu Asn
50 55 60

Ala Ala Asp Asp Val Asp Lys Arg Leu Asp Ala Gly Glu Ala Pro Ala
65 70 75 80

Ser Ala Leu Ala Gly Val Pro Leu Ala Leu Lys Asp Val Phe Thr Thr
 85 90 95
 Thr Asp Ala Pro Thr Thr Ala Ala Ser Lys Met Leu Glu Gly Tyr Met
 100 105 110
 Ser Pro Tyr Asp Ala Thr Val Thr Arg Lys Ile Arg Glu Ala Gly Ile
 115 120 125
 Pro Ile Leu Gly Lys Thr Asn Met Asp Glu Phe Ala Met Gly Ser Ser
 130 135 140
 Thr Glu Asn Ser Ala Tyr Gly Pro Thr His Asn Pro Trp Asp Leu Glu
 145 150 155 160
 Arg Thr Ala Gly Gly Ser Gly Gly Gly Ser Ser Ala Ala Leu Ala Ala
 165 170 175
 Gly Gln Ala Pro Leu Ala Ile Gly Thr Asp Thr Gly Gly Ser Ile Arg
 180 185 190
 Gln Pro Ala Ala Leu Thr Asn Thr Val Gly Val Lys Pro Thr Tyr Gly
 195 200 205
 Thr Val Ser Arg Tyr Gly Leu Ile Ala Cys Ala Ser Ser Leu Asp Gln
 210 215 220
 Gly Gly Pro Thr Ala Arg Thr Val Leu Asp Thr Ala Leu Leu His Glu
 225 230 235 240
 Val Ile Ala Gly His Asp Ala Phe Asp Ala Thr Ser Val Asn Arg Pro
 245 250 255
 Val Ala Pro Val Val Gln Ala Ala Arg Glu Gly Ala Asn Gly Asp Leu
 260 265 270
 Lys Gly Val Lys Val Gly Val Val Lys Gln Phe Asp Arg Asp Gly Tyr
 275 280 285
 Gln Pro Gly Val Leu Glu Ala Phe His Ala Ser Val Glu Gln Met Arg
 290 295 300
 Ser Gln Gly Ala Glu Ile Val Glu Val Asp Cys Pro His Phe Asp Asp
 305 310 315 320
 Ala Leu Gly Ala Tyr Tyr Leu Ile Leu Pro Cys Glu Val Ser Ser Asn
 325 330 335
 Leu Ala Arg Phe Asp Gly Met Arg Tyr Gly Leu Arg Ala Gly Asp Asp
 340 345 350
 Gly Thr Arg Ser Ala Asp Glu Val Met Ala Tyr Thr Arg Ala Gln Gly
 355 360 365
 Phe Gly Pro Glu Val Lys Arg Arg Ile Ile Leu Gly Thr Tyr Ala Leu
 370 375 380
 Ser Val Gly Tyr Tyr Asp Ala Tyr Tyr Leu Gln Ala Gln Arg Val Arg
 385 390 395 400
 Thr Leu Ile Ala Gln Asp Phe Ala Lys Ala Tyr Glu Gln Val Asp Ile

	405		410		415
Leu Val Ser Pro Thr Thr Pro Thr Thr Ala Phe Lys Leu Gly Glu Lys					
	420		425		430
Val Thr Asp Pro Leu Glu Met Tyr Asn Phe Asp Leu Cys Thr Leu Pro					
	435		440		445
Leu Asn Leu Ala Gly Leu Ala Gly Met Ser Leu Pro Ser Gly Leu Ala					
	450		455		460
Ser Asp Thr Gly Leu Pro Val Gly Leu Gln Leu Met Ala Pro Ala Phe					
465		470		475	480
Gln Asp Asp Arg Leu Tyr Arg Val Gly Ala Ala Phe Glu Ala Gly Arg					
	485		490		495

Lys

<210> 375
 <211> 420
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(397)
 <223> RXA00210

<400> 375
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 cttgtacca ttgtgactag cgaagaggat cagaaaccaa gtg cct gag att tcg 115
 Val Pro Glu Ile Ser 5
 1
 cgc gac cag gtc gct cac ctt gcc aaa ctt tcc aga ctg gcg ctc act 163
 Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser Arg Leu Ala Leu Thr 20
 10 15
 gag gaa gaa ctc gag cag ttt gct gga cag atc gat gac att gtc gga 211
 Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile Asp Asp Ile Val Gly 35
 25 30
 tat gtt tcc gca gtt caa aac gtc gac gcc gca ggt gtt gag cct atg 259
 Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala Gly Val Glu Pro Met 50
 40 45
 agc cac ccg cac agc atc gcc acc acc atg cgt gaa gat gtc gtg cac 307
 Ser His Pro His Ser Ile Ala Thr Thr Met Arg Glu Asp Val Val His 65
 55 60
 aag acc ctc gat gct gcg gct gcg ttg gac caa gcg ccc gct gtc gag 355
 Lys Thr Leu Asp Ala Ala Ala Ala Leu Asp Gln Ala Pro Ala Val Glu 85
 70 75 80
 gat gga cgt ttt atg gtt ccg cag att ctg ggt gag ggc gac 397
 Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly Glu Gly Asp 95
 90 95

taataattat gaccaacaag tac

420

<210> 376

<211> 99

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Val Pro Glu Ile Ser Arg Asp Gln Val Ala His Leu Ala Lys Leu Ser
1 5 10 15

Arg Leu Ala Leu Thr Glu Glu Glu Leu Glu Gln Phe Ala Gly Gln Ile
20 25 30

Asp Asp Ile Val Gly Tyr Val Ser Ala Val Gln Asn Val Asp Ala Ala
35 40 45

Gly Val Glu Pro Met Ser His Pro His Ser Ile Ala Thr Thr Met Arg
50 55 60

Glu Asp Val Val His Lys Thr Leu Asp Ala Ala Ala Leu Asp Gln
65 70 75 80

Ala Pro Ala Val Glu Asp Gly Arg Phe Met Val Pro Gln Ile Leu Gly
85 90 95

Glu Gly Asp

<210> 377

<211> 1260

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1237)

<223> RXA02686

<400> 377

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tggttacaca gcttaaccg ccgaactaag gtgggtgtcc atg tct gtt gct caa 115
Met Ser Val Ala Gln
1 5

tta gcg aac cgc ttg gcc caa ctc tcc ccc gcc gag cat ggt ttt gca 163
Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala Glu His Gly Phe Ala
10 15 20

tgg ttc gac cct gaa atc acc gct ggc cat ggc gtt ggc ccg ttg cat 211
Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly Val Gly Pro Leu His
25 30 35

ggc atg gtg att cca gcc aag gac ctc aac gat gtc gca ggc atg ccc 259
Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp Val Ala Gly Met Pro
40 45 50

acc gcg ttc gga aat gca tct cgg cga aag gta gca aca gat acc gat	307
Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val Ala Thr Asp Thr Asp	
55 60 65	
ccg ttc atc caa aat ctc atc gac cgc ggc gcg atc atc gct ggc aaa	355
Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala Ile Ile Ala Gly Lys	
70 75 80 85	
acc caa acc agc gag ctc ggc atg acg gcg tat tgc gaa ccc atc gac	403
Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr Cys Glu Pro Ile Asp	
90 95 100	
atg gac gca ccc agc aac ccg gtt ttg cct ggt cac acg ccc ggc ggt	451
Met Asp Ala Pro Ser Asn Pro Val Leu Pro Gly His Thr Pro Gly Gly	
105 110 115	
tcg tcg ggt ggt gcg gcg gtt gcc gtt gcc agg tcg ctt gtc gac gcc	499
Ser Ser Gly Gly Ala Ala Val Ala Val Ala Arg Ser Leu Val Asp Ala	
120 125 130	
gcc cac gcc tca gac gga ggc ggc tcg atc cgg gtt cca gcc gcc gcg	547
Ala His Ala Ser Asp Gly Gly Gly Ser Ile Arg Val Pro Ala Ala Ala	
135 140 145	
tgc ggg ctg gtc ggg ttt aaa ccc gcc cac gat tcc agc ggc gga aac	595
Cys Gly Leu Val Gly Phe Lys Pro Ala His Asp Ser Ser Gly Gly Asn	
150 155 160 165	
ccc tcc acg cag ggg ttt atc acc cgc gat gtg gcc acc caa gtg cgc	643
Pro Ser Thr Gln Gly Phe Ile Thr Arg Asp Val Ala Thr Gln Val Arg	
170 175 180	
ttg cac gca ctt caa cca cgc acc agg cgc ctg cgc atc ggc gtt ctc	691
Leu His Ala Leu Gln Pro Arg Thr Arg Arg Leu Arg Ile Gly Val Leu	
185 190 195	
gct gag ccc atc cat gct aat tcg ctt gtc gac gcc ccc ttc ctg agc	739
Ala Glu Pro Ile His Ala Asn Ser Leu Val Asp Ala Pro Phe Leu Ser	
200 205 210	
atc ctc gaa tcc acc gcc cac ctc ctg gag aaa gct ggc cac gaa ata	787
Ile Leu Glu Ser Thr Ala His Leu Leu Glu Lys Ala Gly His Glu Ile	
215 220 225	
gtg tcc gta ccc ctc cct tat ggc gct tgg gct ttt gac gct tat aca	835
Val Ser Val Pro Leu Pro Tyr Gly Ala Trp Ala Phe Asp Ala Tyr Thr	
230 235 240 245	
gaa gtt ttc atg atg aaa tcc gct gga cta acc aac ctg ggt agc ccc	883
Glu Val Phe Met Met Lys Ser Ala Gly Leu Thr Asn Leu Gly Ser Pro	
250 255 260	
att aca aga tgg ttg agt gaa caa ggc cgt agt ctt tct cct tct gat	931
Ile Thr Arg Trp Leu Ser Glu Gln Gly Arg Ser Leu Ser Pro Ser Asp	
265 270 275	
aga caa tca agt gtc aag gct ttt gat tcc gtg gct gag act gta cac	979
Arg Gln Ser Ser Val Lys Ala Phe Asp Ser Val Ala Glu Thr Val His	
280 285 290	
gga gca tgg gac atc gat gtt tta tta acc cct acc ttg gct tat gca	1027

Gly Ala Trp Asp Ile Asp Val Leu Leu Thr Pro Thr Leu Ala Tyr Ala
 295 300 305
 cct ccc aag att ggg tac ttt tca tcc atg cca cct gaa gaa gac ttc 1075
 Pro Pro Lys Ile Gly Tyr Phe Ser Ser Met Pro Pro Glu Glu Asp Phe
 310 315 320 325
 ctt gca caa acc aaa tgg acg ccg tgg gca acg ctg ttc aac atg acc 1123
 Leu Ala Gln Thr Lys Trp Thr Pro Trp Ala Thr Leu Phe Asn Met Thr
 330 335 340
 ggt ggt gca gcc atc agc gtg cct gtt gaa ggt gtc ggc att cat ctt 1171
 Gly Gly Ala Ala Ile Ser Val Pro Val Glu Gly Val Gly Ile His Leu
 345 350 355
 ggt ggg ata cgc gta cga gat gaa gac ctc tta gga tta gca gca ttt 1219
 Gly Gly Ile Arg Val Arg Asp Glu Asp Leu Leu Gly Leu Ala Ala Phe
 360 365 370
 gtg gaa aga gct gtg gca tgagtagttc agtaatgtca ccg 1260
 Val Glu Arg Ala Val Ala
 375

<210> 378

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 378

Met Ser Val Ala Gln Leu Ala Asn Arg Leu Ala Gln Leu Ser Pro Ala
 1 5 10 15
 Glu His Gly Phe Ala Trp Phe Asp Pro Glu Ile Thr Ala Gly His Gly
 20 25 30
 Val Gly Pro Leu His Gly Met Val Ile Pro Ala Lys Asp Leu Asn Asp
 35 40 45
 Val Ala Gly Met Pro Thr Ala Phe Gly Asn Ala Ser Arg Arg Lys Val
 50 55 60
 Ala Thr Asp Thr Asp Pro Phe Ile Gln Asn Leu Ile Asp Arg Gly Ala
 65 70 75 80
 Ile Ile Ala Gly Lys Thr Gln Thr Ser Glu Leu Gly Met Thr Ala Tyr
 85 90 95
 Cys Glu Pro Ile Asp Met Asp Ala Pro Ser Asn Pro Val Leu Pro Gly
 100 105 110
 His Thr Pro Gly Gly Ser Ser Gly Gly Ala Ala Val Ala Val Ala Arg
 115 120 125
 Ser Leu Val Asp Ala Ala His Ala Ser Asp Gly Gly Gly Ser Ile Arg
 130 135 140
 Val Pro Ala Ala Ala Cys Gly Leu Val Gly Phe Lys Pro Ala His Asp
 145 150 155 160
 Ser Ser Gly Gly Asn Pro Ser Thr Gln Gly Phe Ile Thr Arg Asp Val

165					170					175					
Ala	Thr	Gln	Val	Arg	Leu	His	Ala	Leu	Gln	Pro	Arg	Thr	Arg	Arg	Leu
			180					185					190		
Arg	Ile	Gly	Val	Leu	Ala	Glu	Pro	Ile	His	Ala	Asn	Ser	Leu	Val	Asp
		195					200					205			
Ala	Pro	Phe	Leu	Ser	Ile	Leu	Glu	Ser	Thr	Ala	His	Leu	Leu	Glu	Lys
	210					215					220				
Ala	Gly	His	Glu	Ile	Val	Ser	Val	Pro	Leu	Pro	Tyr	Gly	Ala	Trp	Ala
225					230					235					240
Phe	Asp	Ala	Tyr	Thr	Glu	Val	Phe	Met	Met	Lys	Ser	Ala	Gly	Leu	Thr
				245					250					255	
Asn	Leu	Gly	Ser	Pro	Ile	Thr	Arg	Trp	Leu	Ser	Glu	Gln	Gly	Arg	Ser
			260					265					270		
Leu	Ser	Pro	Ser	Asp	Arg	Gln	Ser	Ser	Val	Lys	Ala	Phe	Asp	Ser	Val
		275					280					285			
Ala	Glu	Thr	Val	His	Gly	Ala	Trp	Asp	Ile	Asp	Val	Leu	Leu	Thr	Pro
	290					295					300				
Thr	Leu	Ala	Tyr	Ala	Pro	Pro	Lys	Ile	Gly	Tyr	Phe	Ser	Ser	Met	Pro
305					310					315					320
Pro	Glu	Glu	Asp	Phe	Leu	Ala	Gln	Thr	Lys	Trp	Thr	Pro	Trp	Ala	Thr
				325					330					335	
Leu	Phe	Asn	Met	Thr	Gly	Gly	Ala	Ala	Ile	Ser	Val	Pro	Val	Glu	Gly
			340					345					350		
Val	Gly	Ile	His	Leu	Gly	Gly	Ile	Arg	Val	Arg	Asp	Glu	Asp	Leu	Leu
		355					360					365			
Gly	Leu	Ala	Ala	Phe	Val	Glu	Arg	Ala	Val	Ala					
	370					375									

<210> 379

<211> 886

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(886)

<223> RXA02625

<400> 379

ctcaattaag cagcaatccg agccggggga gcgctgtcag aaatggaccg tgccacccca 60

tgacaacatg	cttgacacaat	gatgactaga	ataatgaccc	atg	act	gca	gcc	ttt	115
				Met	Thr	Ala	Ala	Phe	
				1				5	

tat	gat	ctg	atg	gac	ttc	gat	gaa	gtt	cta	gag	aaa	tat	gac	ccg	gtg	163
Tyr	Asp	Leu	Met	Asp	Phe	Asp	Glu	Val	Leu	Glu	Lys	Tyr	Asp	Pro	Val	

10										15					20					
atg gga ctt gag gtc cac gtc gaa ctg ggc act gag acc aag atg ttc	211																			
Met Gly Leu Glu Val His Val Glu Leu Gly Thr Glu Thr Lys Met Phe																				
25 30 35																				
tct gca tct tct gca cac ttt ggc gct gaa ccc aat agc aat gtt gac	259																			
Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro Asn Ser Asn Val Asp																				
40 45 50																				
cca gtt tct ttg ggt ctc cca ggc gca ctt cct gtg gtt aac gcc aag	307																			
Pro Val Ser Leu Gly Leu Pro Gly Ala Leu Pro Val Val Asn Ala Lys																				
55 60 65																				
ggc gtg gag tgg gca att aag att gga ctg gcg ctg aac tgc agc atc	355																			
Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala Leu Asn Cys Ser Ile																				
70 75 80 85																				
gct gag tcc tca cgc ttt gca cgt aag aac tac ttc tac ccg gat cag	403																			
Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr Phe Tyr Pro Asp Gln																				
90 95 100																				
cct aag aac tac cag atc tcc cag tat gac gag cca atc gca tac gac	451																			
Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu Pro Ile Ala Tyr Asp																				
105 110 115																				
ggc tac ctg gat gtt gtt ctg gag gac ggc acc gag tgg cgt gtg gaa	499																			
Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr Glu Trp Arg Val Glu																				
120 125 130																				
atc gaa cgc gct cac atg gag gaa gac acc gga aag ctc acc cac ctg	547																			
Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly Lys Leu Thr His Leu																				
135 140 145																				
ggt ggt act tct ggt cgt att cac ggc gca acc gct tct ttg gtg gac	595																			
Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr Ala Ser Leu Val Asp																				
150 155 160 165																				
tgc aac cgt gca ggc gtc cct ttg att gag gtt gtc acc aag cca atc	643																			
Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val Val Thr Lys Pro Ile																				
170 175 180																				
gaa ggc gct ggc gct cgc gct cca gag atc gct aag gct tat gtc tcc	691																			
Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala Lys Ala Tyr Val Ser																				
185 190 195																				
gca ctg cgc gat ctg gtt aag gcg ctc ggt gtg tcc gac ggc cgc ttg	739																			
Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val Ser Asp Gly Arg Leu																				
200 205 210																				
gat cag ggt tct atg cgt gtc gac gcc aac ctg tcc ctg cgc ccg atc	787																			
Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu Ser Leu Arg Pro Ile																				
215 220 225																				
ggc cag gag gaa ttc ggc acc cgt acc gaa acc aag aac atc aac tcc	835																			
Gly Gln Glu Glu Phe Gly Thr Arg Thr Glu Thr Lys Asn Ile Asn Ser																				
230 235 240 245																				
ctg aag tcc gtt gag cag gcc agc acc ttt gag atg cag cgc cag gct	883																			
Leu Lys Ser Val Glu Gln Ala Ser Thr Phe Glu Met Gln Arg Gln Ala																				
250 255 260																				

cag
Gln

886

<210> 380
<211> 262
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 380
Met Thr Ala Ala Phe Tyr Asp Leu Met Asp Phe Asp Glu Val Leu Glu
1 5 10 15
Lys Tyr Asp Pro Val Met Gly Leu Glu Val His Val Glu Leu Gly Thr
20 25 30
Glu Thr Lys Met Phe Ser Ala Ser Ser Ala His Phe Gly Ala Glu Pro
35 40 45
Asn Ser Asn Val Asp Pro Val Ser Leu Gly Leu Pro Gly Ala Leu Pro
50 55 60
Val Val Asn Ala Lys Gly Val Glu Trp Ala Ile Lys Ile Gly Leu Ala
65 70 75 80
Leu Asn Cys Ser Ile Ala Glu Ser Ser Arg Phe Ala Arg Lys Asn Tyr
85 90 95
Phe Tyr Pro Asp Gln Pro Lys Asn Tyr Gln Ile Ser Gln Tyr Asp Glu
100 105 110
Pro Ile Ala Tyr Asp Gly Tyr Leu Asp Val Val Leu Glu Asp Gly Thr
115 120 125
Glu Trp Arg Val Glu Ile Glu Arg Ala His Met Glu Glu Asp Thr Gly
130 135 140
Lys Leu Thr His Leu Gly Gly Thr Ser Gly Arg Ile His Gly Ala Thr
145 150 155 160
Ala Ser Leu Val Asp Cys Asn Arg Ala Gly Val Pro Leu Ile Glu Val
165 170 175
Val Thr Lys Pro Ile Glu Gly Ala Gly Ala Arg Ala Pro Glu Ile Ala
180 185 190
Lys Ala Tyr Val Ser Ala Leu Arg Asp Leu Val Lys Ala Leu Gly Val
195 200 205
Ser Asp Gly Arg Leu Asp Gln Gly Ser Met Arg Val Asp Ala Asn Leu
210 215 220
Ser Leu Arg Pro Ile Gly Gln Glu Glu Phe Gly Thr Arg Thr Glu Thr
225 230 235 240
Lys Asn Ile Asn Ser Leu Lys Ser Val Glu Gln Ala Ser Thr Phe Glu
245 250 255
Met Gln Arg Gln Ala Gln

260

<210> 381
 <211> 659
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(636)
 <223> RXA01398

<400> 381
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 Lys Glu Thr Ala Glu Asp Tyr Arg Tyr Phe Asn Asp Pro Asp Leu Pro
 1 5 10 15
 cca gtg att gcg cct cgt gag tgg gtg gaa gaa atc cgc gca act ctt 96
 Pro Val Ile Ala Pro Arg Glu Trp Val Glu Glu Ile Arg Ala Thr Leu
 20 25 30
 cca gag ctg cct tgg gtt cgc cgt gca cgt atc cag gaa gag tgg aag 144
 Pro Glu Leu Pro Trp Val Arg Arg Ala Arg Ile Gln Glu Glu Trp Lys
 35 40 45
 ctt tcc gac gcc gag atg cgc gac ctc atc aac gcc aac gcg ctc gac 192
 Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp
 50 55 60
 ctc atc atc gag acc gtg gaa gcg ggt acc act cct gat gaa gct cgt 240
 Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg
 65 70 75 80
 gct tgg tgg gtt tct tac atc tct cag aag gct aac gag tct ggt gtc 288
 Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val
 85 90 95
 gag ctc gat gct ctc ggt gtt gcg cca gct cac gtt gct cgc gtc gtt 336
 Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val
 100 105 110
 gcg ctt gtt tct gaa ggc aag ctg acc aat aag ctg gca cgt cag gct 384
 Ala Leu Val Ser Glu Gly Lys Leu Thr Asn Lys Leu Ala Arg Gln Ala
 115 120 125
 atc gac ggc gtt att gct ggc gaa ggc gat gtg gac gcg gtt gtt gct 432
 Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala
 130 135 140
 gct cgt gga ctg gaa gtt gtt cgc gat gac ggc gca att gaa aag gct 480
 Ala Arg Gly Leu Glu Val Val Arg Asp Asp Gly Ala Ile Glu Lys Ala
 145 150 155 160
 gtc gat gat gcc ttg gct gca aac cca gac atc gtg gag aag tac cgc 528
 Val Asp Asp Ala Leu Ala Ala Asn Pro Asp Ile Val Glu Lys Tyr Arg
 165 170 175
 gct ggc aac acc aag gtc acc ggc gcc atc gtt ggt gct gtc atg aag 576
 Ala Gly Asn Thr Lys Val Thr Gly Ala Ile Val Gly Ala Val Met Lys
 180 185 190

gcg acc cgc ggt aag gct gac cca gct cag gtg aac cag ctg atc gca 624
 Ala Thr Arg Gly Lys Ala Asp Pro Ala Gln Val Asn Gln Leu Ile Ala
 195 200 205

aag aag ttg gct taagcttttt gccgttgagc tgc 659
 Lys Lys Leu Ala
 210

<210> 382

<211> 212

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Lys Glu Thr Ala Glu Asp Tyr Arg Tyr Phe Asn Asp Pro Asp Leu Pro
 1 5 10 15

Pro Val Ile Ala Pro Arg Glu Trp Val Glu Glu Ile Arg Ala Thr Leu
 20 25 30

Pro Glu Leu Pro Trp Val Arg Arg Ala Arg Ile Gln Glu Glu Trp Lys
 35 40 45

Leu Ser Asp Ala Glu Met Arg Asp Leu Ile Asn Ala Asn Ala Leu Asp
 50 55 60

Leu Ile Ile Glu Thr Val Glu Ala Gly Thr Thr Pro Asp Glu Ala Arg
 65 70 75 80

Ala Trp Trp Val Ser Tyr Ile Ser Gln Lys Ala Asn Glu Ser Gly Val
 85 90 95

Glu Leu Asp Ala Leu Gly Val Ala Pro Ala His Val Ala Arg Val Val
 100 105 110

Ala Leu Val Ser Glu Gly Lys Leu Thr Asn Lys Leu Ala Arg Gln Ala
 115 120 125

Ile Asp Gly Val Ile Ala Gly Glu Gly Asp Val Asp Ala Val Val Ala
 130 135 140

Ala Arg Gly Leu Glu Val Val Arg Asp Asp Gly Ala Ile Glu Lys Ala
 145 150 155 160

Val Asp Asp Ala Leu Ala Ala Asn Pro Asp Ile Val Glu Lys Tyr Arg
 165 170 175

Ala Gly Asn Thr Lys Val Thr Gly Ala Ile Val Gly Ala Val Met Lys
 180 185 190

Ala Thr Arg Gly Lys Ala Asp Pro Ala Gln Val Asn Gln Leu Ile Ala
 195 200 205

Lys Lys Leu Ala
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<210> 383

<211> 1026

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA02228

<400> 383

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gttgctcgct ggacttttta acttaaggga gatctagatc gtg gta aca ccg atc 115
                               Val Val Thr Pro Ile
                               1 5

gca gtg gtt gga ccc act gca tct gga aaa tca gct ttg gga att gct 163
Ala Val Val Gly Pro Thr Ala Ser Gly Lys Ser Ala Leu Gly Ile Ala
                               10 15 20

cta gcc cac aag ctt gac ggt gaa gta gtc aat gtg gat tcc atg cag 211
Leu Ala His Lys Leu Asp Gly Glu Val Val Asn Val Asp Ser Met Gln
                               25 30 35

ctg tac aaa ggc atg gac atc ggc acg gca aag ctg act gtc gaa gaa 259
Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys Leu Thr Val Glu Glu
                               40 45 50

cgc gaa ggc att gcg cat cat cag ctc gat gtc tgg gac gtt acc gaa 307
Arg Glu Gly Ile Ala His His Gln Leu Asp Val Trp Asp Val Thr Glu
                               55 60 65

act gcg tca gtg gcg agg ttt caa tcc gac gcc gtt gcc gat gtg gaa 355
Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala Val Ala Asp Val Glu
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gat att atg tcc cgt ggc aaa acc ccc atc ttg gtt ggc ggc tcc atg 403
Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu Val Gly Gly Ser Met
                               90 95 100

ttg tac gtc caa tct ttg gtc gat gat tgg caa ttc cca cct acc gac 451
Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln Phe Pro Pro Thr Asp
                               105 110 115

agc gct gtt cgc gca cgc ttt gag gcc cgc ttg gca gac atc ggt gtc 499
Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu Ala Asp Ile Gly Val
                               120 125 130

gaa gca cta cac gct gaa ctt act cag ctt gac cca gaa gca gca gcc 547
Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp Pro Glu Ala Ala Ala
                               135 140 145

gtc atc gaa agc aat gat ccc cga cgc acc gtc cga gca tta gaa gtc 595
Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val Arg Ala Leu Glu Val
                               150 155 160 165

att gaa cta acc ggc cag ccc ttc caa gca agc caa ccg ccc aaa gac 643
Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser Gln Pro Pro Lys Asp
                               170 175 180

gcg cca cct cgc tgg gga act cga atc att ggc ctg aaa acc act cca 691
Ala Pro Pro Arg Trp Gly Thr Arg Ile Ile Gly Leu Lys Thr Thr Pro

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185	190	195	
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Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr Ala Arg Met Phe Glu			
200	205	210	
caa ggc ttt gtc gcc gaa gtg gaa cac ctt gtg cag caa gga ctc atc			787
Gln Gly Phe Val Ala Glu Val Glu His Leu Val Gln Gln Gly Leu Ile			
215	220	225	
gct gac tcc acc gcg gga cga gca atc ggc tac tcc caa gta ctg gca			835
Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr Ser Gln Val Leu Ala			
230	235	240	245
gcc atg gca ggg gag atg acc tgg gaa gac gcc ttc gaa cgc acg gtc			883
Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala Phe Glu Arg Thr Val			
250	255	260	
acc gga acc aga cgc tat gtc agg cgc caa cgc agc tgg ttc aac aga			931
Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg Ser Trp Phe Asn Arg			
265	270	275	
gac cac cgc gtg tcc tgg gtc gac gcc tct ggc gat ccc acc gca caa			979
Asp His Arg Val Ser Trp Val Asp Ala Ser Gly Asp Pro Thr Ala Gln			
280	285	290	
gcc ttg gag att ttg ggt cta caa tagcgagggt gaatttgacc atc			1026
Ala Leu Glu Ile Leu Gly Leu Gln			
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<210> 384

<211> 301

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

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20 25 30	
Val Asp Ser Met Gln Leu Tyr Lys Gly Met Asp Ile Gly Thr Ala Lys	
35 40 45	
Leu Thr Val Glu Glu Arg Glu Gly Ile Ala His His Gln Leu Asp Val	
50 55 60	
Trp Asp Val Thr Glu Thr Ala Ser Val Ala Arg Phe Gln Ser Asp Ala	
65 70 75 80	
Val Ala Asp Val Glu Asp Ile Met Ser Arg Gly Lys Thr Pro Ile Leu	
85 90 95	
Val Gly Gly Ser Met Leu Tyr Val Gln Ser Leu Val Asp Asp Trp Gln	
100 105 110	
Phe Pro Pro Thr Asp Ser Ala Val Arg Ala Arg Phe Glu Ala Arg Leu	
115 120 125	

Ala Asp Ile Gly Val Glu Ala Leu His Ala Glu Leu Thr Gln Leu Asp
 130 135 140

Pro Glu Ala Ala Ala Val Ile Glu Ser Asn Asp Pro Arg Arg Thr Val
 145 150 155 160

Arg Ala Leu Glu Val Ile Glu Leu Thr Gly Gln Pro Phe Gln Ala Ser
 165 170 175

Gln Pro Pro Lys Asp Ala Pro Pro Arg Trp Gly Thr Arg Ile Ile Gly
 180 185 190

Leu Lys Thr Thr Pro Glu Trp Leu Asn Pro Arg Ile Glu Gln Arg Thr
 195 200 205

Ala Arg Met Phe Glu Gln Gly Phe Val Ala Glu Val Glu His Leu Val
 210 215 220

Gln Gln Gly Leu Ile Ala Asp Ser Thr Ala Gly Arg Ala Ile Gly Tyr
 225 230 235 240

Ser Gln Val Leu Ala Ala Met Ala Gly Glu Met Thr Trp Glu Asp Ala
 245 250 255

Phe Glu Arg Thr Val Thr Gly Thr Arg Arg Tyr Val Arg Arg Gln Arg
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Ser Trp Phe Asn Arg Asp His Arg Val Ser Trp Val Asp Ala Ser Gly
 275 280 285

Asp Pro Thr Ala Gln Ala Leu Glu Ile Leu Gly Leu Gln
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<210> 385

<211> 1515

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1492)

<223> RXA02502

<400> 385

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 Met Val Ser Val Leu
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atc gta ggg atg tgc cac agg tct gcg cct gtg tgc ctt ctt gaa cgt 163
 Ile Val Gly Met Ser His Arg Ser Ala Pro Val Ser Leu Leu Glu Arg
 10 15 20

ctg agc atg gat gat tca gta cgt ggt gaa aca act caa gca ctc ctg 211
 Leu Ser Met Asp Asp Ser Val Arg Gly Glu Thr Thr Gln Ala Leu Leu
 25 30 35

ggt agg gcg tct tta agc gag gcc ctc att gtc tct acg tgt aac cgc 259
 Gly Arg Ala Ser Leu Ser Glu Ala Leu Ile Val Ser Thr Cys Asn Arg

40					45					50							
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Leu	Glu	Val	Tyr	Thr	Val	Thr	Ser	Ser	Phe	His	Thr	Gly	Val	Asn	Asp		
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Val	Val	Glu	Val	Leu	His	Glu	Ala	Ser	Gly	Val	Asp	Ile	Glu	Thr	Leu		
70					75					80					85		
cgc	gga	tat	ctt	tat	gtc	cgt	tac	gcc	gat	gct	gct	gct	gaa	cac	atg	403	
Arg	Gly	Tyr	Leu	Tyr	Val	Arg	Tyr	Ala	Asp	Ala	Ala	Ala	Glu	His	Met		
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ttg	gtg	gtg	act	tcc	ggg	ttg	gat	tcc	atg	gtg	ttg	ggg	gag	cag	cag	451	
Leu	Val	Val	Thr	Ser	Gly	Leu	Asp	Ser	Met	Val	Leu	Gly	Glu	Gln	Gln		
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atc	att	ggg	cag	gtg	cgc	act	gcg	tac	caa	gca	gct	aat	gaa	tat	ggg	499	
Ile	Ile	Gly	Gln	Val	Arg	Thr	Ala	Tyr	Gln	Ala	Ala	Asn	Glu	Tyr	Gly		
120					125					130							
tct	gtc	ggg	cct	gct	ttg	cat	tca	ctt	acc	cag	acc	gcg	ctg	cat	acc	547	
Ser	Val	Gly	Pro	Ala	Leu	His	Ser	Leu	Thr	Gln	Thr	Ala	Leu	His	Thr		
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ggc	aag	cgc	gtg	cat	tcg	gag	act	gct	att	gat	gat	gct	ggg	gca	tcg	595	
Gly	Lys	Arg	Val	His	Ser	Glu	Thr	Ala	Ile	Asp	Asp	Ala	Gly	Ala	Ser		
150					155					160					165		
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Met	Val	Ser	Phe	Ala	Val	Asp	Arg	Ala	Leu	Val	Gln	Met	Gly	Leu	Asp		
170					175					180							
tcg	gag	gca	gaa	gcc	cca	cta	tct	ggc	aag	aca	gcc	ttg	gtg	ttg	ggc	691	
Ser	Glu	Ala	Glu	Ala	Pro	Leu	Ser	Gly	Lys	Thr	Ala	Leu	Val	Leu	Gly		
185					190					195							
gct	ggc	gcg	atg	agt	tct	ctt	gca	gcc	act	cac	ctt	ggg	cgc	gct	gga	739	
Ala	Gly	Ala	Met	Ser	Ser	Leu	Ala	Ala	Thr	His	Leu	Gly	Arg	Ala	Gly		
200					205					210							
att	tcc	aac	ttg	atc	atg	gcc	aac	cgc	act	ctg	gaa	cgt	gcc	gaa	agg	787	
Ile	Ser	Asn	Leu	Ile	Met	Ala	Asn	Arg	Thr	Leu	Glu	Arg	Ala	Glu	Arg		
215					220					225							
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Leu	Ala	Glu	His	Ser	Leu	Glu	Ala	Gly	Val	Pro	Ala	Glu	Val	Val	Glu		
230					235					240					245		
tac	gat	cag	cga	gct	tcc	gcc	tac	aat	cgc	gtt	gac	ctg	gta	gtt	tcc	883	
Tyr	Asp	Gln	Arg	Ala	Ser	Ala	Tyr	Asn	Arg	Val	Asp	Leu	Val	Val	Ser		
250					255					260							
gcc	acg	gga	gcg	gat	gat	ttc	acc	gtg	aag	cct	gag	gat	att	cca	gaa	931	
Ala	Thr	Gly	Ala	Asp	Asp	Phe	Thr	Val	Lys	Pro	Glu	Asp	Ile	Pro	Glu		
265					270					275							
ggg	gct	tcg	ttg	atg	ttg	gtg	gat	ttg	tcc	atg	cca	cga	gac	atc	gat	979	
Gly	Ala	Ser	Leu	Met	Leu	Val	Asp	Leu	Ser	Met	Pro	Arg	Asp	Ile	Asp		
280					285					290							

gat gct tgt gcg gat ctg ccg ggc gtt gat ttg gtg aac atc gaa cgc 1027
Asp Ala Cys Ala Asp Leu Pro Gly Val Asp Leu Val Asn Ile Glu Arg
295 300 305

ctg cac aag gcc tcc cgt gag ggt gga tcg ggc atg gcg cca agc gag 1075
Leu His Lys Ala Ser Arg Glu Gly Gly Ser Gly Met Ala Pro Ser Glu
310 315 320 325

gaa gaa gct ttg gcg att gtt cgg gaa gag ttg gat tct ttc acc tct 1123
Glu Glu Ala Leu Ala Ile Val Arg Glu Glu Leu Asp Ser Phe Thr Ser
330 335 340

gag cag cgc att cgc gat atc gtt cca gct gtg tcc gcg ttg cgc agg 1171
Glu Gln Arg Ile Arg Asp Ile Val Pro Ala Val Ser Ala Leu Arg Arg
345 350 355

cag gcc gcg tcg gtg gga agc gat gaa ttg gat cga ctc cgc caa cgt 1219
Gln Ala Ala Ser Val Gly Ser Asp Glu Leu Asp Arg Leu Arg Gln Arg
360 365 370

gcc ccc ggg att tcc gag gtg gaa tgg ggg gaa gtg gag aaa aca ggg 1267
Ala Pro Gly Ile Ser Glu Val Glu Trp Gly Glu Val Glu Lys Thr Gly
375 380 385

aga cgg gtc gtc gat aag ctt ctt cat gaa ccc act gtg cgc gtc aag 1315
Arg Arg Val Val Asp Lys Leu Leu His Glu Pro Thr Val Arg Val Lys
390 395 400 405

gaa ctg gcg gcc cgg tcc ggc agc atc tct tat gat tca gct ctg caa 1363
Glu Leu Ala Ala Arg Ser Gly Ser Ile Ser Tyr Asp Ser Ala Leu Gln
410 415 420

gag ctg ttc ggt ttg gag tcg ctg gcg agc acc gca gca ccg gca acc 1411
Glu Leu Phe Gly Leu Glu Ser Leu Ala Ser Thr Ala Ala Pro Ala Thr
425 430 435

acg tcc gtc aac gcg tca gaa ctg ccg gat gcg ggt atc gtc gca ttc 1459
Thr Ser Val Asn Ala Ser Glu Leu Pro Asp Ala Gly Ile Val Ala Phe
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gta 1515

<210> 386

<211> 464

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

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Thr Gln Ala Leu Leu Gly Arg Ala Ser Leu Ser Glu Ala Leu Ile Val

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Asp	Ile	Glu	Thr	Leu	Arg	Gly	Tyr	Leu	Tyr	Val	Arg	Tyr	Ala	Asp	Ala	
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Ala	Ala	Glu	His	Met	Leu	Val	Val	Thr	Ser	Gly	Leu	Asp	Ser	Met	Val	
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Leu	Gly	Glu	Gln	Gln	Ile	Ile	Gly	Gln	Val	Arg	Thr	Ala	Tyr	Gln	Ala	
					115					120					125	
Ala	Asn	Glu	Tyr	Gly	Ser	Val	Gly	Pro	Ala	Leu	His	Ser	Leu	Thr	Gln	
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Thr	Ala	Leu	His	Thr	Gly	Lys	Arg	Val	His	Ser	Glu	Thr	Ala	Ile	Asp	
145					150					155					160	
Asp	Ala	Gly	Ala	Ser	Met	Val	Ser	Phe	Ala	Val	Asp	Arg	Ala	Leu	Val	
					165					170					175	
Gln	Met	Gly	Leu	Asp	Ser	Glu	Ala	Glu	Ala	Pro	Leu	Ser	Gly	Lys	Thr	
					180					185					190	
Ala	Leu	Val	Leu	Gly	Ala	Gly	Ala	Met	Ser	Ser	Leu	Ala	Ala	Thr	His	
					195					200					205	
Leu	Gly	Arg	Ala	Gly	Ile	Ser	Asn	Leu	Ile	Met	Ala	Asn	Arg	Thr	Leu	
210					215					220						
Glu	Arg	Ala	Glu	Arg	Leu	Ala	Glu	His	Ser	Leu	Glu	Ala	Gly	Val	Pro	
225					230					235					240	
Ala	Glu	Val	Val	Glu	Tyr	Asp	Gln	Arg	Ala	Ser	Ala	Tyr	Asn	Arg	Val	
					245					250					255	
Asp	Leu	Val	Val	Ser	Ala	Thr	Gly	Ala	Asp	Asp	Phe	Thr	Val	Lys	Pro	
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Glu	Asp	Ile	Pro	Glu	Gly	Ala	Ser	Leu	Met	Leu	Val	Asp	Leu	Ser	Met	
					275					280					285	
Pro	Arg	Asp	Ile	Asp	Asp	Ala	Cys	Ala	Asp	Leu	Pro	Gly	Val	Asp	Leu	
290					295					300						
Val	Asn	Ile	Glu	Arg	Leu	His	Lys	Ala	Ser	Arg	Glu	Gly	Gly	Ser	Gly	
305					310					315					320	
Met	Ala	Pro	Ser	Glu	Glu	Glu	Ala	Leu	Ala	Ile	Val	Arg	Glu	Glu	Leu	
					325					330					335	
Asp	Ser	Phe	Thr	Ser	Glu	Gln	Arg	Ile	Arg	Asp	Ile	Val	Pro	Ala	Val	
					340					345					350	
Ser	Ala	Leu	Arg	Arg	Gln	Ala	Ala	Ser	Val	Gly	Ser	Asp	Glu	Leu	Asp	
355					360					365						

Arg Leu Arg Gln Arg Ala Pro Gly Ile Ser Glu Val Glu Trp Gly Glu
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Val Glu Lys Thr Gly Arg Arg Val Val Asp Lys Leu Leu His Glu Pro
 385 390 395 400

Thr Val Arg Val Lys Glu Leu Ala Ala Arg Ser Gly Ser Ile Ser Tyr
 405 410 415

Asp Ser Ala Leu Gln Glu Leu Phe Gly Leu Glu Ser Leu Ala Ser Thr
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Ala Ala Pro Ala Thr Thr Ser Val Asn Ala Ser Glu Leu Pro Asp Ala
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Gly Ile Val Ala Phe Val Asn Ala Pro Ser Ala Thr Gln Thr Arg Glu
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<210> 387

<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(874)

<223> RXA02182

<400> 387

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 Val Lys Lys Leu Ala
 1 5

tcc ata gcg atc ctc tcc agc ctc cct ttg gct tcg tgt tcc act cct 163
 Ser Ile Ala Ile Leu Ser Ser Leu Pro Leu Ala Ser Cys Ser Thr Pro
 10 15 20

cca aca gat tca gag gct gtc gtt gag cat ctg gtt cca gaa att atc 211
 Pro Thr Asp Ser Glu Ala Val Val Glu His Leu Val Pro Glu Ile Ile
 25 30 35

tcc acc cac tct ttt gat tcc acc tcg ttt act cag ggg ttg gaa tta 259
 Ser Thr His Ser Phe Asp Ser Thr Ser Phe Thr Gln Gly Leu Glu Leu
 40 45 50

gat ggc gac gag ctg att gtg gga act ggc caa tac ggt ggt tcc cga 307
 Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln Tyr Gly Gly Ser Arg
 55 60 65

atc tat cgc agc tcc gtt gat ggc cag gaa tct gtt tcc caa tcg ctt 355
 Ile Tyr Arg Ser Ser Val Asp Gly Gln Glu Ser Val Ser Gln Ser Leu
 70 75 80 85

gat cca gaa ttc ttc ggt gaa ggc atc acc aag tct ggt gat gcc atc 403
 Asp Pro Glu Phe Phe Gly Glu Gly Ile Thr Lys Ser Gly Asp Ala Ile
 90 95 100

tgg	cag	ctg	aca	tgg	aat	gaa	ggt	gtc	gct	ttc	aag	cgt	gat	gca	gat	451
Trp	Gln	Leu	Thr	Trp	Asn	Glu	Gly	Val	Ala	Phe	Lys	Arg	Asp	Ala	Asp	
			105					110					115			

act ctc gag gag tta gat cgc gtt tca tat aat ggc cag ggg tgg gga 499
Thr Leu Glu Glu Leu Asp Arg Val Ser Tyr Asn Gly Gln Gly Trp Gly
120 125 130

att tgc tca act gac gat gcc ctc atc acc tct gat gga agc tcc acc 547
Ile Cys Ser Thr Asp Asp Ala Leu Ile Thr Ser Asp Gly Ser Ser Thr
135 140 145

ctc acc ttt agg gat ccg gaa acc ttt gca gag aac agc act gta gat 595
Leu Thr Phe Arg Asp Pro Glu Thr Phe Ala Glu Asn Ser Thr Val Asp
150 155 160 165

gtg aca cta gac ggc tct ccg gtt ggg aac ctc aat gag ctc gaa tgc 643
Val Thr Leu Asp Gly Ser Pro Val Gly Asn Leu Asn Glu Leu Glu Cys
170 175 180

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gtt gat ggc gag gta tat gcc aat att ttc ctc gat aca gac atc atg    691
Val Asp Gly Glu Val Tyr Ala Asn Ile Phe Leu Asp Thr Asp Ile Met
      185                      190                      195

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cga atc gat ccg aac tcc ggc gaa gtc acc gca gtg atc gat gcc tca 739
Arg Ile Asp Pro Asn Ser Gly Glu Val Thr Ala Val Ile Asp Ala Ser
200 205 210

aat att cct aac aac gcc aca cca gat aca aac aat gtg ctc aac ggc 787
Asn Ile Pro Asn Asn Ala Thr Pro Asp Thr Asn Asn Val Leu Asn Gly
215 220 225

att gca cat att ccg gat tcc gat cgt ttt tat atc act ggt aag cgt 835
Ile Ala His Ile Pro Asp Ser Asp Arg Phe Tyr Ile Thr Gly Lys Arg
230 235 240 245

tgg cct gac ctc tat gag gtt aga ttc gtc cct gct gac tagaatcaag 884
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actcatggca agc 897

<210> 388

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

Val Lys Lys Leu Ala Ser Ile Ala Ile Leu Ser Ser Leu Pro Leu Ala
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20 25 30

Val Pro Glu Ile Ile Ser Thr His Ser Phe Asp Ser Thr Ser Phe Thr
35 40 45

Gln Gly Leu Glu Leu Asp Gly Asp Glu Leu Ile Val Gly Thr Gly Gln
50 55 60

Tyr Gly Gly Ser Arg Ile Tyr Arg Ser Ser Val Asp Gly Gln Glu Ser
 65 70 75 80
 Val Ser Gln Ser Leu Asp Pro Glu Phe Phe Gly Glu Gly Ile Thr Lys
 85 90 95
 Ser Gly Asp Ala Ile Trp Gln Leu Thr Trp Asn Glu Gly Val Ala Phe
 100 105 110
 Lys Arg Asp Ala Asp Thr Leu Glu Glu Leu Asp Arg Val Ser Tyr Asn
 115 120 125
 Gly Gln Gly Trp Gly Ile Cys Ser Thr Asp Asp Ala Leu Ile Thr Ser
 130 135 140
 Asp Gly Ser Ser Thr Leu Thr Phe Arg Asp Pro Glu Thr Phe Ala Glu
 145 150 155 160
 Asn Ser Thr Val Asp Val Thr Leu Asp Gly Ser Pro Val Gly Asn Leu
 165 170 175
 Asn Glu Leu Glu Cys Val Asp Gly Glu Val Tyr Ala Asn Ile Phe Leu
 180 185 190
 Asp Thr Asp Ile Met Arg Ile Asp Pro Asn Ser Gly Glu Val Thr Ala
 195 200 205
 Val Ile Asp Ala Ser Asn Ile Pro Asn Asn Ala Thr Pro Asp Thr Asn
 210 215 220
 Asn Val Leu Asn Gly Ile Ala His Ile Pro Asp Ser Asp Arg Phe Tyr
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 Ile Thr Gly Lys Arg Trp Pro Asp Leu Tyr Glu Val Arg Phe Val Pro
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 Ala Asp

<210> 389

<211> 786

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(763)

<223> RXN00211

<400> 389

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 Met Ser Phe Leu Ile
 1 5

cgc gtc ctg ttg tcc gac acc cca ggc agc ctc gcg tta ctc gct gaa 163
 Arg Val Leu Leu Ser Asp Thr Pro Gly Ser Leu Ala Leu Leu Ala Glu
 10 15 20

gcc ctt ggg att gta gag gcc aat att caa tcc gtg gac gtg gtg gaa 211
 Ala Leu Gly Ile Val Glu Ala Asn Ile Gln Ser Val Asp Val Val Glu
 25 30 35

cgc ttc ccc aat ggc acg gtc atg gac gat ctg gtg atc tcc atc cct 259
 Arg Phe Pro Asn Gly Thr Val Met Asp Asp Leu Val Ile Ser Ile Pro
 40 45 50

cgc gat gtc atg gca gac acc atc atc acc gca gct gaa gaa gtc gac 307
 Arg Asp Val Met Ala Asp Thr Ile Ile Thr Ala Ala Glu Glu Val Asp
 55 60 65

ggc gtg gag att gat tcc atc cgc cca ttc tcc ggg act gtt gac cgc 355
 Gly Val Glu Ile Asp Ser Ile Arg Pro Phe Ser Gly Thr Val Asp Arg
 70 75 80 85

cgc gga cag atc caa atg ctg gct gct gtt gct cac caa cgc cgc gat 403
 Arg Gly Gln Ile Gln Met Leu Ala Ala Val Ala His Gln Arg Arg Asp
 90 95 100

atc acc gca gcg atg gaa gaa atg gtc gat gtc atc ccc cgc acc atg 451
 Ile Thr Ala Ala Met Glu Glu Met Val Asp Val Ile Pro Arg Thr Met
 105 110 115

acc tct ggt tgg gct ttg gtc att gat cta aaa gga ccc atc act cgc 499
 Thr Ser Gly Trp Ala Leu Val Ile Asp Leu Lys Gly Pro Ile Thr Arg
 120 125 130

atc gct ggt tcc cta gca gcg ccc gaa gat gac ggc acc gtt ccg gag 547
 Ile Ala Gly Ser Leu Ala Ala Pro Glu Asp Asp Gly Thr Val Pro Glu
 135 140 145

aac atc gtt ctc aaa gaa gct cgc atg ctc aac ccg gaa aac gat ccg 595
 Asn Ile Val Leu Lys Glu Ala Arg Met Leu Asn Pro Glu Asn Asp Pro
 150 155 160 165

tgg att cca gag tcc tgg aca ctg ctt gat tct tcc ctt gcc atc gct 643
 Trp Ile Pro Glu Ser Trp Thr Leu Leu Asp Ser Ser Leu Ala Ile Ala
 170 175 180

ccg atc ggc aag cac ggc ctg gct ctg att atc ggt cgc cct ggt ggc 691
 Pro Ile Gly Lys His Gly Leu Ala Leu Ile Ile Gly Arg Pro Gly Gly
 185 190 195

cct gat ttc ttg gcc agc gaa gtg gag cac tta ggc caa gtc ggt gac 739
 Pro Asp Phe Leu Ala Ser Glu Val Glu His Leu Gly Gln Val Gly Asp
 200 205 210

att atc gga gca atg ctt caa aaa taatctgagc tgtttaaaaa atg 786
 Ile Ile Gly Ala Met Leu Gln Lys
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<210> 390

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

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<213> Corynebacterium glutamicum
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<223> RXN00669
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gtggggcgctg acgtcgaaaa gcaaaaaaatg aaaggcagac atg gac aat tca acg 115
Met Asp Asn Ser Thr
1 5

gtg cga atc cgg ctg gat cta gcg tat gac ggc acg gat ttt cat ggc 163
Val Arg Ile Arg Leu Asp Leu Ala Tyr Asp Gly Thr Asp Phe His Gly
10 15 20

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tgg gcg aag cag ggg acc agc gat cta cgc acc gtg caa aaa gtg ttg	211
Trp Ala Lys Gln Gly Thr Ser Asp Leu Arg Thr Val Gln Lys Val Leu	
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gaa gac aat ttg agc atg gtg ctg cgt gag act gtt gaa ttg act gtg	259
Glu Asp Asn Leu Ser Met Val Leu Arg Glu Thr Val Glu Leu Thr Val	
40 45 50	
gcc ggg cga acc gat gcg ggg gtg cat gcg gcg ggc cag gtg gcg cac	307
Ala Gly Arg Thr Asp Ala Gly Val His Ala Ala Gly Gln Val Ala His	
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ttt gat att ccg gca cac gct tta gag cag cgc agt att gat ggc gat	355
Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg Ser Ile Asp Gly Asp	
70 75 80 85	
cca agc aag ttg gtt cgg cgc ttg ggt cgg ttg ctg ccc gat gat att	403
Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu Leu Pro Asp Asp Ile	
90 95 100	
cgg gtg cat ggc gta cgt ttt gcc gag ccc ggg ttt gat gcg cga ttt	451
Arg Val His Gly Val Arg Phe Ala Glu Pro Gly Phe Asp Ala Arg Phe	
105 110 115	
tcc gcg atg cgc agg cac tac gtt tat cgc att acg acg cat ccc gcc	499
Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile Thr Thr His Pro Ala	
120 125 130	
ggc gcg ctg cct acg cgc cgc cac gac acg gcg cag tgg cca aaa cct	547
Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala Gln Trp Pro Lys Pro	
135 140 145	
gtc gaa cta gag cgg atg caa tta gcc gcc gat gca ctg ctg ggg ctg	595
Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp Ala Leu Leu Gly Leu	
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cat gat ttt gtg gcg ttt tgc aaa gct aag cca cat gcg acg acg gtg	643
His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro His Ala Thr Thr Val	
170 175 180	
cgt gaa cta caa aaa ttt gcg tgg aaa gac gtc tcc act gac atc gaa	691
Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val Ser Thr Asp Ile Glu	
185 190 195	
ccg cag gtg tat gaa gca cac gtg gtg gcc gat gct ttt tgc tgg tcg	739
Pro Gln Val Tyr Glu Ala His Val Val Ala Asp Ala Phe Cys Trp Ser	
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atg gtg cgc tcg ctg gtc ggc tcc tgc atg gcc gtg ggc gaa gga cgc	787
Met Val Arg Ser Leu Val Gly Ser Cys Met Ala Val Gly Glu Gly Arg	
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cgc gga tca ggg ttt act gca gaa ttg ctt gat gca agc gaa cgc agc	835
Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp Ala Ser Glu Arg Ser	
230 235 240 245	
ccc atg gtt cca gta gca cct gcg aaa ggt ttg agc ttg gtt ggc gtg	883
Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu Ser Leu Val Gly Val	
250 255 260	

gat tat cct tcc gct gat aag tta cag gaa aga gcg ctg gaa acc cga 931
 Asp Tyr Pro Ser Ala Asp Lys Leu Gln Glu Arg Ala Leu Glu Thr Arg
 265 270 275

gct gtt cgc gag ttt ccg gac gcg tcc gcg agc cta aaa cta gat gat 979
 Ala Val Arg Glu Phe Pro Asp Ala Ser Ala Ser Leu Lys Leu Asp Asp
 280 285 290

gag taaaagggac taaactcgtc tct 1005
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<210> 392

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

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Val Gln Lys Val Leu Glu Asp Asn Leu Ser Met Val Leu Arg Glu Thr
 35 40 45

Val Glu Leu Thr Val Ala Gly Arg Thr Asp Ala Gly Val His Ala Ala
 50 55 60

Gly Gln Val Ala His Phe Asp Ile Pro Ala His Ala Leu Glu Gln Arg
 65 70 75 80

Ser Ile Asp Gly Asp Pro Ser Lys Leu Val Arg Arg Leu Gly Arg Leu
 85 90 95

Leu Pro Asp Asp Ile Arg Val His Gly Val Arg Phe Ala Glu Pro Gly
 100 105 110

Phe Asp Ala Arg Phe Ser Ala Met Arg Arg His Tyr Val Tyr Arg Ile
 115 120 125

Thr Thr His Pro Ala Gly Ala Leu Pro Thr Arg Arg His Asp Thr Ala
 130 135 140

Gln Trp Pro Lys Pro Val Glu Leu Glu Arg Met Gln Leu Ala Ala Asp
 145 150 155 160

Ala Leu Leu Gly Leu His Asp Phe Val Ala Phe Cys Lys Ala Lys Pro
 165 170 175

His Ala Thr Thr Val Arg Glu Leu Gln Lys Phe Ala Trp Lys Asp Val
 180 185 190

Ser Thr Asp Ile Glu Pro Gln Val Tyr Glu Ala His Val Val Ala Asp
 195 200 205

Ala Phe Cys Trp Ser Met Val Arg Ser Leu Val Gly Ser Cys Met Ala
 210 215 220

Val Gly Glu Gly Arg Arg Gly Ser Gly Phe Thr Ala Glu Leu Leu Asp
 225 230 235 240

Ala Ser Glu Arg Ser Pro Met Val Pro Val Ala Pro Ala Lys Gly Leu
 245 250 255

Ser Leu Val Gly Val Asp Tyr Pro Ser Ala Asp Lys Leu Gln Glu Arg
 260 265 270

Ala Leu Glu Thr Arg Ala Val Arg Glu Phe Pro Asp Ala Ser Ala Ser
 275 280 285

Leu Lys Leu Asp Asp Glu
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 <212> DNA
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 <222> (101)..(1030)
 <223> RXN02651

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 Met Asn Asn Arg Gln
 1 5

agc aga acc ctt ccc gta cca gaa gga ctg gca ggc atg cgt gtg gac 163
 Ser Arg Thr Leu Pro Val Pro Glu Gly Leu Ala Gly Met Arg Val Asp
 10 15 20

gca gca ctg tcc aag ttg ctg gga att tca cgc acc gta gct gca gaa 211
 Ala Ala Leu Ser Lys Leu Leu Gly Ile Ser Arg Thr Val Ala Ala Glu
 25 30 35

ctc gcc acc gcc ggc gat gtc agc gtt gat ggg gct gtg gta ggt aaa 259
 Leu Ala Thr Ala Gly Asp Val Ser Val Asp Gly Ala Val Val Gly Lys
 40 45 50

agc gag cgg ctc gtt gcc gat tcc atg ctg gat gtc ttg ctg cct gaa 307
 Ser Glu Arg Leu Val Ala Asp Ser Met Leu Asp Val Leu Leu Pro Glu
 55 60 65

cca gca gct ccg ttg atg ccc aag gaa gaa atc gtt ccc ggc ctg gat 355
 Pro Ala Ala Pro Leu Met Pro Lys Glu Glu Ile Val Pro Gly Leu Asp
 70 75 80 85

att ttg tac tct gat gac gat gtc atc gca gtc aac aaa ccc gtc ggc 403
 Ile Leu Tyr Ser Asp Asp Asp Val Ile Ala Val Asn Lys Pro Val Gly
 90 95 100

gtg gcg gca cat ccc acc gtg ggt tgg gaa ggc cca act gtg gtg ggc 451
 Val Ala Ala His Pro Thr Val Gly Trp Glu Gly Pro Thr Val Val Gly
 105 110 115

gga ctt gca gct gca ggt ttc cgc att tcc acc tcc ggc cca cca gag 499
 Gly Leu Ala Ala Ala Gly Phe Arg Ile Ser Thr Ser Gly Pro Pro Glu
 120 125 130

cgc aag ggt att gtg cag cgc ctt gac gtt ggc acg tct ggc gtg atg 547
 Arg Lys Gly Ile Val Gln Arg Leu Asp Val Gly Thr Ser Gly Val Met
 135 140 145

gtg gtt gct gcc tct gaa cgt gga tac acc gtg ctc aag cgc gct ttc 595
 Val Val Ala Ala Ser Glu Arg Gly Tyr Thr Val Leu Lys Arg Ala Phe
 150 155 160 165

cgg gac cgc acc gtg gac aag acc tac cac gcg ttg gtg caa ggc cac 643
 Arg Asp Arg Thr Val Asp Lys Thr Tyr His Ala Leu Val Gln Gly His
 170 175 180

cct gat ccg ctg acc gga acc atc gaa gca ccg atc ggc cgc cac ccc 691
 Pro Asp Pro Leu Thr Gly Thr Ile Glu Ala Pro Ile Gly Arg His Pro
 185 190 195

tca gca ggt tgg cgt ttc gca gta aca act gaa ggc aaa cac gcc gtc 739
 Ser Ala Gly Trp Arg Phe Ala Val Thr Thr Glu Gly Lys His Ala Val
 200 205 210

aca cac tac gaa acc ctg gag gcc ttc caa gag gca acc ctg ctg aaa 787
 Thr His Tyr Glu Thr Leu Glu Ala Phe Gln Glu Ala Thr Leu Leu Lys
 215 220 225

atc cac ctg gaa act ggc cgc acc cac cag atc cgc gtg cat ttc tcc 835
 Ile His Leu Glu Thr Gly Arg Thr His Gln Ile Arg Val His Phe Ser
 230 235 240 245

gcg ctg cac cac cca tgc tgt ggc gac ccc atg tac ggc tct gat cct 883
 Ala Leu His His Pro Cys Cys Gly Asp Pro Met Tyr Gly Ser Asp Pro
 250 255 260

gcg ttg tcc gag cgc ctt ggc ctt aac cgt cag tgg ctg cac gcc gtc 931
 Ala Leu Ser Glu Arg Leu Gly Leu Asn Arg Gln Trp Leu His Ala Val
 265 270 275

tcg ctt gga ttc aac cac cca gca gat ggc cga tgg atg gaa atc gtc 979
 Ser Leu Gly Phe Asn His Pro Ala Asp Gly Arg Trp Met Glu Ile Val
 280 285 290

tcc cca tat cca act gat ctc caa cac gct tta gac gtt ctc cgc gag 1027
 Ser Pro Tyr Pro Thr Asp Leu Gln His Ala Leu Asp Val Leu Arg Glu
 295 300 305

caa taatggatgg tgtcgataaa ggg 1053
 Gln
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<210> 394

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

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 35 40 45
 Ala Val Val Gly Lys Ser Glu Arg Leu Val Ala Asp Ser Met Leu Asp
 50 55 60
 Val Leu Leu Pro Glu Pro Ala Ala Pro Leu Met Pro Lys Glu Glu Ile
 65 70 75 80
 Val Pro Gly Leu Asp Ile Leu Tyr Ser Asp Asp Asp Val Ile Ala Val
 85 90 95
 Asn Lys Pro Val Gly Val Ala Ala His Pro Thr Val Gly Trp Glu Gly
 100 105 110
 Pro Thr Val Val Gly Gly Leu Ala Ala Ala Gly Phe Arg Ile Ser Thr
 115 120 125
 Ser Gly Pro Pro Glu Arg Lys Gly Ile Val Gln Arg Leu Asp Val Gly
 130 135 140
 Thr Ser Gly Val Met Val Val Ala Ala Ser Glu Arg Gly Tyr Thr Val
 145 150 155 160
 Leu Lys Arg Ala Phe Arg Asp Arg Thr Val Asp Lys Thr Tyr His Ala
 165 170 175
 Leu Val Gln Gly His Pro Asp Pro Leu Thr Gly Thr Ile Glu Ala Pro
 180 185 190
 Ile Gly Arg His Pro Ser Ala Gly Trp Arg Phe Ala Val Thr Thr Glu
 195 200 205
 Gly Lys His Ala Val Thr His Tyr Glu Thr Leu Glu Ala Phe Gln Glu
 210 215 220
 Ala Thr Leu Leu Lys Ile His Leu Glu Thr Gly Arg Thr His Gln Ile
 225 230 235 240
 Arg Val His Phe Ser Ala Leu His His Pro Cys Cys Gly Asp Pro Met
 245 250 255
 Tyr Gly Ser Asp Pro Ala Leu Ser Glu Arg Leu Gly Leu Asn Arg Gln
 260 265 270
 Trp Leu His Ala Val Ser Leu Gly Phe Asn His Pro Ala Asp Gly Arg
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 Asp Val Leu Arg Glu Gln
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<210> 395

<211> 2647

<212> DNA

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<222> (101)..(2647)

<223> RXA01344

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                                   Val Leu Glu Gly Pro
                                   1 5

atc ttg gca gtc tcc cgc cag acc aag tca gtc gtc gat att ccc ggt 163
Ile Leu Ala Val Ser Arg Gln Thr Lys Ser Val Val Asp Ile Pro Gly
                                   10 15 20

gca ccg cag cgt tat tct ttc gcg aag gtg tcc gca ccc att gag gtg 211
Ala Pro Gln Arg Tyr Ser Phe Ala Lys Val Ser Ala Pro Ile Glu Val
                                   25 30 35

ccc ggg cta cta gat ctt caa ctg gat tct tac tcc tgg ctg att ggt 259
Pro Gly Leu Leu Asp Leu Gln Leu Asp Ser Tyr Ser Trp Leu Ile Gly
                                   40 45 50

acg cct gag tgg cgt gct cgt cag aag gaa gaa ttc ggc gag gga gcc 307
Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu Phe Gly Glu Gly Ala
                                   55 60 65

cgc gta acc agc ggc ctt gag aac att ctc gag gag ctc tcc cca atc 355
Arg Val Thr Ser Gly Leu Glu Asn Ile Leu Glu Glu Leu Ser Pro Ile
                                   70 75 80 85

cag gat tac tct gga aac atg tcc ctg agc ctt tcg gag cca cgc ttc 403
Gln Asp Tyr Ser Gly Asn Met Ser Leu Ser Leu Ser Glu Pro Arg Phe
                                   90 95 100

gaa gac gtc aag aac acc att gac gag gcg aaa gaa aag gac atc aac 451
Glu Asp Val Lys Asn Thr Ile Asp Glu Ala Lys Glu Lys Asp Ile Asn
                                   105 110 115

tac gcg gcg cca ctg tat gtg acc gcg gag ttc gtc aac aac acc acc 499
Tyr Ala Ala Pro Leu Tyr Val Thr Ala Glu Phe Val Asn Asn Thr Thr
                                   120 125 130

ggt gaa atc aag tct cag act gtc ttc atc ggc gat ttc cca atg atg 547
Gly Glu Ile Lys Ser Gln Thr Val Phe Ile Gly Asp Phe Pro Met Met
                                   135 140 145

acg gac aag gga acg ttc atc atc aac gga acc gaa cgc gtt gtg gtc 595
Thr Asp Lys Gly Thr Phe Ile Ile Asn Gly Thr Glu Arg Val Val Val
                                   150 155 160 165

agc cag ctc gtc cgc tcc ccg ggc gtg tac ttt gac cag acc atc gat 643
Ser Gln Leu Val Arg Ser Pro Gly Val Tyr Phe Asp Gln Thr Ile Asp
                                   170 175 180

aag tca act gag cgt cca ctg cac gcc gtg aag gtt att cct tcc cgt 691
Lys Ser Thr Glu Arg Pro Leu His Ala Val Lys Val Ile Pro Ser Arg

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185										190										195																			
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cgt	att	gac	cgc	aag	cgt	cgc	cag	cca	gtc	acc	gta	ctg	ctg	aag	gct	787																							
Arg	Ile	Asp	Arg	Lys	Arg	Arg	Gln	Pro	Val	Thr	Val	Leu	Leu	Lys	Ala																								
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Leu	Gly	Trp	Thr	Thr	Glu	Gln	Ile	Thr	Glu	Arg	Phe	Gly	Phe	Ser	Glu																								
230										235										240										245									
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Ile	Met	Met	Ser	Thr	Leu	Glu	Ser	Asp	Gly	Val	Ala	Asn	Thr	Asp	Glu																								
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gca	ttg	ctg	gag	atc	tac	cgc	aag	cag	cgt	cca	ggc	gag	cag	cct	acc	931																							
Ala	Leu	Leu	Glu	Ile	Tyr	Arg	Lys	Gln	Arg	Pro	Gly	Glu	Gln	Pro	Thr																								
265										270										275																			
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Arg	Asp	Leu	Ala	Gln	Ser	Leu	Leu	Asp	Asn	Ser	Phe	Phe	Arg	Ala	Lys																								
280										285										290																			
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Arg	Tyr	Asp	Leu	Ala	Arg	Val	Gly	Arg	Tyr	Lys	Ile	Asn	Arg	Lys	Leu																								
295										300										305																			
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Gly	Leu	Gly	Gly	Asp	His	Asp	Gly	Leu	Met	Thr	Leu	Thr	Glu	Glu	Asp																								
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Ile	Ala	Thr	Thr	Ile	Glu	Tyr	Leu	Val	Arg	Leu	His	Ala	Gly	Glu	Arg																								
330										335										340																			
gtc	atg	act	tct	cca	aat	ggt	gaa	gag	atc	cca	gtc	gag	acc	gat	gac	1171																							
Val	Met	Thr	Ser	Pro	Asn	Gly	Glu	Glu	Ile	Pro	Val	Glu	Thr	Asp	Asp																								
345										350										355																			
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Ile	Asp	His	Phe	Gly	Asn	Arg	Arg	Leu	Arg	Thr	Val	Gly	Glu	Leu	Ile																								
360										365										370																			
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Glu	Arg	Met	Thr	Thr	Gln	Asp	Ala	Glu	Ser	Ile	Thr	Pro	Thr	Ser	Leu																								
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Ile	Asn	Val	Arg	Pro	Val	Ser	Ala	Ala	Ile	Arg	Glu	Phe	Phe	Gly	Thr																								
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acc	cca	tac	cgt	cgc	atc	atc	gac	ggc	aag	ctg	acc	gac	cag	att	gac	1651
Thr	Pro	Tyr	Arg	Arg	Ile	Ile	Asp	Gly	Lys	Leu	Thr	Asp	Gln	Ile	Asp	
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tac	ctt	acc	gct	gat	gag	gaa	gac	cgc	ttc	gtt	gtt	gcg	cag	gca	aac	1699
Tyr	Leu	Thr	Ala	Asp	Glu	Glu	Asp	Arg	Phe	Val	Val	Ala	Gln	Ala	Asn	
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acg	cac	tac	gac	gaa	gag	ggc	aac	atc	acc	gat	gag	acc	gtc	act	gtt	1747
Thr	His	Tyr	Asp	Glu	Glu	Gly	Asn	Ile	Thr	Asp	Glu	Thr	Val	Thr	Val	
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cgt	ctg	aag	gac	ggc	gac	atc	gcc	atg	gtt	ggc	cgc	aac	gcg	gtt	gat	1795
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Tyr	Met	Asp	Val	Ser	Pro	Arg	Gln	Met	Val	Ser	Val	Gly	Thr	Ala	Met	
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Ile	Pro	Phe	Leu	Glu	His	Asp	Asp	Ala	Asn	Arg	Ala	Leu	Met	Gly	Ala	
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Asn	Met	Gln	Lys	Gln	Ala	Val	Pro	Leu	Ile	Arg	Ala	Glu	Ala	Pro	Phe	
		600					605					610				
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Val	Ile	Thr	Pro	Val	Ala	Gly	Val	Val	Glu	Asn	Val	Ser	Ala	Asp	Phe	
	630				635					640					645	
atc	acc	atc	atg	gct	gat	gac	ggc	aag	cgc	gaa	acc	tac	ctg	ctg	cgt	2083
Ile	Thr	Ile	Met	Ala	Asp	Asp	Gly	Lys	Arg	Glu	Thr	Tyr	Leu	Leu	Arg	
				650					655					660		
aag	ttc	cag	cgc	acc	aac	cag	ggc	acc	agc	tac	aac	cag	aag	cct	ttg	2131
Lys	Phe	Gln	Arg	Thr	Asn	Gln	Gly	Thr	Ser	Tyr	Asn	Gln	Lys	Pro	Leu	
			665					670					675			

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 680 685 690

cca ggt acc ttc aat ggt gaa atg tcc ctt ggc cgt aac ctt ctg gtt 2227
 Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly Arg Asn Leu Leu Val
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gcg ttc atg cct tgg gaa ggc cac aac tac gag gat gcg atc atc ctc 2275
 Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu Asp Ala Ile Ile Leu
 710 715 720 725

aac cag aac atc gtt gag cag gac atc ttg acc tcg atc cac atc gag 2323
 Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr Ser Ile His Ile Glu
 730 735 740

gag cac gag atc gat gcc cgc gac act aag ctt ggc gcc gaa gaa atc 2371
 Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu Gly Ala Glu Glu Ile
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 Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val Leu Lys Asp Leu Asp
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gac cgc ggt att gtc cgc atc ggt gct gat gtt cgt gac ggc gac atc 2467
 Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val Arg Asp Gly Asp Ile
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ctg gtc ggt aag gtc acc cct aag ggc gag acc gag ctc acc ccg gaa 2515
 Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr Glu Leu Thr Pro Glu
 790 795 800 805

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 Glu Arg Leu Leu Arg Ala Ile Phe Gly Glu Lys Ala Arg Glu Val Arg
 810 815 820

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 Asp Thr Ser Met Lys Val Pro His Gly Glu Thr Gly Lys Val Ile Gly
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35 40 45

Ser Trp Leu Ile Gly Thr Pro Glu Trp Arg Ala Arg Gln Lys Glu Glu

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Glu	Leu	Ser	Pro	Ile 85	Gln	Asp	Tyr	Ser	Gly 90	Asn	Met	Ser	Leu	Ser	Leu 95
Ser	Glu	Pro	Arg 100	Phe	Glu	Asp	Val	Lys 105	Asn	Thr	Ile	Asp	Glu	Ala	Lys 110
Glu	Lys	Asp 115	Ile	Asn	Tyr	Ala	Ala 120	Pro	Leu	Tyr	Val	Thr	Ala	Glu	Phe 125
Val	Asn 130	Asn	Thr	Thr	Gly	Glu 135	Ile	Lys	Ser	Gln	Thr 140	Val	Phe	Ile	Gly
Asp 145	Phe	Pro	Met	Met	Thr	Asp 150	Lys	Gly	Thr	Phe	Ile	Ile	Asn	Gly	Thr 160
Glu	Arg	Val	Val	Val	Ser	Gln	Leu	Val	Arg 170	Ser	Pro	Gly	Val	Tyr	Phe 175
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Val	Ile	Pro 195	Ser	Arg	Gly	Ala	Trp 200	Leu	Glu	Phe	Asp	Val	Asp	Lys	Arg 205
Asp 210	Ser	Val	Gly	Val	Arg	Ile 215	Asp	Arg	Lys	Arg	Arg	Gln	Pro	Val	Thr 220
Val 225	Leu	Leu	Lys	Ala	Leu	Gly 230	Trp	Thr	Thr	Glu	Gln	Ile	Thr	Glu	Arg 240
Phe	Gly	Phe	Ser	Glu 245	Ile	Met	Met	Ser	Thr 250	Leu	Glu	Ser	Asp	Gly	Val 255
Ala	Asn	Thr	Asp 260	Glu	Ala	Leu	Leu	Glu 265	Ile	Tyr	Arg	Lys	Gln	Arg	Pro 270
Gly	Glu	Gln	Pro	Thr	Arg	Asp	Leu	Ala 280	Gln	Ser	Leu	Leu	Asp	Asn	Ser 285
Phe 290	Phe	Arg	Ala	Lys	Arg	Tyr 295	Asp	Leu	Ala	Arg	Val	Gly	Arg	Tyr	Lys 300
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Leu	Thr	Glu	Glu	Asp 325	Ile	Ala	Thr	Thr	Ile 330	Glu	Tyr	Leu	Val	Arg	Leu 335
His	Ala	Gly	Glu	Arg	Val	Met	Thr	Ser 345	Pro	Asn	Gly	Glu	Glu	Ile	Pro 350
Val	Glu	Thr 355	Asp	Asp	Ile	Asp	His 360	Phe	Gly	Asn	Arg	Arg	Leu	Arg	Thr 365
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 Ser Leu Ser Gly Leu Thr His Lys Arg Arg Leu Ser Ala Leu Gly Pro
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 Pro Ser His Tyr Gly Arg Met Cys Pro Ile Glu Thr Pro Glu Gly Pro
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 Thr Asp Gln Ile Asp Tyr Leu Thr Ala Asp Glu Glu Asp Arg Phe Val
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 Val Gly Thr Ala Met Ile Pro Phe Leu Glu His Asp Asp Ala Asn Arg
 580 585 590
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 Ala Glu Ala Pro Phe Val Gly Thr Gly Met Glu Gln Arg Ala Ala Tyr
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 Val Ser Ala Asp Phe Ile Thr Ile Met Ala Asp Asp Gly Lys Arg Glu
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 Thr Tyr Leu Leu Arg Lys Phe Gln Arg Thr Asn Gln Gly Thr Ser Tyr
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 Val Ile Ala Asp Gly Pro Gly Thr Phe Asn Gly Glu Met Ser Leu Gly
 690 695 700

Arg Asn Leu Leu Val Ala Phe Met Pro Trp Glu Gly His Asn Tyr Glu
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 Asp Ala Ile Ile Leu Asn Gln Asn Ile Val Glu Gln Asp Ile Leu Thr
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 Ser Ile His Ile Glu Glu His Glu Ile Asp Ala Arg Asp Thr Lys Leu
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 Gly Ala Glu Glu Ile Thr Arg Asp Ile Pro Asn Val Ser Glu Glu Val
 755 760 765
 Leu Lys Asp Leu Asp Asp Arg Gly Ile Val Arg Ile Gly Ala Asp Val
 770 775 780
 Arg Asp Gly Asp Ile Leu Val Gly Lys Val Thr Pro Lys Gly Glu Thr
 785 790 795 800
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 Val Leu Asp Val Asn 1 5
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 Val Phe Asp Glu Leu Arg Ile Gly Leu Ala Thr Ala Asp Asp Ile Arg 10 15 20
 cgt tgg tcc aag ggt gag gtc aag aag ccg gag acc atc aac tac cga 211
 Arg Trp Ser Lys Gly Glu Val Lys Lys Pro Glu Thr Ile Asn Tyr Arg 25 30 35
 acc ctc aag cct gag aag gac ggt ctg ttc tgc gag cgt atc ttc ggt 259
 Thr Leu Lys Pro Glu Lys Asp Gly Leu Phe Cys Glu Arg Ile Phe Gly 40 45 50
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Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys Tyr Lys Arg Val Arg
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 Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val Glu Val Thr Lys Ser
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 Lys Val Arg Arg Glu Arg Met Gly His Ile Glu Leu Ala Ala Pro Val
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 35 40 45

Glu Arg Ile Phe Gly Pro Thr Arg Asp Trp Glu Cys Ala Cys Gly Lys
 50 55 60

Tyr Lys Arg Val Arg Tyr Lys Gly Ile Ile Cys Glu Arg Cys Gly Val
 65 70 75 80

Glu Val Thr Lys Ser Lys Val Arg Arg Glu Arg Met Gly His Ile Glu
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Leu Ser Ala Asn Gly Thr Pro Met Lys Leu Ala Gly Asp Asp Asp Asp
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Phe Asp Gln Ala Gly Ala Ser Ile Gly Ile Asn Leu Ser Arg Asp Glu
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Val Ser Gly Arg Val Leu Ala Gly Asp Ala Thr Asn Ala Ala Gly Glu
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Cys	Gln	Thr	Pro	Thr	Gly	Val	Cys	Ala	Lys	Cys	Tyr	Gly	Lys	Ser	Met	
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gag ctg cgt tct gag atc atg ggt atc acc aag gcc tct ctc gca act 1008
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Cys Gln Thr Pro Thr Gly Val Cys Ala Lys Cys Tyr Gly Lys Ser Met

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Ile Asp Gln Leu His Pro Asp Gln Arg Ile Ala Leu Ile Leu Val Asp 145															
ctc ggc ggc tac acc gta gaa gat gtg gcc gaa atc gaa gga atc aaa 595															
Leu Gly Gly Tyr Thr Val Glu Asp Val Ala Glu Ile Glu Gly Ile Lys 165															

gta ggt acc gtt aaa tca cgc cga ggg cgc gca cgc aaa gcg ttg cgc 643
 Val Gly Thr Val Lys Ser Arg Arg Gly Arg Ala Arg Lys Ala Leu Arg
 170 175 180

gcc ctt tta cat gca gat ttc ttc ggg ccc gaa gat ggc tcc ata cag 691
 Ala Leu Leu His Ala Asp Phe Phe Gly Pro Glu Asp Gly Ser Ile Gln
 185 190 195

tgc gaa agc aac tgatggaagt ttttcaaagt gtc 726
 Cys Glu Ser Asn
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<210> 404

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 404

Met Thr Val Leu Pro Lys Asn His Asp Leu Ser Asp Thr Gln Leu Val
 1 5 10 15

Lys Gln Phe Ile Ser Gly Asp Ser Arg Ala Phe Ser Thr Ile Ile His
 20 25 30

Arg His Glu Arg His Met Met Gln Ala Ala Arg Lys Tyr Gly Arg Lys
 35 40 45

Pro Glu Asp Ala Gln Asp Ile Leu Gln Glu Ala Leu Phe Arg Ala Ser
 50 55 60

Arg Asn Met His Leu Tyr Arg Ala Glu Ala Ala Leu Gly Thr Trp Leu
 65 70 75 80

His Lys Leu Val Leu Asn Ser Gly Phe Asp Trp Ala Thr His Arg Ser
 85 90 95

Gln Val Glu Phe Pro Ile Leu Asn Glu Pro Thr Ile Asp Leu Glu Lys
 100 105 110

Asp Pro Arg Leu Ala Thr Asp Pro Leu Gly Tyr Leu Asp Val Ala Met
 115 120 125

Thr Ile Arg Ser Ala Ile Asp Gln Leu His Pro Asp Gln Arg Ile Ala
 130 135 140

Leu Ile Leu Val Asp Leu Gly Gly Tyr Thr Val Glu Asp Val Ala Glu
 145 150 155 160

Ile Glu Gly Ile Lys Val Gly Thr Val Lys Ser Arg Arg Gly Arg Ala
 165 170 175

Arg Lys Ala Leu Arg Ala Leu Leu His Ala Asp Phe Phe Gly Pro Glu
 180 185 190

Asp Gly Ser Ile Gln Cys Glu Ser Asn
 195 200

<210> 405


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<222> (101)..(718)
<223> RXA02456
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gga atg tta aag gaa gta gcg aag gaa caa ggc att ggt ctt gaa cat 691

Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly Ile Gly Leu Glu His
 185 190 195

ccc gac atg aag aaa aat tcg gag gca taacgatgac gaatctcaac cgc 741
 Pro Asp Met Lys Lys Asn Ser Glu Ala
 200 205

<210> 406
 <211> 206
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 406
 Met Ala Glu Asn Arg Thr Gly Thr Val Asp Gly Asp Ala Leu Ala Ala
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Arg Phe Glu Glu Glu Ala Leu Pro Leu Leu Asp Gln Leu Tyr Gly Gly
 20 25 30

Ala Leu Arg Met Thr Arg Asn Pro Ala Asp Ala Glu Asp Leu Val Gln
 35 40 45

Asp Thr Tyr Ile Lys Ala Tyr Gln Ala Phe Ala Ser Phe Lys Pro Gly
 50 55 60

Thr Asn Leu Lys Ala Trp Leu Tyr Arg Ile Met Thr Asn Thr Tyr Ile
 65 70 75 80

Asn Met Tyr Arg Lys Lys Gln Arg Gln Pro Ser Gln Thr Ser Ala Asp
 85 90 95

Glu Ile Thr Asp Tyr Gln Leu Val Glu Ser Gln Ser His Thr Ser Thr
 100 105 110

Gly Leu Glu Ser Ala Glu Val Glu Ala Leu Lys Asn Leu Pro Asp Gly
 115 120 125

Lys Ile Gly Asp Ala Met Asn Gln Leu Ser Pro Glu Tyr Arg Met Val
 130 135 140

Val Tyr Tyr Ala Asp Val Glu Asp Leu Ala Tyr Lys Glu Ile Ala Glu
 145 150 155 160

Ile Met Asp Val Pro Leu Gly Thr Val Met Ser Arg Leu His Arg Gly
 165 170 175

Arg Lys Gln Leu Arg Gly Met Leu Lys Glu Val Ala Lys Glu Gln Gly
 180 185 190

Ile Gly Leu Glu His Pro Asp Met Lys Lys Asn Ser Glu Ala
 195 200 205

<210> 407
 <211> 793
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<223> RXA00304

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acc aat gag gaa ctc gca gaa gag tcc ggc att gaa gag tcc aag att 739
Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile Glu Glu Ser Lys Ile
200 205 210

gaa atg ctg ctt cgt cag tct cgc gat cca gtg agc ttg gac atg cca 787
 Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val Ser Leu Asp Met Pro
 215 220 225

gtc ggc 793
 Val Gly
 230

<210> 408

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 408

Met Thr Ala Pro Ser Thr Gln Asp Leu Ala Thr Thr Glu Arg Glu Val
 1 5 10 15

Asp Pro Gly Ser Arg Arg Gly Gln Thr Asn Asp Asn Pro Ser Gln Asp
 20 25 30

Leu Val Arg Val Tyr Leu Asn Gly Ile Gly Lys Thr Ala Leu Leu Thr
 35 40 45

Ala Glu Asp Glu Val Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr
 50 55 60

Ala Glu His Leu Leu Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met
 65 70 75 80

Lys Arg Asp Leu Lys Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser
 85 90 95

His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg
 100 105 110

Tyr Thr Gly Arg Gly Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn
 115 120 125

Leu Gly Leu Ile Arg Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe
 130 135 140

Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg
 145 150 155 160

Gly Met Ala Asp Gln Ser Arg Thr Ile Arg Leu Pro Val His Leu Val
 165 170 175

Glu Gln Val Asn Lys Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His
 180 185 190

Leu Gly Arg Glu Ala Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile
 195 200 205

Glu Glu Ser Lys Ile Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val
 210 215 220

Ser Leu Asp Met Pro Val Gly
 225 230

<210> 409
 <211> 687
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(664)
 <223> RXA00495

<400> 409

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attaaacttt tagggttttg atgcaggaag gtgcgagaac ttg gct gat act gag 115
                                   Leu Ala Asp Thr Glu
                                   1      5

cgc gag ctc gct gac ctg gta ccg cag gca acg gcg ggc gat cgt cgg 163
Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr Ala Gly Asp Arg Arg
      10      15      20

gca ttg caa aga ata atg gag att att cac ccc att gtt ttg cgt tat 211
Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro Ile Val Leu Arg Tyr
      25      30      35

gct cgc gct cgt att gga ggt gga cgc cag cca acg gca gaa gac gtt 259
Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro Thr Ala Glu Asp Val
      40      45      50

gct caa gaa atc tgc ctg gcg gta gcc acc tcc att agg aac ttt gtc 307
Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser Ile Arg Asn Phe Val
      55      60      65

gac cag ggt agg ccg ttc atg gcg ttt gtc tac ggc att gca tct aac 355
Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr Gly Ile Ala Ser Asn
      70      75      80      85

aag gtc gca gat gct cac agg gcg atg tcg agg gat aaa tcg act cct 403
Lys Val Ala Asp Ala His Arg Ala Met Ser Arg Asp Lys Ser Thr Pro
      90      95      100

att gag gaa gtc cca gaa act tca cca gat act ttt acc ccc gaa gac 451
Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr Phe Thr Pro Glu Asp
      105      110      115

ttt gcg ctg gtc agc gat gga agt aac aga gtt agg gaa ctt ctc gat 499
Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val Arg Glu Leu Leu Asp
      120      125      130

cta ctg agt gaa aag gca cgc gac att ctt atc ttg aga gtt atc gtt 547
Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile Leu Arg Val Ile Val
      135      140      145

ggg ctt tcc gca gaa gaa act gca gag atg gtg ggc agc acc cca ggt 595
Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val Gly Ser Thr Pro Gly
      150      155      160      165

gct gta cga gtt gcc caa cac agg gca ctc acg aca ctt cga agc aca 643
Ala Val Arg Val Ala Gln His Arg Ala Leu Thr Thr Leu Arg Ser Thr
      170      175      180

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ctt gag cag cag gag aac aag taatgactcg acgtctacat ggt
 Leu Glu Gln Gln Glu Asn Lys
 185

687

<210> 410
 <211> 188
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 410
 Leu Ala Asp Thr Glu Arg Glu Leu Ala Asp Leu Val Pro Gln Ala Thr
 1 5 10 15
 Ala Gly Asp Arg Arg Ala Leu Gln Arg Ile Met Glu Ile Ile His Pro
 20 25 30
 Ile Val Leu Arg Tyr Ala Arg Ala Arg Ile Gly Gly Gly Arg Gln Pro
 35 40 45
 Thr Ala Glu Asp Val Ala Gln Glu Ile Cys Leu Ala Val Ala Thr Ser
 50 55 60
 Ile Arg Asn Phe Val Asp Gln Gly Arg Pro Phe Met Ala Phe Val Tyr
 65 70 75 80
 Gly Ile Ala Ser Asn Lys Val Ala Asp Ala His Arg Ala Met Ser Arg
 85 90 95
 Asp Lys Ser Thr Pro Ile Glu Glu Val Pro Glu Thr Ser Pro Asp Thr
 100 105 110
 Phe Thr Pro Glu Asp Phe Ala Leu Val Ser Asp Gly Ser Asn Arg Val
 115 120 125
 Arg Glu Leu Leu Asp Leu Leu Ser Glu Lys Ala Arg Asp Ile Leu Ile
 130 135 140
 Leu Arg Val Ile Val Gly Leu Ser Ala Glu Glu Thr Ala Glu Met Val
 145 150 155 160
 Gly Ser Thr Pro Gly Ala Val Arg Val Ala Gln His Arg Ala Leu Thr
 165 170 175
 Thr Leu Arg Ser Thr Leu Glu Gln Gln Glu Asn Lys
 180 185

<210> 411
 <211> 608
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(585)
 <223> RXA00532

<400> 411
 gca att gtg aag tca aaa gag cgt aac gac gcc cac gtc acc gag ctg 48

Ala	Ile	Val	Lys	Ser	Lys	Glu	Arg	Asn	Asp	Ala	His	Val	Thr	Glu	Leu	
1				5					10					15		
gcc	cta	gcc	gcc	ggc	cgt	ggc	gac	cgc	gca	gct	ctc	acc	gat	ttc	atc	96
Ala	Leu	Ala	Ala	Gly	Arg	Gly	Asp	Arg	Ala	Ala	Leu	Thr	Asp	Phe	Ile	
			20					25					30			
cgg	gaa	acc	caa	gac	gat	gtc	tgg	cgt	ctc	ctc	gcc	cac	ctt	ggc	ggc	144
Arg	Glu	Thr	Gln	Asp	Asp	Val	Trp	Arg	Leu	Leu	Ala	His	Leu	Gly	Gly	
		35					40					45				
cac	gaa	atc	gcc	gac	gat	cta	acc	caa	gaa	act	tat	ctg	cgg	gtc	atg	192
His	Glu	Ile	Ala	Asp	Asp	Leu	Thr	Gln	Glu	Thr	Tyr	Leu	Arg	Val	Met	
	50					55					60					
agc	gcc	ctc	ccc	cgc	ttc	gca	gcg	cgc	tcc	tcg	gcg	cgc	acc	tgg	cta	240
Ser	Ala	Leu	Pro	Arg	Phe	Ala	Ala	Arg	Ser	Ser	Ala	Arg	Thr	Trp	Leu	
65					70				75					80		
cta	tcg	cta	gcc	cgg	cgc	gtc	tgg	gtc	gac	aac	atc	cga	cac	gac	atg	288
Leu	Ser	Leu	Ala	Arg	Arg	Val	Trp	Val	Asp	Asn	Ile	Arg	His	Asp	Met	
				85					90					95		
gca	cgc	ccc	cgc	aaa	tcc	atc	gtc	gaa	tac	gaa	gac	acc	ggg	gcc	acc	336
Ala	Arg	Pro	Arg	Lys	Ser	Ile	Val	Glu	Tyr	Glu	Asp	Thr	Gly	Ala	Thr	
			100					105					110			
gac	gcg	agc	aac	gca	ggc	atc	tgg	tcc	gag	tgg	atc	gac	gtg	cgc	acg	384
Asp	Ala	Ser	Asn	Ala	Gly	Ile	Trp	Ser	Glu	Trp	Ile	Asp	Val	Arg	Thr	
		115				120						125				
ctt	atc	gac	gcc	ctc	cca	ccc	gaa	cgc	cgc	gaa	gcc	ctc	atc	ctc	acc	432
Leu	Ile	Asp	Ala	Leu	Pro	Pro	Glu	Arg	Arg	Glu	Ala	Leu	Ile	Leu	Thr	
	130					135					140					
caa	gtg	ttg	ggc	tac	acc	tac	gaa	gaa	gcc	gca	aaa	atc	gcc	gac	gtc	480
Gln	Val	Leu	Gly	Tyr	Thr	Tyr	Glu	Glu	Ala	Ala	Lys	Ile	Ala	Asp	Val	
145					150					155					160	
cga	gtc	gga	aca	atc	cgt	tcc	cgc	gta	gcc	cgc	gcc	aga	gcg	gac	ctc	528
Arg	Val	Gly	Thr	Ile	Arg	Ser	Arg	Val	Ala	Arg	Ala	Arg	Ala	Asp	Leu	
				165					170					175		
att	gct	gca	aca	gct	acc	ggg	gat	tcc	tca	gcc	gaa	gat	ggc	aaa	tcc	576
Ile	Ala	Ala	Thr	Ala	Thr	Gly	Asp	Ser	Ser	Ala	Glu	Asp	Gly	Lys	Ser	
			180				185						190			
gcc	caa	ggg	tagcagatga	gctacgtcaa	cgg											608
Ala	Gln	Gly														
		195														

<210> 412

<211> 195

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

Ala	Ile	Val	Lys	Ser	Lys	Glu	Arg	Asn	Asp	Ala	His	Val	Thr	Glu	Leu
1				5					10					15	

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<210> 413
<211> 765
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(742)  
<223> RXA01530
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<400> 413

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ctggttgctt ccttggcaaa gacgctacac cggccgtggc atg gca ttc ctg gac 115
Met Ala Phe Leu Asp
1 5

ctc atc cag gaa ggc aac ctc ggt ctg att cgt gcc gta gag aag ttc 163
Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg Ala Val Glu Lys Phe
10 15 20

gac tac tcc aag ggc tac aag ttc tcc acc tac gca acc tgg tgg atc 211
Asp Tyr Ser Lys Gly Tyr Lys Phe Ser Thr Tyr Ala Thr Trp Trp Ile
25 30 35

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<210> 414
<211> 214
<212> PRT
<213> Corynebacterium glutamicum
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<400> 414
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   1             5             10             15

Ala  Val  Glu  Lys  Phe  Asp  Tyr  Ser  Lys  Gly  Tyr  Lys  Phe  Ser  Thr  Tyr
           20             25             30

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Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Ala Met Ala Asp Gln
 35 40 45

Ala Arg Thr Ile Arg Ile Pro Val His Met Val Glu Val Ile Asn Lys
 50 55 60

Leu Gly Arg Ile Gln Arg Glu Leu Leu Gln Glu Leu Gly Arg Glu Pro
 65 70 75 80

Thr Pro Gln Glu Leu Ser Lys Glu Met Asp Ile Ser Glu Glu Lys Val
 85 90 95

Leu Glu Ile Gln Gln Tyr Ala Arg Glu Pro Ile Ser Leu Asp Gln Thr
 100 105 110

Ile Gly Asp Glu Gly Asp Ser Gln Leu Gly Asp Phe Ile Glu Asp Ser
 115 120 125

Glu Ala Val Val Ala Val Asp Ala Val Ser Phe Thr Leu Leu Gln Asp
 130 135 140

Gln Leu Gln Asp Val Leu Glu Thr Leu Ser Glu Arg Glu Ala Gly Val
 145 150 155 160

Val Lys Leu Arg Phe Gly Leu Thr Asp Gly Met Pro Arg Thr Leu Asp
 165 170 175

Glu Ile Gly Gln Val Tyr Gly Val Thr Arg Glu Arg Ile Arg Gln Ile
 180 185 190

Glu Ser Lys Thr Met Ser Lys Leu Arg His Pro Ser Arg Ser Gln Val
 195 200 205

Leu Arg Asp Tyr Leu Asp
 210

<210> 415

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXA01531

<400> 415

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agatgtcgat gaaaatgcac caggagccgt ggagagcagc atg gta gaa aac aac 115
 Met Val Glu Asn Asn
 1 5

gta gca aaa aag acg gtc gct aaa aag acc gca cgc aag acc gca cgc 163
 Val Ala Lys Lys Thr Val Ala Lys Lys Thr Ala Arg Lys Thr Ala Arg
 10 15 20

aaa gca gcc ccg cgc gtg gca acc cca ttg gga gtc gca tct gag tct 211
 Lys Ala Ala Pro Arg Val Ala Thr Pro Leu Gly Val Ala Ser Glu Ser

25					30					35						
ccc	att	tcg	gcc	acc	cct	gcg	cgc	agc	atc	gat	gga	acc	tca	acc	cct	259
Pro	Ile	Ser	Ala	Thr	Pro	Ala	Arg	Ser	Ile	Asp	Gly	Thr	Ser	Thr	Pro	
		40					45					50				
ggt	gaa	gct	gct	gac	acc	ata	gag	acc	acc	gcc	cct	gca	gcg	aag	gct	307
Val	Glu	Ala	Ala	Asp	Thr	Ile	Glu	Thr	Thr	Ala	Pro	Ala	Ala	Lys	Ala	
	55					60					65					
cct	gcg	gcc	aag	gct	ccc	gct	aaa	aag	gtt	gcc	aag	aag	aca	gct	cgc	355
Pro	Ala	Ala	Lys	Ala	Pro	Ala	Lys	Lys	Val	Ala	Lys	Lys	Thr	Ala	Arg	
	70				75					80					85	
aag	gca	cct	gcg	aaa	aag	act	gtc	gcc	aag	aaa	gcc	aca	acc	gcc	aag	403
Lys	Ala	Pro	Ala	Lys	Lys	Thr	Val	Ala	Lys	Lys	Ala	Thr	Thr	Ala	Lys	
				90					95					100		
gct	gca	cct	gca	act	gcc	aag	gac	gaa	aac	gca	cct	gtt	gat	gac	gac	451
Ala	Ala	Pro	Ala	Thr	Ala	Lys	Asp	Glu	Asn	Ala	Pro	Val	Asp	Asp	Asp	
			105					110					115			
gag	gag	aac	ctc	gct	cag	gat	gaa	cag	gac	ttc	gac	ggc	gat	gac	ttc	499
Glu	Glu	Asn	Leu	Ala	Gln	Asp	Glu	Gln	Asp	Phe	Asp	Gly	Asp	Asp	Phe	
		120					125					130				
gta	gac	ggc	atc	gaa	gac	gaa	gaa	gat	gaa	gac	ggc	gtc	gaa	gcc	ctc	547
Val	Asp	Gly	Ile	Glu	Asp	Glu	Glu	Asp	Glu	Asp	Gly	Val	Glu	Ala	Leu	
	135					140					145					
ggt	gaa	gaa	agc	gaa	gac	gac	gaa	gag	gac	ggc	tca	tcc	gtt	tgg	gat	595
Gly	Glu	Glu	Ser	Glu	Asp	Asp	Glu	Glu	Asp	Gly	Ser	Ser	Val	Trp	Asp	
	150				155					160					165	
gaa	gac	gaa	tcc	gca	acc	ctg	cgt	cag	gca	cgt	aaa	gat	gcc	gag	ctc	643
Glu	Asp	Glu	Ser	Ala	Thr	Leu	Arg	Gln	Ala	Arg	Lys	Asp	Ala	Glu	Leu	
				170					175					180		
acc	gct	tcc	gcc	gac	tct	gtt	cgc	gct	tac	ctg	aag	caa	atc	ggg	aaa	691
Thr	Ala	Ser	Ala	Asp	Ser	Val	Arg	Ala	Tyr	Leu	Lys	Gln	Ile	Gly	Lys	
			185					190					195			
gtt	gcc	ctg	ctg	aac	gct	gaa	cag	gaa	gtc	tcc	ctg	gca	aag	cgc	atc	739
Val	Ala	Leu	Leu	Asn	Ala	Glu	Gln	Glu	Val	Ser	Leu	Ala	Lys	Arg	Ile	
		200					205					210				
gaa	gca	ggc	ctt	tac	gcc	acc	cac	cgc	atg	gag	gaa	atg	gaa	gaa	gct	787
Glu	Ala	Gly	Leu	Tyr	Ala	Thr	His	Arg	Met	Glu	Glu	Met	Glu	Glu	Ala	
	215					220					225					
ttc	gca	gcc	ggt	gac	aag	gac	gcg	aaa	ctc	acc	cca	gcc	gtc	aag	cgt	835
Phe	Ala	Ala	Gly	Asp	Lys	Asp	Ala	Lys	Leu	Thr	Pro	Ala	Val	Lys	Arg	
	230				235					240					245	
gac	ctc	cgc	gcc	atc	gct	cgt	gac	ggc	cgc	aag	gcg	aaa	aac	cac	ctc	883
Asp	Leu	Arg	Ala	Ile	Ala	Arg	Asp	Gly	Arg	Lys	Ala	Lys	Asn	His	Leu	
			250					255						260		
ctg	gaa	gcc	aac	ctt	cgt	ctg	gtt	gtc	tcc	ctg	gca	aag	acg	cta	cac	931
Leu	Glu	Ala	Asn	Leu	Arg	Leu	Val	Val	Ser	Leu	Ala	Lys	Thr	Leu	His	
			265					270					275			

cgg ccg tgg cat ggc att cct gga cct cat cca gga agg caa cct cgg 979
 Arg Pro Trp His Gly Ile Pro Gly Pro His Pro Gly Arg Gln Pro Arg
 280 285 290
 tct gat tcg tgc cgt aga gaa gtt cga cta ctc caa ggg cta caa gtt 1027
 Ser Asp Ser Cys Arg Arg Glu Val Arg Leu Leu Gln Gly Leu Gln Val
 295 300 305
 ctc cac cta cgc aac ctg gtg gat ccg tca ggc aat cac ccg cgc cat 1075
 Leu His Leu Arg Asn Leu Val Asp Pro Ser Gly Asn His Pro Arg His
 310 315 320 325
 ggc cga cca agc acg aac cat ccg tat ccc agt cca cat ggt 1117
 Gly Arg Pro Ser Thr Asn His Pro Tyr Pro Ser Pro His Gly
 330 335
 tgaagtgatc aacaaacttg gtc 1140

<210> 416

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

Met Val Glu Asn Asn Val Ala Lys Lys Thr Val Ala Lys Lys Thr Ala
 1 5 10 15
 Arg Lys Thr Ala Arg Lys Ala Ala Pro Arg Val Ala Thr Pro Leu Gly
 20 25 30
 Val Ala Ser Glu Ser Pro Ile Ser Ala Thr Pro Ala Arg Ser Ile Asp
 35 40 45
 Gly Thr Ser Thr Pro Val Glu Ala Ala Asp Thr Ile Glu Thr Thr Ala
 50 55 60
 Pro Ala Ala Lys Ala Pro Ala Ala Lys Ala Pro Ala Lys Lys Val Ala
 65 70 75 80
 Lys Lys Thr Ala Arg Lys Ala Pro Ala Lys Lys Thr Val Ala Lys Lys
 85 90 95
 Ala Thr Thr Ala Lys Ala Ala Pro Ala Thr Ala Lys Asp Glu Asn Ala
 100 105 110
 Pro Val Asp Asp Asp Glu Glu Asn Leu Ala Gln Asp Glu Gln Asp Phe
 115 120 125
 Asp Gly Asp Asp Phe Val Asp Gly Ile Glu Asp Glu Glu Asp Glu Asp
 130 135 140
 Gly Val Glu Ala Leu Gly Glu Glu Ser Glu Asp Asp Glu Glu Asp Gly
 145 150 155 160
 Ser Ser Val Trp Asp Glu Asp Glu Ser Ala Thr Leu Arg Gln Ala Arg
 165 170 175
 Lys Asp Ala Glu Leu Thr Ala Ser Ala Asp Ser Val Arg Ala Tyr Leu
 180 185 190

Lys Gln Ile Gly Lys Val Ala Leu Leu Asn Ala Glu Gln Glu Val Ser
 195 200 205
 Leu Ala Lys Arg Ile Glu Ala Gly Leu Tyr Ala Thr His Arg Met Glu
 210 215 220
 Glu Met Glu Glu Ala Phe Ala Ala Gly Asp Lys Asp Ala Lys Leu Thr
 225 230 235 240
 Pro Ala Val Lys Arg Asp Leu Arg Ala Ile Ala Arg Asp Gly Arg Lys
 245 250 255
 Ala Lys Asn His Leu Leu Glu Ala Asn Leu Arg Leu Val Val Ser Leu
 260 265 270
 Ala Lys Thr Leu His Arg Pro Trp His Gly Ile Pro Gly Pro His Pro
 275 280 285
 Gly Arg Gln Pro Arg Ser Asp Ser Cys Arg Arg Glu Val Arg Leu Leu
 290 295 300
 Gln Gly Leu Gln Val Leu His Leu Arg Asn Leu Val Asp Pro Ser Gly
 305 310 315 320
 Asn His Pro Arg His Gly Arg Pro Ser Thr Asn His Pro Tyr Pro Ser
 325 330 335
 Pro His Gly

<210> 417

<211> 771

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(748)

<223> RXA02065

<400> 417

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acaggatgta atctagattt cccaagttca gtggggcaaa atg act tat atg aaa 115
 Met Thr Tyr Met Lys
 1 5

aag aag tcc cga gat gac gca ccc gtc gta atc gaa acc gtt caa gca 163
 Lys Lys Ser Arg Asp Asp Ala Pro Val Val Ile Glu Thr Val Gln Ala
 10 15 20

gaa cat gct gaa gaa ctc acg ggc act gca gca ttc gat gct gga cag 211
 Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala Phe Asp Ala Gly Gln
 25 30 35

gca gac atg cca aca tgg ggc gag cta gtc gca gaa cat gca gat agc 259
 Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala Glu His Ala Asp Ser
 40 45 50

gtt tac cgc ctc gcg tac cgt ctt tcc ggc aac cag cac gat gct gaa 307
 Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn Gln His Asp Ala Glu
 55 60 65
 gac ctg acc caa gaa aca ttc atg cgt gtc ttc cgc tcg ttg aag agc 355
 Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe Arg Ser Leu Lys Ser
 70 75 80 85
 tac cag cca ggc acc ttt gag ggc tgg ctg cac cgc atc acc acc aac 403
 Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His Arg Ile Thr Thr Asn
 90 95 100
 ttg ttc ctt gat atg gtt cgc cac cgc ggc aag atc cgc atg gag gcg 451
 Leu Phe Leu Asp Met Val Arg His Arg Gly Lys Ile Arg Met Glu Ala
 105 110 115
 ctg cct gaa gat tat gag cgc gtt ccg ggc aat gac atc acc cca gag 499
 Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn Asp Ile Thr Pro Glu
 120 125 130
 cag gca tac acc gaa gct aac ctt gac cca gct ctg cag gca gcc ctc 547
 Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala Leu Gln Ala Ala Leu
 135 140 145
 gat gag ttg agc cca gac ttc cgc gtg gca gtg atc ctc tgt gat gtt 595
 Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val Ile Leu Cys Asp Val
 150 155 160 165
 gtt ggt atg agc tat gac gaa atc gca gag acc ctc gga gtg aaa atg 643
 Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr Leu Gly Val Lys Met
 170 175 180
 ggt acc gtg cgt tcc cgt att cac cgt gga cgc agc cag ctt cgt gca 691
 Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg Ser Gln Leu Arg Ala
 185 190 195
 agt ttg gaa gct gca gca atg acc agc gag gaa gtt tct ttg ttg gtt 739
 Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu Val Ser Leu Leu Val
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 cca acc cac taaagttggt gtgttttctg aca 771
 Pro Thr His
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<210> 418

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

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Glu Thr Val Gln Ala Glu His Ala Glu Glu Leu Thr Gly Thr Ala Ala
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Phe Asp Ala Gly Gln Ala Asp Met Pro Thr Trp Gly Glu Leu Val Ala
 35 40 45

Glu His Ala Asp Ser Val Tyr Arg Leu Ala Tyr Arg Leu Ser Gly Asn

50	55	60
Gln His Asp Ala Glu Asp Leu Thr Gln Glu Thr Phe Met Arg Val Phe 65 70 75 80		
Arg Ser Leu Lys Ser Tyr Gln Pro Gly Thr Phe Glu Gly Trp Leu His 85 90 95		
Arg Ile Thr Thr Asn Leu Phe Leu Asp Met Val Arg His Arg Gly Lys 100 105 110		
Ile Arg Met Glu Ala Leu Pro Glu Asp Tyr Glu Arg Val Pro Gly Asn 115 120 125		
Asp Ile Thr Pro Glu Gln Ala Tyr Thr Glu Ala Asn Leu Asp Pro Ala 130 135 140		
Leu Gln Ala Ala Leu Asp Glu Leu Ser Pro Asp Phe Arg Val Ala Val 145 150 155 160		
Ile Leu Cys Asp Val Val Gly Met Ser Tyr Asp Glu Ile Ala Glu Thr 165 170 175		
Leu Gly Val Lys Met Gly Thr Val Arg Ser Arg Ile His Arg Gly Arg 180 185 190		
Ser Gln Leu Arg Ala Ser Leu Glu Ala Ala Ala Met Thr Ser Glu Glu 195 200 205		
Val Ser Leu Leu Val Pro Thr His 210 215		

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<211> 645

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<220>

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<222> (101)..(622)

<223> RXA00588

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Met Ala Ser Val Asp	
1 5	

aag caa tac atc acc cca gaa acc aag gcc aag ctg gag gaa gag ctc	163
Lys Gln Tyr Ile Thr Pro Glu Thr Lys Ala Lys Leu Glu Glu Glu Leu	
10 15 20	

aac gcc ctc atc gca cac cgc cct gca gtt gct gcg gaa atc aat gag	211
Asn Ala Leu Ile Ala His Arg Pro Ala Val Ala Ala Glu Ile Asn Glu	
25 30 35	

cgc cgt gaa gaa ggc gac ctc aag gaa aac gct ggc tat gac gcc gct	259
Arg Arg Glu Glu Gly Asp Leu Lys Glu Asn Ala Gly Tyr Asp Ala Ala	
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cgt gaa atg cag gac cag gaa gag gcc cgc atc aag cag atc tat gag 307
 Arg Glu Met Gln Asp Gln Glu Glu Ala Arg Ile Lys Gln Ile Tyr Glu
 55 60 65
 ctg ctg gcc aac tcc acc act gag cgc gaa ggc atc atc gaa ggt gtc 355
 Leu Leu Ala Asn Ser Thr Glu Arg Glu Gly Ile Ile Glu Gly Val
 70 75 80 85
 gca aac gtt ggc tcc gtt gtt cac gtc tac tac gac ggc gac gag aac 403
 Ala Asn Val Gly Ser Val Val His Val Tyr Tyr Asp Gly Asp Glu Asn
 90 95 100
 gac aag gaa acc ttc ctc atc ggt acc cgt gct ggc gct tcc gag aac 451
 Asp Lys Glu Thr Phe Leu Ile Gly Thr Arg Ala Gly Ala Ser Glu Asn
 105 110 115
 cca gat ctt gag acc tac tct gag cag tcc cca ctc ggc gct gca att 499
 Pro Asp Leu Glu Thr Tyr Ser Glu Gln Ser Pro Leu Gly Ala Ala Ile
 120 125 130
 ctc gga gct cag gaa ggc gac acc cgt cag tac acc gct cca aat ggt 547
 Leu Gly Ala Gln Glu Gly Asp Thr Arg Gln Tyr Thr Ala Pro Asn Gly
 135 140 145
 tcc gtt atc tcc gta act gtt gtt tct gca gaa cca tac aac tca gca 595
 Ser Val Ile Ser Val Thr Val Val Ser Ala Glu Pro Tyr Asn Ser Ala
 150 155 160 165
 aaa gcc gcg aca ctc cgc ggc aaa aac taaccaagga tttaaaagtc ttc 645
 Lys Ala Ala Thr Leu Arg Gly Lys Asn
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<210> 420

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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 20 25 30
 Ala Glu Ile Asn Glu Arg Arg Glu Glu Gly Asp Leu Lys Glu Asn Ala
 35 40 45
 Gly Tyr Asp Ala Ala Arg Glu Met Gln Asp Gln Glu Glu Ala Arg Ile
 50 55 60
 Lys Gln Ile Tyr Glu Leu Leu Ala Asn Ser Thr Thr Glu Arg Glu Gly
 65 70 75 80
 Ile Ile Glu Gly Val Ala Asn Val Gly Ser Val Val His Val Tyr Tyr
 85 90 95
 Asp Gly Asp Glu Asn Asp Lys Glu Thr Phe Leu Ile Gly Thr Arg Ala
 100 105 110

Gly Ala Ser Glu Asn Pro Asp Leu Glu Thr Tyr Ser Glu Gln Ser Pro
 115 120 125

Leu Gly Ala Ala Ile Leu Gly Ala Gln Glu Gly Asp Thr Arg Gln Tyr
 130 135 140

Thr Ala Pro Asn Gly Ser Val Ile Ser Val Thr Val Val Ser Ala Glu
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Pro Tyr Asn Ser Ala Lys Ala Ala Thr Leu Arg Gly Lys Asn
 165 170

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1320)
 <223> RXN01724

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gcg caa act tca act gca cct gct tca gca cca tct gaa gag act ccc 96
 Ala Gln Thr Ser Thr Ala Pro Ala Ser Ala Pro Ser Glu Glu Thr Pro
 20 25 30

gca gct ccc gct cgt cgt gga cgt cgc cgt gta acc acc acc gcg acc 144
 Ala Ala Pro Ala Arg Arg Gly Arg Arg Val Thr Thr Thr Ala Thr
 35 40 45

acc cca gag cca gca gcg cct gca caa tcc cag cct gca gaa gct caa 192
 Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser Gln Pro Ala Glu Ala Gln
 50 55 60

cca gca cag act cag gct gca cag caa gaa gaa ctt cct gtt gca gcg 240
 Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala
 65 70 75 80

aag gag tcc gca cca gct aca gaa aac act cag ggc caa gct cag ggc 288
 Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr Gln Gly Gln Ala Gln Gly
 85 90 95

caa gct cag ggc caa gct cag ggc gat gag cac gat gat cgt ttt gag 336
 Gln Ala Gln Gly Gln Ala Gln Gly Asp Glu His Asp Asp Arg Phe Glu
 100 105 110

tcc cgt tct gct gca cgc cga gca cgc cgc aac cgt cag cgc cag atc 384
 Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile
 115 120 125

cac cgc gat ggc gat gac aat gcg aat gca aac aca gag tct gag cag 432
 His Arg Asp Gly Asp Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln
 130 135 140

aac acc cct gcc cag aac gca acc gca cag gct gag tct gag cag act 480

Asn 145	Thr	Pro	Ala	Gln	Asn 150	Ala	Thr	Ala	Gln	Ala 155	Glu	Ser	Glu	Gln	Thr 160	
gca	gct	cct	gca	cag	gct	gaa	gca	gct	gag	cag	aac	cag	aac	gat	aac	528
Ala	Ala	Pro	Ala	Gln 165	Ala	Glu	Ala	Ala	Glu 170	Gln	Asn	Gln	Asn	Asp 175	Asn	
agc	gag	tcc	tcc	gag	aac	cgc	agc	gat	aac	tac	cgc	aac	aac	aat	cgt	576
Ser	Glu	Ser	Ser 180	Glu	Asn	Arg	Ser	Asp 185	Asn	Tyr	Arg	Asn	Asn	Asn	Arg	
cgt	tcc	cgc	aac	aac	cgg	aac	aat	cgc	aat	tac	cgc	gat	aac	aac	gag	624
Arg	Ser	Arg	Asn 195	Asn	Arg	Asn	Asn	Arg	Asn	Tyr	Arg	Asp 205	Asn	Asn	Glu	
tcc	tct	gat	aat	gca	gga	cag	tcc	agc	aat	gat	gat	gcc	gac	aac	aat	672
Ser	Ser	Asp	Asn	Ala	Gly	Gln 215	Ser	Ser	Asn	Asp 220	Ala	Asp	Asn	Asn	Asn	
cag	gca	cgg	tct	gag	gac	aat	aac	gac	gat	cgc	cgt	tct	cgt	aat	aac	720
Gln	Ala	Arg	Ser	Glu	Asp	Asn 230	Asn	Asp	Asp	Arg	Arg	Ser	Arg	Asn	Asn 240	
cgt	aac	aac	gac	cgc	aat	gat	cgt	aac	gat	cgc	aat	gac	cgc	gac	aac	768
Arg	Asn	Asn	Asp	Arg	Asn	Asp 245	Arg	Asn	Asp 250	Arg	Asn	Asp	Arg	Asp 255	Asn	
gac	gac	aac	gat	gat	cgc	cgc	aac	cgt	cgc	gga	cgc	cgc	aat	cgc	cgt	816
Asp	Asp	Asn	Asp 260	Asp	Arg	Arg	Asn	Arg 265	Arg	Gly	Arg	Arg	Asn	Arg	Arg	
gga	cgc	aac	gac	cgt	aac	gat	cgc	gac	aac	cga	gat	aac	cgg	gat	aac	864
Gly	Arg	Asn 275	Asp	Arg	Asn	Asp 280	Arg	Asp	Asn	Arg	Asp 285	Asn	Arg	Asp	Asn	
cgc	gac	aac	agc	aac	gat	ggc	gac	aac	aac	cag	caa	gat	gag	ctg	cag	912
Arg	Asp 290	Asn	Ser	Asn	Asp	Gly 295	Asp	Asn	Asn	Gln	Gln 300	Asp	Glu	Leu	Gln	
cag	gta	gca	ggc	atc	ctg	gac	atc	gtg	gac	cat	aac	gtc	gca	ttc	gtg	960
Gln	Val	Ala	Gly	Ile	Leu 310	Asp	Ile	Val	Asp 315	His	Asn	Val	Ala	Phe	Val 320	
cgc	acc	acc	ggt	tac	cac	gct	gca	cct	tct	gac	gtg	ttt	gtc	agc	aac	1008
Arg	Thr	Thr	Gly 325	Tyr	His	Ala	Ala	Pro	Ser 330	Asp	Val	Phe	Val	Ser	Asn 335	
cag	ctg	atc	cgc	cgt	atg	ggt	ctt	cgt	tcc	ggt	gac	gcc	att	gaa	ggt	1056
Gln	Leu	Ile	Arg 340	Arg	Met	Gly	Leu	Arg 345	Ser	Gly	Asp	Ala	Ile	Glu	Gly	
cag	gtt	cgt	atg	aac	cag	ggt	ggt	ggc	aac	cac	aac	aac	cat	ggt	cgc	1104
Gln	Val 355	Arg	Met	Asn	Gln	Gly 360	Gly	Gly	Asn	His	Asn	Asn	His	Gly	Arg	
aac	cgt	cag	aag	tac	aac	aac	ttg	gtg	cgc	gtg	gag	atg	gtt	aac	ggt	1152
Asn	Arg	Gln	Lys	Tyr	Asn	Asn 375	Leu	Val	Arg	Val	Glu 380	Met	Val	Asn	Gly	
ctt	cct	gct	gaa	gag	act	cgc	aac	cgt	cct	gag	ttc	ggc	aag	ctg	act	1200
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Ala	Gln	Thr	Ser 20	Thr	Ala	Pro	Ala	Ser 25	Ala	Pro	Ser	Glu	Glu 30	Thr	Pro
Ala	Ala	Pro 35	Ala	Arg	Arg	Gly	Arg 40	Arg	Arg	Val	Thr	Thr 45	Thr	Ala	Thr
Thr	Pro 50	Glu	Pro	Ala	Ala	Pro 55	Ala	Gln	Ser	Gln	Pro 60	Ala	Glu	Ala	Gln
Pro 65	Ala	Gln	Thr	Gln	Ala 70	Ala	Gln	Gln	Glu	Glu 75	Leu	Pro	Val	Ala	Ala 80
Lys	Glu	Ser	Ala	Pro 85	Ala	Thr	Glu	Asn	Thr 90	Gln	Gly	Gln	Ala	Gln 95	Gly
Gln	Ala	Gln	Gly 100	Gln	Ala	Gln	Gly	Asp 105	Glu	His	Asp	Asp	Arg 110	Phe	Glu
Ser	Arg	Ser 115	Ala	Ala	Arg	Arg	Ala 120	Arg	Arg	Asn	Arg	Gln 125	Arg	Gln	Ile
His	Arg 130	Asp	Gly	Asp	Asp	Asn 135	Ala	Asn	Ala	Asn	Thr 140	Glu	Ser	Glu	Gln
Asn 145	Thr	Pro	Ala	Gln	Asn 150	Ala	Thr	Ala	Gln	Ala 155	Glu	Ser	Glu	Gln	Thr 160
Ala	Ala	Pro	Ala	Gln 165	Ala	Glu	Ala	Ala	Glu 170	Gln	Asn	Gln	Asn	Asp 175	Asn
Ser	Glu	Ser	Ser 180	Glu	Asn	Arg	Ser	Asp 185	Asn	Tyr	Arg	Asn	Asn 190	Asn	Arg
Arg	Ser	Arg 195	Asn	Asn	Arg	Asn	Asn 200	Arg	Asn	Tyr	Arg	Asp 205	Asn	Asn	Glu
Ser	Ser	Asp	Asn	Ala	Gly	Gln	Ser	Ser	Asn	Asp	Asp	Ala	Asp	Asn	Asn

210	215	220
Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp Arg Arg Ser Arg Asn Asn		
225	230	235 240
Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp Arg Asn Asp Arg Asp Asn		
	245	250 255
Asp Asp Asn Asp Asp Arg Arg Asn Arg Arg Gly Arg Arg Asn Arg Arg		
	260	265 270
Gly Arg Asn Asp Arg Asn Asp Arg Asp Asn Arg Asp Asn Arg Asp Asn		
	275	280 285
Arg Asp Asn Ser Asn Asp Gly Asp Asn Asn Gln Gln Asp Glu Leu Gln		
	290	295 300
Gln Val Ala Gly Ile Leu Asp Ile Val Asp His Asn Val Ala Phe Val		
305	310	315 320
Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe Val Ser Asn		
	325	330 335
Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala Ile Glu Gly		
	340	345 350
Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn His Gly Arg		
	355	360 365
Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met Val Asn Gly		
	370	375 380
Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly Lys Leu Thr		
385	390	395 400
Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu Gln Lys Ile		
	405	410 415
Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly Lys Gly Gln		
	420	425 430
Leu Cys Phe Asp Cys Val Ala Thr		
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<210> 423

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> FRXA01723

<220>

<223> All occurrences of Xaa = any amino acid

<220>

<223> All occurrences of n = any nucleotide

<400> 423

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Val Asp Xaa Ser Arg
1 5

gta acc acc acc gcg acc acc cca gag cca gca gcg cct gca caa tcc 163
Val Thr Thr Thr Ala Thr Thr Pro Glu Pro Ala Ala Pro Ala Gln Ser
10 15 20

cag cct gca gaa gct caa cca gca cag act cag gct gca cag caa gaa 211
Gln Pro Ala Glu Ala Gln Pro Ala Gln Thr Gln Ala Ala Gln Gln Glu
25 30 35

gaa ctt cct gtt gca gcg aag gag tcc gca cca gct aca gaa aac act 259
Glu Leu Pro Val Ala Ala Lys Glu Ser Ala Pro Ala Thr Glu Asn Thr
40 45 50

cag ggc caa kcy cag ggc caa gct cag ggc saa gct cag ggc gat gag 307
Gln Gly Gln Xaa Gln Gly Gln Ala Gln Gly Xaa Ala Gln Gly Asp Glu
55 60 65

cac gat gat cgy ttt gag tcc cgt tct gct gca cgc cga gca cgc cgc 355
His Asp Asp Xaa Phe Glu Ser Arg Ser Ala Ala Arg Arg Ala Arg Arg
70 75 80 85

aac cgt cag cgc cag atc cac cgc gat ggc gat gac aat gcg aat gca 403
Asn Arg Gln Arg Gln Ile His Arg Asp Gly Asp Asp Asn Ala Asn Ala
90 95 100

aac aca gag tct gag cag aac acc cct gcc cag aac gca acc gca cag 451
Asn Thr Glu Ser Glu Gln Asn Thr Pro Ala Gln Asn Ala Thr Ala Gln
105 110 115

gct gag tct gag cag act gca gct cct gca cag gct gaa gca gct gag 499
Ala Glu Ser Glu Gln Thr Ala Ala Pro Ala Gln Ala Glu Ala Ala Glu
120 125 130

cag aac cag aac gat aac agc gag tcc tcc gag aac cgc agc gat aac 547
Gln Asn Gln Asn Asp Asn Ser Glu Ser Ser Glu Asn Arg Ser Asp Asn
135 140 145

tac cgc aac aac aat cgt cgt tcc cgc aac aac cgg aac aat cgc aat 595
Tyr Arg Asn Asn Asn Arg Arg Ser Arg Asn Asn Arg Asn Asn Arg Asn
150 155 160 165

tac cgc gat aac aac gag tcc tct gat aat gca gga cag tcc agc aat 643
Tyr Arg Asp Asn Asn Glu Ser Ser Asp Asn Ala Gly Gln Ser Ser Asn
170 175 180

gat gat gcc gac aac aat cag gca cgg tct gag gac aat aac gac gat 691
Asp Asp Ala Asp Asn Asn Gln Ala Arg Ser Glu Asp Asn Asn Asp Asp
185 190 195

cgc cgt tct cgt aat aac cgt aac aac gac cgc aat gat cgt aac gat 739
Arg Arg Ser Arg Asn Asn Arg Asn Asn Asp Arg Asn Asp Arg Asn Asp
200 205 210

cgc aat gac cgc gac aac gac gac aac gat gat cgc cgc aac cgt cgc 787
Arg Asn Asp Arg Asp Asn Asp Asp Asn Asp Asp Arg Arg Asn Arg Arg

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215	220	225	
gga cgc cgc aat cgc cgt	gga ncn gca acg acc	gta acg atc gcg aca	835
Gly Arg Arg Asn Arg Arg	Gly Xaa Ala Thr Thr	Val Thr Ile Ala Thr	
230	235	240	245
acc gag ata acc ggg ata acc gcg aca aca gca acg atg gcg aca aca			883
Thr Glu Ile Thr Gly Ile Thr Ala Thr Thr Ala Thr Met Ala Thr Thr			
	250	255	260
acc agc aag atn gag nct gca gca ggt agc agg cat cct gga cat cgt			931
Thr Ser Lys Xaa Glu Xaa Ala Ala Gly Ser Arg His Pro Gly His Arg			
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Gly Pro			

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<211> 279

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 424

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Ala Ala Gln Gln Glu Glu Leu Pro Val Ala Ala Lys Glu Ser Ala Pro	
35 40 45	
Ala Thr Glu Asn Thr Gln Gly Gln Xaa Gln Gly Gln Ala Gln Gly Xaa	
50 55 60	
Ala Gln Gly Asp Glu His Asp Asp Xaa Phe Glu Ser Arg Ser Ala Ala	
65 70 75 80	
Arg Arg Ala Arg Arg Asn Arg Gln Arg Gln Ile His Arg Asp Gly Asp	
85 90 95	
Asp Asn Ala Asn Ala Asn Thr Glu Ser Glu Gln Asn Thr Pro Ala Gln	
100 105 110	
Asn Ala Thr Ala Gln Ala Glu Ser Glu Gln Thr Ala Ala Pro Ala Gln	
115 120 125	
Ala Glu Ala Ala Glu Gln Asn Gln Asn Asp Asn Ser Glu Ser Ser Glu	
130 135 140	
Asn Arg Ser Asp Asn Tyr Arg Asn Asn Asn Arg Arg Ser Arg Asn Asn	
145 150 155 160	
Arg Asn Asn Arg Asn Tyr Arg Asp Asn Asn Glu Ser Ser Asp Asn Ala	
165 170 175	

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Val Asp His Asn Val																115
1 5																
gca ttc gtg cgc acc acc ggt tac cac gct gca cct tct gac gtg ttt																163
Ala Phe Val Arg Thr Thr Gly Tyr His Ala Ala Pro Ser Asp Val Phe																
10 15 20																
gtc agc aac cag ctg atc cgc cgt atg ggt ctt cgt tcc ggt gac gcc																211
Val Ser Asn Gln Leu Ile Arg Arg Met Gly Leu Arg Ser Gly Asp Ala																
25 30 35																
att gaa ggt cag gtt cgt atg aac cag ggt ggt ggc aac cac aac aac																259
Ile Glu Gly Gln Val Arg Met Asn Gln Gly Gly Gly Asn His Asn Asn																
40 45 50																
cat ggt cgc aac cgt cag aag tac aac aac ttg gtg cgc gtg gag atg																307
His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu Val Arg Val Glu Met																
55 60 65																
gtt aac ggt ctt cct gct gaa gag act cgc aac cgt cct gag ttc ggc																355
Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn Arg Pro Glu Phe Gly																
70 75 80 85																
aag ctg act cct ctg tac ccg aac cag cgt ctg cgt ttg gaa act gag																403
Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu Arg Leu Glu Thr Glu																

90 95 100
 cag aag att ctt acc act cgt gtg atc gac ttg atc atg cct att ggt 451
 Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu Ile Met Pro Ile Gly
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 aag gga cag ctg tgc ttt gat tgt gtc gcc acc taaggctggt aagaccacga 504
 Lys Gly Gln Leu Cys Phe Asp Cys Val Ala Thr
 120 125
 tcc 507

<210> 426
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Gly Asn His Asn Asn His Gly Arg Asn Arg Gln Lys Tyr Asn Asn Leu
 50 55 60
 Val Arg Val Glu Met Val Asn Gly Leu Pro Ala Glu Glu Thr Arg Asn
 65 70 75 80
 Arg Pro Glu Phe Gly Lys Leu Thr Pro Leu Tyr Pro Asn Gln Arg Leu
 85 90 95
 Arg Leu Glu Thr Glu Gln Lys Ile Leu Thr Thr Arg Val Ile Asp Leu
 100 105 110
 Ile Met Pro Ile Gly Lys Gly Gln Leu Cys Phe Asp Cys Val Ala Thr
 115 120 125

<210> 427
 <211> 330
 <212> DNA
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 <222> (101)..(307)
 <223> RXN01725

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 Leu Ile Val Ser Pro
 1 5

cct aag gct ggt aag acc acg atc ctg cag aac att gcg aac gct att 163
 Pro Lys Ala Gly Lys Thr Thr Ile Leu Gln Asn Ile Ala Asn Ala Ile
 10 15 20

tcc acc aac aac cca gag tgc tac ctc atg gtt gtt ttg gtt gat gag 211
 Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val Val Leu Val Asp Glu
 25 30 35

cgt ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg 259
 Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val
 40 45 50

att tct tct act ttc gat cgt cca cca tca gag cac act gcg gtt gct 307
 Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu His Thr Ala Val Ala
 55 60 65

tgagctggcg attgagcgtg cga 330

<210> 428
 <211> 69
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 428
 Leu Ile Val Ser Pro Pro Lys Ala Gly Lys Thr Thr Ile Leu Gln Asn
 1 5 10 15

Ile Ala Asn Ala Ile Ser Thr Asn Asn Pro Glu Cys Tyr Leu Met Val
 20 25 30

Val Leu Val Asp Glu Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser
 35 40 45

Val Asn Gly Glu Val Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu
 50 55 60

His Thr Ala Val Ala
 65

<210> 429
 <211> 231
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(208)
 <223> FRXA01725

<400> 429
 tgattgtgtc gccacctaag gctggttaaga ccacgatcct gcagaaacat tgcgaacgct 60

atttccacca acaaccaga gtgctacctc atggcttggtt ttg gtt gat gag cgt 115
 Leu Val Asp Glu Arg
 1 5

ccg aaa gaa gtt act gat atg cag cgc tcc gtc aac ggc gaa gtg att 163
 Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val Asn Gly Glu Val Ile
 10 15 20

tgagctggcg attgagcgtg cga 231

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<400> 430
Leu Val Asp Glu Arg Pro Lys Glu Val Thr Asp Met Gln Arg Ser Val
  1              5              10              15
Asn Gly Glu Val Ile Ser Ser Thr Phe Asp Arg Pro Pro Ser Glu His
      20              25              30
Thr Ala Val Ala
      35

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<222> (101)..(673)
<223> RXA01726
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tcttctactt tcgatcgtcc accatcagag cacactgcgg ttg ctt gag ctg gcg																115
Leu Leu Glu Leu Ala																5
1																
att gag cgt gcg aag cgc ctg gtg gag cag ggc cag gac gtc gtt gtt																163
Ile Glu Arg Ala Lys Arg Leu Val Glu Gln Gly Gln Asp Val Val Val																20
10 15																
ctg ctt gac tcc att act cgt ttg ggc cgt gcg tac aac aac agc tca																211
Leu Leu Asp Ser Ile Thr Arg Leu Gly Arg Ala Tyr Asn Asn Ser Ser																35
25 30																
cct gca tcg gga cgt att ttg tcc ggt ggt gtg gat tcc aat gca ctg																259
Pro Ala Ser Gly Arg Ile Leu Ser Gly Gly Val Asp Ser Asn Ala Leu																50
40 45																
tac ccg ccg aag cgt ttc ttg ggt gct gct cga aac atc gaa aat ggt																307
Tyr Pro Pro Lys Arg Phe Leu Gly Ala Ala Arg Asn Ile Glu Asn Gly																65
55 60																
gga tct ttg acc atc atc gca act gcc atg gtg gaa acc ggc tct gct																355
Gly Ser Leu Thr Ile Ile Ala Thr Ala Met Val Glu Thr Gly Ser Ala																85
70 75 80																

ggt gac acc gtg atc ttc gag gag ttc aag ggc act ggt aac gct gag 403
 Gly Asp Thr Val Ile Phe Glu Glu Phe Lys Gly Thr Gly Asn Ala Glu
 90 95 100

ctg aag ctg gat cgt aag atc tct gag cgc cgc gtt ttc cca gct gtg 451
 Leu Lys Leu Asp Arg Lys Ile Ser Glu Arg Arg Val Phe Pro Ala Val
 105 110 115

gat gtt aat cct tct ggt act cgt aag gac gag ctg ttg ctc aac ccg 499
 Asp Val Asn Pro Ser Gly Thr Arg Lys Asp Glu Leu Leu Leu Asn Pro
 120 125 130

gac gag gct cgc att atg cac aag ctg cgt cgt att ctg tct gca ctt 547
 Asp Glu Ala Arg Ile Met His Lys Leu Arg Arg Ile Leu Ser Ala Leu
 135 140 145

gat aat cag caa gcc att gat ctg ttg atc aag cag ctg aag aag acc 595
 Asp Asn Gln Gln Ala Ile Asp Leu Leu Ile Lys Gln Leu Lys Lys Thr
 150 155 160 165

aag tcc aat gcg gaa ttc ctc atg cag gtt gct tcc agc gct cca atg 643
 Lys Ser Asn Ala Glu Phe Leu Met Gln Val Ala Ser Ser Ala Pro Met
 170 175 180

gca ggc aca gaa aaa gag gag gat tac tcc taatggcatc gcagggtttct gca 696
 Ala Gly Thr Glu Lys Glu Glu Asp Tyr Ser
 185 190

<210> 432

<211> 191

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Leu Leu Glu Leu Ala Ile Glu Arg Ala Lys Arg Leu Val Glu Gln Gly
 1 5 10 15

Gln Asp Val Val Val Leu Leu Asp Ser Ile Thr Arg Leu Gly Arg Ala
 20 25 30

Tyr Asn Asn Ser Ser Pro Ala Ser Gly Arg Ile Leu Ser Gly Gly Val
 35 40 45

Asp Ser Asn Ala Leu Tyr Pro Pro Lys Arg Phe Leu Gly Ala Ala Arg
 50 55 60

Asn Ile Glu Asn Gly Gly Ser Leu Thr Ile Ile Ala Thr Ala Met Val
 65 70 75 80

Glu Thr Gly Ser Ala Gly Asp Thr Val Ile Phe Glu Glu Phe Lys Gly
 85 90 95

Thr Gly Asn Ala Glu Leu Lys Leu Asp Arg Lys Ile Ser Glu Arg Arg
 100 105 110

Val Phe Pro Ala Val Asp Val Asn Pro Ser Gly Thr Arg Lys Asp Glu
 115 120 125

Leu Leu Leu Asn Pro Asp Glu Ala Arg Ile Met His Lys Leu Arg Arg
 130 135 140

Ile Leu Ser Ala Leu Asp Asn Gln Gln Ala Ile Asp Leu Leu Ile Lys
145 150 155 160

Gln Leu Lys Lys Thr Lys Ser Asn Ala Glu Phe Leu Met Gln Val Ala
165 170 175

Ser Ser Ala Pro Met Ala Gly Thr Glu Lys Glu Glu Asp Tyr Ser
180 185 190

<210> 433

<211> 1887

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1887)

<223> RXA00736

<400> 433

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Ala Gly Leu Val Phe Pro Lys Val Arg Lys His Arg Asp Gly Ala Ala
1 5 10 15

atg ccg ttg gtg gtt att aca gaa acc gat ctg act ggt aac cgt gtt 96
Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val
20 25 30

ggc gat att gca ggg gcg aaa cgt cga cct gca aaa cgc cgc aac aag 144
Gly Asp Ile Ala Gly Ala Lys Arg Arg Pro Ala Lys Arg Arg Asn Lys
35 40 45

gtg gat cct ttg gcg ctg gag cca ggg gat ttg gtg gtt cat gaa acc 192
Val Asp Pro Leu Ala Leu Glu Pro Gly Asp Leu Val Val His Glu Thr
50 55 60

cac ggc att ggt cgt ttt gtg aag atg act gaa cga acc att tct gcg 240
His Gly Ile Gly Arg Phe Val Lys Met Thr Glu Arg Thr Ile Ser Ala
65 70 75 80

ggt gat gag acc tcg cgc cgt gaa tac att gtg ctg gag tac gcg cca 288
Gly Asp Glu Thr Ser Arg Arg Glu Tyr Ile Val Leu Glu Tyr Ala Pro
85 90 95

tct aag cgc gga cag ccc ggc gat cag ctg tat gtg ccg atg gat gcg 336
Ser Lys Arg Gly Gln Pro Gly Asp Gln Leu Tyr Val Pro Met Asp Ala
100 105 110

ctg gat atg ctc agc cgc tac gtc ggt ggc gag aag ccg acg ctg tcc 384
Leu Asp Met Leu Ser Arg Tyr Val Gly Gly Glu Lys Pro Thr Leu Ser
115 120 125

aaa atg ggt ggt tct gac tgg aag aac gcc aag aag aag gct cgc gct 432
Lys Met Gly Gly Ser Asp Trp Lys Asn Ala Lys Lys Lys Ala Arg Ala
130 135 140

gcc gtg cgt gaa atc gcc ggt gag ctg gta gaa ctc tac gct aag cgc 480
Ala Val Arg Glu Ile Ala Gly Glu Leu Val Glu Leu Tyr Ala Lys Arg
145 150 155 160

caa tcc gcg ccg ggt cac ccg ttt gcg ccg gat acg ccg tgg caa aaa	528
Gln Ser Ala Pro Gly His Pro Phe Ala Pro Asp Thr Pro Trp Gln Lys	
165 170 175	
gag atg gaa gat aac ttc ccc tac gtt gag acc gaa gac cag atg ttg	576
Glu Met Glu Asp Asn Phe Pro Tyr Val Glu Thr Glu Asp Gln Met Leu	
180 185 190	
gcg atc gat gcg gtc aag gag gac atg gag aaa agt gtc ccc atg gac	624
Ala Ile Asp Ala Val Lys Glu Asp Met Glu Lys Ser Val Pro Met Asp	
195 200 205	
cgc gtc atc atc ggc gat gtg ggt tat ggc aag acg gaa gtg gcg gtg	672
Arg Val Ile Ile Gly Asp Val Gly Tyr Gly Lys Thr Glu Val Ala Val	
210 215 220	
cgc gcg gcg ttc aag gct gtg caa gac ggc aag cag gta gcc gtt ctg	720
Arg Ala Ala Phe Lys Ala Val Gln Asp Gly Lys Gln Val Ala Val Leu	
225 230 235 240	
gtg ccc acc acg ttg ctt gcg cag cag cac cag tcc acg ttt gaa gag	768
Val Pro Thr Thr Leu Leu Ala Gln Gln His Gln Ser Thr Phe Glu Glu	
245 250 255	
cgt atg act ggt ttc cct gtc acc atc aag gga ttg tca cgc ttt act	816
Arg Met Thr Gly Phe Pro Val Thr Ile Lys Gly Leu Ser Arg Phe Thr	
260 265 270	
tcg cct gcg gaa tcg cgg gag att ctc tcc ggt ttg gct gca gga tcg	864
Ser Pro Ala Glu Ser Arg Glu Ile Leu Ser Gly Leu Ala Ala Gly Ser	
275 280 285	
gtg gat atc gtc atc ggt act cac cgt ttg ctg cag act ggc gtg cag	912
Val Asp Ile Val Ile Gly Thr His Arg Leu Leu Gln Thr Gly Val Gln	
290 295 300	
tgg aaa aac cta ggg ctt gtc att gtg gat gag gag cag cgt ttc ggc	960
Trp Lys Asn Leu Gly Leu Val Ile Val Asp Glu Glu Gln Arg Phe Gly	
305 310 315 320	
gtg gaa cat aag gag cac atc aag gct ctg cgt act cac gtg gat gtg	1008
Val Glu His Lys Glu His Ile Lys Ala Leu Arg Thr His Val Asp Val	
325 330 335	
ctg acc atg tcc gcg acc ccg att ccg cgc acc ctg gaa atg tcc atg	1056
Leu Thr Met Ser Ala Thr Pro Ile Pro Arg Thr Leu Glu Met Ser Met	
340 345 350	
gcc ggt atc cgt gag atg acc acc atg ctc acc ccg ccg gaa gat cgc	1104
Ala Gly Ile Arg Glu Met Thr Met Leu Thr Pro Pro Glu Asp Arg	
355 360 365	
cac cca att ctt acc tat gtg gga ccg tat gaa gac aag cag gtc gcg	1152
His Pro Ile Leu Thr Tyr Val Gly Pro Tyr Glu Asp Lys Gln Val Ala	
370 375 380	
gca tca att cgc cgt gag ctg ctg cgc gat ggc cag gtc ttt ttc atc	1200
Ala Ser Ile Arg Arg Glu Leu Leu Arg Asp Gly Gln Val Phe Phe Ile	
385 390 395 400	

cac aac aag gtg gca gat att gag aag aag gcc cgc gag atc cgc gat	1248
His Asn Lys Val Ala Asp Ile Glu Lys Lys Ala Arg Glu Ile Arg Asp	
405 410 415	
cta gtt ccc gaa gcc cga gtg gtc gtt gcc cac ggc cag atg agt gaa	1296
Leu Val Pro Glu Ala Arg Val Val Val Ala His Gly Gln Met Ser Glu	
420 425 430	
gag ctg ctg gaa caa acc gtt caa ggt ttc tgg gac cgc gaa tac gat	1344
Glu Leu Leu Glu Gln Thr Val Gln Gly Phe Trp Asp Arg Glu Tyr Asp	
435 440 445	
gtg ctg gtg tgt acc acc atc gtg gaa act ggt ctg gat att tcc aac	1392
Val Leu Val Cys Thr Thr Ile Val Glu Thr Gly Leu Asp Ile Ser Asn	
450 455 460	
gcc aac acg ctt atc gtg gaa aat gcc cac cac atg ggc ttg tct cag	1440
Ala Asn Thr Leu Ile Val Glu Asn Ala His His Met Gly Leu Ser Gln	
465 470 475 480	
ctg cac cag ctg cgt ggc cgc gtg ggt cgt tcc cgt gag cgc ggt tac	1488
Leu His Gln Leu Arg Gly Arg Val Gly Arg Ser Arg Glu Arg Gly Tyr	
485 490 495	
gcc tac ttc ctg tat cca aag ggc gcg aca ctg act gaa atg tcc tac	1536
Ala Tyr Phe Leu Tyr Pro Lys Gly Ala Thr Leu Thr Glu Met Ser Tyr	
500 505 510	
gac cgc ctg gca acg att gcc caa aac aat gat ttg ggt gcc ggt atg	1584
Asp Arg Leu Ala Thr Ile Ala Gln Asn Asn Asp Leu Gly Ala Gly Met	
515 520 525	
gcg gtt gcc atg aag gat ttg gaa atg cgt ggc gcc gcc aac gtg ctg	1632
Ala Val Ala Met Lys Asp Leu Glu Met Arg Gly Ala Gly Asn Val Leu	
530 535 540	
ggt gca gaa caa tca ggc cat atc gct ggc gtg ggc ttt gac ctg tac	1680
Gly Ala Glu Gln Ser Gly His Ile Ala Gly Val Gly Phe Asp Leu Tyr	
545 550 555 560	
gtt cgc ctc gtc ggc gaa gca gtg gaa gcc tac cgc gcg ctg gct gat	1728
Val Arg Leu Val Gly Glu Ala Val Glu Ala Tyr Arg Ala Leu Ala Asp	
565 570 575	
ggc aaa gtt gtt gat ggc acc gtc aag gga cca aag gaa atc cgc gtg	1776
Gly Lys Val Val Asp Gly Thr Val Lys Gly Pro Lys Glu Ile Arg Val	
580 585 590	
gac ctt ccc gtg gat gcc cac att ccc gaa aag tac atc aac gcc gag	1824
Asp Leu Pro Val Asp Ala His Ile Pro Glu Lys Tyr Ile Asn Ala Glu	
595 600 605	
cgt ctg cgt ctg gaa atc tac cgc aag ctc gcg cag tcc gaa tcg gaa	1872
Arg Leu Arg Leu Glu Ile Tyr Arg Lys Leu Ala Gln Ser Glu Ser Glu	
610 615 620	
gtg gat ctg cgc ctt	1887
Val Asp Leu Arg Leu	
625	

<210> 434
 <211> 629
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 434

Ala	Gly	Leu	Val	Phe	Pro	Lys	Val	Arg	Lys	His	Arg	Asp	Gly	Ala	Ala	1	5	10	15
Met	Pro	Leu	Val	Val	Ile	Thr	Glu	Thr	Asp	Leu	Thr	Gly	Asn	Arg	Val	20	25	30	
Gly	Asp	Ile	Ala	Gly	Ala	Lys	Arg	Arg	Pro	Ala	Lys	Arg	Arg	Asn	Lys	35	40	45	
Val	Asp	Pro	Leu	Ala	Leu	Glu	Pro	Gly	Asp	Leu	Val	Val	His	Glu	Thr	50	55	60	
His	Gly	Ile	Gly	Arg	Phe	Val	Lys	Met	Thr	Glu	Arg	Thr	Ile	Ser	Ala	65	70	75	80
Gly	Asp	Glu	Thr	Ser	Arg	Arg	Glu	Tyr	Ile	Val	Leu	Glu	Tyr	Ala	Pro	85	90	95	
Ser	Lys	Arg	Gly	Gln	Pro	Gly	Asp	Gln	Leu	Tyr	Val	Pro	Met	Asp	Ala	100	105	110	
Leu	Asp	Met	Leu	Ser	Arg	Tyr	Val	Gly	Gly	Glu	Lys	Pro	Thr	Leu	Ser	115	120	125	
Lys	Met	Gly	Gly	Ser	Asp	Trp	Lys	Asn	Ala	Lys	Lys	Lys	Ala	Arg	Ala	130	135	140	
Ala	Val	Arg	Glu	Ile	Ala	Gly	Glu	Leu	Val	Glu	Leu	Tyr	Ala	Lys	Arg	145	150	155	160
Gln	Ser	Ala	Pro	Gly	His	Pro	Phe	Ala	Pro	Asp	Thr	Pro	Trp	Gln	Lys	165	170	175	
Glu	Met	Glu	Asp	Asn	Phe	Pro	Tyr	Val	Glu	Thr	Glu	Asp	Gln	Met	Leu	180	185	190	
Ala	Ile	Asp	Ala	Val	Lys	Glu	Asp	Met	Glu	Lys	Ser	Val	Pro	Met	Asp	195	200	205	
Arg	Val	Ile	Ile	Gly	Asp	Val	Gly	Tyr	Gly	Lys	Thr	Glu	Val	Ala	Val	210	215	220	
Arg	Ala	Ala	Phe	Lys	Ala	Val	Gln	Asp	Gly	Lys	Gln	Val	Ala	Val	Leu	225	230	235	240
Val	Pro	Thr	Thr	Leu	Leu	Ala	Gln	Gln	His	Gln	Ser	Thr	Phe	Glu	Glu	245	250	255	
Arg	Met	Thr	Gly	Phe	Pro	Val	Thr	Ile	Lys	Gly	Leu	Ser	Arg	Phe	Thr	260	265	270	
Ser	Pro	Ala	Glu	Ser	Arg	Glu	Ile	Leu	Ser	Gly	Leu	Ala	Ala	Gly	Ser	275	280	285	
Val	Asp	Ile	Val	Ile	Gly	Thr	His	Arg	Leu	Leu	Gln	Thr	Gly	Val	Gln				

290		295		300
Trp 305	Lys Asn Leu Gly	Leu 310	Val Ile Val Asp	Glu 315 Glu Gln Arg Phe Gly 320
Val 325	Glu His Lys	Glu 325	His Ile Lys Ala	Leu 330 Arg Thr His Val Asp 335
Leu 340	Thr Met Ser	Ala 340	Thr Pro Ile Pro	Arg 345 Thr Leu Glu Met Ser Met 350
Ala 355	Gly Ile Arg	Glu 355	Met Thr Thr Met	Leu 360 Thr Pro Pro Glu Asp Arg 365
His 370	Pro Ile Leu Thr	Tyr 375	Val Gly Pro Tyr	Glu 380 Asp Lys Gln Val Ala
Ala 385	Ser Ile Arg Arg	Glu 390	Leu Leu Arg Asp	Gly 395 Gln Val Phe Phe Ile 400
His 405	Asn Lys Val Ala	Asp 405	Ile Glu Lys Lys	Ala 410 Arg Glu Ile Arg Asp 415
Leu 420	Val Pro Glu Ala	Arg 420	Val Val Val Ala	His 425 Gly Gln Met Ser Glu 430
Glu 435	Leu Leu Glu Gln	Thr 440	Val Gln Gly Phe	Trp 445 Asp Arg Glu Tyr Asp
Val 450	Leu Val Cys Thr	Thr 455	Ile Val Glu Thr	Gly 460 Leu Asp Ile Ser Asn
Ala 465	Asn Thr Leu Ile	Val 470	Glu Asn Ala His	His 475 Met Gly Leu Ser Gln 480
Leu 485	His Gln Leu Arg	Gly 485	Arg Val Gly Arg	Ser 490 Arg Glu Arg Gly Tyr 495
Ala 500	Tyr Phe Leu Tyr	Pro 500	Lys Gly Ala Thr	Leu 510 Thr Glu Met Ser Tyr
Asp 515	Arg Leu Ala Thr	Ile 520	Ala Gln Asn Asn	Asp 525 Leu Gly Ala Gly Met
Ala 530	Val Ala Met Lys	Asp 535	Leu Glu Met Arg	Gly 540 Ala Gly Asn Val Leu
Gly 545	Ala Glu Gln Ser	Gly 550	His Ile Ala Gly	Val 555 Gly Phe Asp Leu Tyr 560
Val 565	Arg Leu Val Gly	Glu 565	Ala Val Glu Ala	Tyr 570 Arg Ala Leu Ala Asp 575
Gly 580	Lys Val Val Asp	Gly 585	Thr Val Lys Gly	Pro 590 Lys Glu Ile Arg Val
Asp 595	Leu Pro Val Asp	Ala 600	His Ile Pro Glu	Lys 605 Tyr Ile Asn Ala Glu
Arg 610	Leu Arg Leu Glu	Ile 615	Tyr Arg Lys Leu	Ala 620 Gln Ser Glu Ser Glu

Val Asp Leu Arg Leu
625

<210> 435
<211> 1116
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1093)
<223> RXN00737

<400> 435
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accacattgg attatccggt gcgtgtggag ttctggggcg atg aag gtc tct gac 115
Met Lys Val Ser Asp
1 5
att agg cag ttc tct gtc gcc gat cag cgc acc att cca gaa atc acc 163
Ile Arg Gln Phe Ser Val Ala Asp Gln Arg Thr Ile Pro Glu Ile Thr
10 15 20
atc aag agc att gag att ttc ccg gca cgg gaa ttg ctc att act gaa 211
Ile Lys Ser Ile Glu Ile Phe Pro Ala Arg Glu Leu Leu Ile Thr Glu
25 30 35
gaa gtg gca tcg cgt gcg gag tct ctt att tct aag cac ccg ggc aac 259
Glu Val Ala Ser Arg Ala Glu Ser Leu Ile Ser Lys His Pro Gly Asn
40 45 50
ccg acg ctt gtg gag atg ctg tcg agg att gcg gat tcc caa gat gtt 307
Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala Asp Ser Gln Asp Val
55 60 65
gat ggc atg gag gcg ttg att ccg gcg ctg acg gat acg ccg atg gtt 355
Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr Asp Thr Pro Met Val
70 75 80 85
ccg atg ctg gag ctc atg ccg gaa aac acc cat gtg ttg gtg att gct 403
Pro Met Leu Glu Leu Met Pro Glu Asn Thr His Val Leu Val Ile Ala
90 95 100
ccg gag aag gtg cgc cga cgc att gcg gat ctg gaa gca acc gat gct 451
Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu Glu Ala Thr Asp Ala
105 110 115
gag ttt ttg atg gct ggt tgg gaa gca gct gcg atg ggt gct gat ggt 499
Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala Met Gly Ala Asp Gly
120 125 130
cca gtg gct gcg gaa ggc ctg gac ttg gaa gct tct agc tat cgc agt 547
Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser Ser Tyr Arg Ser
135 140 145
tat gaa agt ttg gag gtt tct gcg tcg aaa agc gat gtg cgt tgg tgg 595
Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp Val Arg Trp Trp
150 155 160 165

act ttc gcg ccg ccg ggc atg ttt gag gcc tcg gag gag gcg acg ctg 643
 Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu Glu Ala Thr Leu
 170 175 180

ccg ctt gat ttt gaa gcc ggg ccg gcg ccg cgc ggt gag ctg ccg aag 691
 Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly Glu Leu Pro Lys
 185 190 195

atc gat gcg atg atg gcg cag ctg ctt gcg cac aca acc ggc ggt ggg 739
 Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr Thr Gly Gly Gly
 200 205 210

cgg gct gcg ttt atc gcg ccg acc caa ggt gcg att aag cgc atg gtc 787
 Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala Ile Lys Arg Met Val
 215 220 225

gat cgt ttc gcg gaa aag ggc att ccc acc cat gtg gcg acc ccg ggt 835
 Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His Val Ala Thr Pro Gly
 230 235 240 245

tgg gag cca acg cct ggt caa gtg act ctt tat cat gcg ctg agc cat 883
 Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr His Ala Leu Ser His
 250 255 260

gct ggc ctg gtg ttt ccg aag gtg cgt aaa cac cgc gat ggc gct gca 931
 Ala Gly Leu Val Phe Pro Lys Val Arg Lys His Arg Asp Gly Ala Ala
 265 270 275

atg ccg ttg gtg gtt att aca gaa acc gat ctg act ggt aac cgt gtt 979
 Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu Thr Gly Asn Arg Val
 280 285 290

ggc gat att gca ggg cga aac gtc gac ctg caa aac gcc gca aca agg 1027
 Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln Asn Ala Ala Thr Arg
 295 300 305

tgg atc ctt tgg cgc tgg agc cag ggg att tgg tgg ttc atg aaa ccc 1075
 Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp Trp Phe Met Lys Pro
 310 315 320 325

acg gca ttg gtc gtt ttg tgaagatgac tgaacgaacc att 1116
 Thr Ala Leu Val Val Leu
 330

<210> 436

<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 436

Met Lys Val Ser Asp Ile Arg Gln Phe Ser Val Ala Asp Gln Arg Thr
 1 5 10 15

Ile Pro Glu Ile Thr Ile Lys Ser Ile Glu Ile Phe Pro Ala Arg Glu
 20 25 30

Leu Leu Ile Thr Glu Glu Val Ala Ser Arg Ala Glu Ser Leu Ile Ser
 35 40 45

Lys His Pro Gly Asn Pro Thr Leu Val Glu Met Leu Ser Arg Ile Ala
 50 55 60
 Asp Ser Gln Asp Val Asp Gly Met Glu Ala Leu Ile Pro Ala Leu Thr
 65 70 75 80
 Asp Thr Pro Met Val Pro Met Leu Glu Leu Met Pro Glu Asn Thr His
 85 90 95
 Val Leu Val Ile Ala Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu
 100 105 110
 Glu Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala
 115 120 125
 Met Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala
 130 135 140
 Ser Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser
 145 150 155 160
 Asp Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser
 165 170 175
 Glu Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg
 180 185 190
 Gly Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His
 195 200 205
 Thr Thr Gly Gly Gly Arg Ala Ala Phe Ile Ala Pro Thr Gln Gly Ala
 210 215 220
 Ile Lys Arg Met Val Asp Arg Phe Ala Glu Lys Gly Ile Pro Thr His
 225 230 235 240
 Val Ala Thr Pro Gly Trp Glu Pro Thr Pro Gly Gln Val Thr Leu Tyr
 245 250 255
 His Ala Leu Ser His Ala Gly Leu Val Phe Pro Lys Val Arg Lys His
 260 265 270
 Arg Asp Gly Ala Ala Met Pro Leu Val Val Ile Thr Glu Thr Asp Leu
 275 280 285
 Thr Gly Asn Arg Val Gly Asp Ile Ala Gly Arg Asn Val Asp Leu Gln
 290 295 300
 Asn Ala Ala Thr Arg Trp Ile Leu Trp Arg Trp Ser Gln Gly Ile Trp
 305 310 315 320
 Trp Phe Met Lys Pro Thr Ala Leu Val Val Leu
 325 330

<210> 437

<211> 480

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(480)

<223> FRXA00737

<400> 437

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His	Pro	Gly	Asn	Pro	Thr	Leu	Val	Glu	Met	Leu	Ser	Arg	Ile	Ala	Asp	
1				5					10					15		
tcc	caa	gat	gtt	gat	ggc	atg	gag	gcg	ttg	att	ccg	gcg	ctg	acg	gat	96
Ser	Gln	Asp	Val	Asp	Gly	Met	Glu	Ala	Leu	Ile	Pro	Ala	Leu	Thr	Asp	
			20					25					30			
acg	ccg	atg	gtt	ccg	atg	ctg	gag	ctc	atg	ccg	gaa	aac	acc	cat	gtg	144
Thr	Pro	Met	Val	Pro	Met	Leu	Glu	Leu	Met	Pro	Glu	Asn	Thr	His	Val	
		35					40					45				
ttg	gtg	att	gct	ccg	gag	aag	gtg	cgc	cga	cgc	att	gcg	gat	ctg	gaa	192
Leu	Val	Ile	Ala	Pro	Glu	Lys	Val	Arg	Arg	Arg	Ile	Ala	Asp	Leu	Glu	
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gca	acc	gat	gct	gag	ttt	ttg	atg	gct	ggc	tgg	gaa	gca	gct	gcg	atg	240
Ala	Thr	Asp	Ala	Glu	Phe	Leu	Met	Ala	Gly	Trp	Glu	Ala	Ala	Ala	Met	
65					70					75					80	
ggc	gct	gat	ggc	cca	gtg	gct	gcg	gaa	ggc	ctg	gac	ttg	gaa	gct	tct	288
Gly	Ala	Asp	Gly	Pro	Val	Ala	Ala	Glu	Gly	Leu	Asp	Leu	Glu	Ala	Ser	
				85					90					95		
agc	tat	cgc	agt	tat	gaa	agt	ttg	gag	gtt	tct	gcg	tcg	aaa	agc	gat	336
Ser	Tyr	Arg	Ser	Tyr	Glu	Ser	Leu	Glu	Val	Ser	Ala	Ser	Lys	Ser	Asp	
			100					105					110			
gtg	cgt	tgg	tgg	act	ttc	gcg	ccg	ccg	ggc	atg	ttt	gag	gcc	tcg	gag	384
Val	Arg	Trp	Trp	Thr	Phe	Ala	Pro	Pro	Gly	Met	Phe	Glu	Ala	Ser	Glu	
		115					120					125				
gag	gcg	acg	ctg	ccg	ctt	gat	ttt	gaa	gcc	ggg	ccg	gcg	ccg	cgc	ggc	432
Glu	Ala	Thr	Leu	Pro	Leu	Asp	Phe	Glu	Ala	Gly	Pro	Ala	Pro	Arg	Gly	
	130					135					140					
gag	ctg	ccg	aag	atc	gat	gcg	atg	atg	gcg	cag	ctg	ctt	gcg	cac	aca	480
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<212> PRT

<213> Corynebacterium glutamicum

<400> 438

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Ser	Gln	Asp	Val	Asp	Gly	Met	Glu	Ala	Leu	Ile	Pro	Ala	Leu	Thr	Asp
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Thr	Pro	Met	Val	Pro	Met	Leu	Glu	Leu	Met	Pro	Glu	Asn	Thr	His	Val
		35					40					45			

Leu Val Ile Ala Pro Glu Lys Val Arg Arg Arg Ile Ala Asp Leu Glu
 50 55 60
 Ala Thr Asp Ala Glu Phe Leu Met Ala Gly Trp Glu Ala Ala Ala Met
 65 70 75 80
 Gly Ala Asp Gly Pro Val Ala Ala Glu Gly Leu Asp Leu Glu Ala Ser
 85 90 95
 Ser Tyr Arg Ser Tyr Glu Ser Leu Glu Val Ser Ala Ser Lys Ser Asp
 100 105 110
 Val Arg Trp Trp Thr Phe Ala Pro Pro Gly Met Phe Glu Ala Ser Glu
 115 120 125
 Glu Ala Thr Leu Pro Leu Asp Phe Glu Ala Gly Pro Ala Pro Arg Gly
 130 135 140
 Glu Leu Pro Lys Ile Asp Ala Met Met Ala Gln Leu Leu Ala His Thr
 145 150 155 160

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 <223> RXN01872

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 Met Gly Asn Asp Gly
 1 5
 gga gac ctg cga atc gac gac cta cgc agc ttc att tca gtc gct caa 163
 Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe Ile Ser Val Ala Gln
 10 15 20
 tca ggc cac cta acc gaa act gcc caa aga tta ggc atc ccg cag ccc 211
 Ser Gly His Leu Thr Glu Thr Ala Gln Arg Leu Gly Ile Pro Gln Pro
 25 30 35
 aca ctt tcc aga cga atc agc cga gtg gaa aaa cac gca ggc acc cca 259
 Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys His Ala Gly Thr Pro
 40 45 50
 ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc aac caa cga ggc cac 307
 Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu Asn Gln Arg Gly His
 55 60 65
 gcc ttc ctc aac cac gcc agc gcc atc gtc gca gaa ttc aac tcc gcc 355
 Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala Glu Phe Asn Ser Ala
 70 75 80 85
 gca act gaa atc aaa cgc ctc atg gac cca gaa aaa ggc aca atc cga 403
 Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu Lys Gly Thr Ile Arg

90										95					100					
ctg	gac	ttc	atg	cat	tcc	ttg	ggc	act	tgg	atg	gtc	ccc	gaa	ctt	atc	451				
Leu	Asp	Phe	Met	His	Ser	Leu	Gly	Thr	Trp	Met	Val	Pro	Glu	Leu	Ile					
			105					110					115							
cga	aca	ttc	cgc	gcc	gaa	cac	ccc	aac	gta	gaa	ttc	caa	ctc	cac	caa	499				
Arg	Thr	Phe	Arg	Ala	Glu	His	Pro	Asn	Val	Glu	Phe	Gln	Leu	His	Gln					
		120					125					130								
gcg	gca	gca	atg	ctc	ctg	gta	gat	cgt	gtt	ttg	gct	gat	gaa	act	gac	547				
Ala	Ala	Ala	Met	Leu	Leu	Val	Asp	Arg	Val	Leu	Ala	Asp	Glu	Thr	Asp					
		135				140					145									
ctc	gca	tta	gtt	ggc	ccc	aaa	cct	gcc	gag	gtt	ggg	acc	tct	tta	ggg	595				
Leu	Ala	Leu	Val	Gly	Pro	Lys	Pro	Ala	Glu	Val	Gly	Thr	Ser	Leu	Gly					
150					155					160					165					
tgg	gcg	cca	ctg	ctt	cgt	caa	cga	ctt	gcc	cta	gct	gtt	ccc	gca	gat	643				
Trp	Ala	Pro	Leu	Leu	Arg	Gln	Arg	Leu	Ala	Leu	Ala	Val	Pro	Ala	Asp					
				170					175					180						
cac	cgg	ctt	gcc	tcc	ttt	tct	ggc	caa	gga	gaa	ttg	ccg	ttg	att	act	691				
His	Arg	Leu	Ala	Ser	Phe	Ser	Gly	Gln	Gly	Glu	Leu	Pro	Leu	Ile	Thr					
			185					190					195							
gcg	gcg	gaa	gaa	cct	ttc	gtg	gcg	atg	cga	gca	ggg	ttc	ggc	acc	cga	739				
Ala	Ala	Glu	Glu	Pro	Phe	Val	Ala	Met	Arg	Ala	Gly	Phe	Gly	Thr	Arg					
		200					205					210								
ctc	ctc	atg	gat	gca	tta	gcc	gaa	gaa	gcc	ggg	ttt	gtt	ccc	aat	gtg	787				
Leu	Leu	Met	Asp	Ala	Leu	Ala	Glu	Glu	Ala	Gly	Phe	Val	Pro	Asn	Val					
		215				220				225										
gtt	ttc	gaa	tcc	atg	gaa	ctc	acc	acc	gtc	gca	ggg	ctt	gtc	agc	gca	835				
Val	Phe	Glu	Ser	Met	Glu	Leu	Thr	Thr	Val	Ala	Gly	Leu	Val	Ser	Ala					
230					235					240					245					
ggg	ctc	ggc	gtt	ggg	gtg	gtt	ccg	atg	gat	gat	ccc	tac	ctt	tcc	aca	883				
Gly	Leu	Gly	Val	Gly	Val	Val	Pro	Met	Asp	Asp	Pro	Tyr	Leu	Ser	Thr					
				250				255						260						
gtg	gga	atc	gtg	caa	cgc	cca	ctt	agt	cca	ccc	gct	tat	agg	gaa		928				
Val	Gly	Ile	Val	Gln	Arg	Pro	Leu	Ser	Pro	Pro	Ala	Tyr	Arg	Glu						
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<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

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Ile	Ser	Val	Ala	Gln	Ser	Gly	His	Leu	Thr	Glu	Thr	Ala	Gln	Arg	Leu
			20					25					30		

Gly	Ile	Pro	Gln	Pro	Thr	Leu	Ser	Arg	Arg	Ile	Ser	Arg	Val	Glu	Lys
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His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
 50 55 60
 Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
 65 70 75 80
 Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
 85 90 95
 Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met
 100 105 110
 Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu
 115 120 125
 Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu
 130 135 140
 Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
 145 150 155 160
 Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu
 165 170 175
 Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu
 180 185 190
 Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala
 195 200 205
 Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly
 210 215 220
 Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr Val Ala
 225 230 235 240
 Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp Asp
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 Ala Tyr Arg Glu
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<210> 441

<211> 865

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(865)

<223> FRXA01872

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gga	gac	ctg	cga	atc	gac	gac	cta	cgc	agc	ttc	att	tca	gtc	gct	caa	163
Gly	Asp	Leu	Arg	Ile	Asp	Asp	Leu	Arg	Ser	Phe	Ile	Ser	Val	Ala	Gln	
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tca	ggc	cac	cta	acc	gaa	act	gcc	caa	aga	tta	ggc	atc	ccg	cag	ccc	211
Ser	Gly	His	Leu	Thr	Glu	Thr	Ala	Gln	Arg	Leu	Gly	Ile	Pro	Gln	Pro	
			25				30				35					
aca	ctt	tcc	aga	cga	atc	agc	cga	gtg	gaa	aaa	cac	gca	ggc	acc	cca	259
Thr	Leu	Ser	Arg	Arg	Ile	Ser	Arg	Val	Glu	Lys	His	Ala	Gly	Thr	Pro	
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ctt	ttc	gac	cgc	gcc	ggc	cgc	aaa	ctc	gtc	ctc	aac	caa	cga	ggc	cac	307
Leu	Phe	Asp	Arg	Ala	Gly	Arg	Lys	Leu	Val	Leu	Asn	Gln	Arg	Gly	His	
		55				60				65						
gcc	ttc	ctc	aac	cac	gcc	agc	gcc	atc	gtc	gca	gaa	ttc	aac	tcc	gcc	355
Ala	Phe	Leu	Asn	His	Ala	Ser	Ala	Ile	Val	Ala	Glu	Phe	Asn	Ser	Ala	
		70				75				80				85		
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Ala	Thr	Glu	Ile	Lys	Arg	Leu	Met	Asp	Pro	Glu	Lys	Gly	Thr	Ile	Arg	
				90				95				100				
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Leu	Asp	Phe	Met	His	Ser	Leu	Gly	Thr	Trp	Met	Val	Pro	Glu	Leu	Ile	
			105				110				115					
cga	aca	ttc	cgc	gcc	gaa	cac	ccc	aac	gta	gaa	ttc	caa	ctc	cac	caa	499
Arg	Thr	Phe	Arg	Ala	Glu	His	Pro	Asn	Val	Glu	Phe	Gln	Leu	His	Gln	
		120				125				130						
gcg	gca	gca	atg	ctc	ctg	gta	gat	cgt	gtt	ttg	gct	gat	gaa	act	gac	547
Ala	Ala	Ala	Met	Leu	Leu	Val	Asp	Arg	Val	Leu	Ala	Asp	Glu	Thr	Asp	
		135				140				145						
ctc	gca	tta	gtt	ggc	ccc	aaa	cct	gcc	gag	gtt	ggt	acc	tct	tta	ggg	595
Leu	Ala	Leu	Val	Gly	Pro	Lys	Pro	Ala	Glu	Val	Gly	Thr	Ser	Leu	Gly	
		150				155				160				165		
tgg	gcg	cca	ctg	ctt	cgt	caa	cga	ctt	gcc	cta	gct	gtt	ccc	gca	gat	643
Trp	Ala	Pro	Leu	Leu	Arg	Gln	Arg	Leu	Ala	Leu	Ala	Val	Pro	Ala	Asp	
				170				175				180				
cac	cgg	ctt	gcc	tcc	ttt	tct	ggc	caa	gga	gaa	ttg	ccg	ttg	att	act	691
His	Arg	Leu	Ala	Ser	Phe	Ser	Gly	Gln	Gly	Glu	Leu	Pro	Leu	Ile	Thr	
			185				190				195					
gcg	gcg	gaa	gaa	cct	ttc	gtg	gcg	atg	cga	gca	ggt	ttc	ggc	acc	cga	739
Ala	Ala	Glu	Glu	Pro	Phe	Val	Ala	Met	Arg	Ala	Gly	Phe	Gly	Thr	Arg	
		200				205				210						
ctc	ctc	atg	gat	gca	tta	gcc	gaa	gaa	gcc	ggt	ttt	gtt	ccc	aat	gtg	787
Leu	Leu	Met	Asp	Ala	Leu	Ala	Glu	Glu	Ala	Gly	Phe	Val	Pro	Asn	Val	
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 Gly Leu Gly Val Gly Val Val Pro Met Asp
 250 255

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 <213> Corynebacterium glutamicum

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 20 25 30
 Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
 35 40 45
 His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
 50 55 60
 Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile Val Ala
 65 70 75 80
 Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp Pro Glu
 85 90 95
 Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr Trp Met
 100 105 110
 Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn Val Glu
 115 120 125
 Phe Gln Leu His Gln Ala Ala Ala Met Leu Leu Val Asp Arg Val Leu
 130 135 140
 Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala Glu Val
 145 150 155 160
 Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu Ala Leu
 165 170 175
 Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln Gly Glu
 180 185 190
 Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met Arg Ala
 195 200 205
 Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu Ala Gly
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 Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met Asp
 245 250 255

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Met Thr Ser Glu Asn 5																
1																
tcc gaa tcc cag gac att tgg cta acc gat gag caa caa gat gtg tgg 163																
Ser Glu Ser Gln Asp Ile Trp Leu Thr Asp Glu Gln Gln Asp Val Trp 20																
10 15																
ctc gat gtg tgg aca atg cga atc ggc ctg cct gct cgc ttg gat gct 211																
Leu Asp Val Trp Thr Met Arg Ile Gly Leu Pro Ala Arg Leu Asp Ala 35																
25 30																
caa ctg aaa gaa gct gcg ggt gtc agc cac ttt gag tac ttc acc atg 259																
Gln Leu Lys Glu Ala Ala Gly Val Ser His Phe Glu Tyr Phe Thr Met 50																
40 45																
gcg cag att tct atg gcc ccg gaa cat cgg gtg cgc atg agt gag ctt 307																
Ala Gln Ile Ser Met Ala Pro Glu His Arg Val Arg Met Ser Glu Leu 65																
55 60																
gct gag ctg tcc gat atg acg cta tcg cat cta tct aga gtg gtt act 355																
Ala Glu Leu Ser Asp Met Thr Leu Ser His Leu Ser Arg Val Val Thr 85																
70 75 80																
cgc cta gaa aag gct ggc tgg gtg aag cgt gtt ccc gat cct gat gat 403																
Arg Leu Glu Lys Ala Gly Trp Val Lys Arg Val Pro Asp Pro Asp Asp 100																
90 95																
ggt cgc gcc acc gtt gct gtg ctc acg gac tct ggg tgg gag aaa gtt 451																
Gly Arg Ala Thr Val Ala Val Leu Thr Asp Ser Gly Trp Glu Lys Val 115																
105 110																
aaa gca aca gcc cct ggt cat gtg aag gaa gtg cgt cgt ttg gtg ttt 499																
Lys Ala Thr Ala Pro Gly His Val Lys Glu Val Arg Arg Leu Val Phe 130																
120 125 130																
gac gat ctc act cca gaa gaa ctc aag gta atg ggc acc gca atg aag 547																
Asp Asp Leu Thr Pro Glu Glu Leu Lys Val Met Gly Thr Ala Met Lys 145																
135 140 145																
aag att gtg aac cga ctc gat atg tcc aac agg ctg ccc cgg gtg 592																
Lys Ile Val Asn Arg Leu Asp Met Ser Asn Arg Leu Pro Arg Val 160																
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 <213> Corynebacterium glutamicum

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 Ala Arg Leu Asp Ala Gln Leu Lys Glu Ala Ala Gly Val Ser His Phe
 35 40 45
 Glu Tyr Phe Thr Met Ala Gln Ile Ser Met Ala Pro Glu His Arg Val
 50 55 60
 Arg Met Ser Glu Leu Ala Glu Leu Ser Asp Met Thr Leu Ser His Leu
 65 70 75 80
 Ser Arg Val Val Thr Arg Leu Glu Lys Ala Gly Trp Val Lys Arg Val
 85 90 95
 Pro Asp Pro Asp Asp Gly Arg Ala Thr Val Ala Val Leu Thr Asp Ser
 100 105 110
 Gly Trp Glu Lys Val Lys Ala Thr Ala Pro Gly His Val Lys Glu Val
 115 120 125
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 Leu Pro Arg Val

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<220>
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 <222> (1)..(999)
 <223> RXN01404

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 Ala Gly Val Ser Lys Ser Leu Val Ser Leu Val Leu Arg Gly Ser Pro
 20 25 30
 aac gtg agc aaa gaa tcc gaa gcc gcg gtc aag acc gcg ata aaa aag 144
 Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys

35					40					45						
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Leu	Asn	Tyr	Gln	Pro	Asn	Arg	Ala	Ala	Ser	Asp	Leu	Ala	Ala	Lys	Arg	
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acg	cag	ctc	att	gca	gtg	ctt	atc	gac	gac	tac	tcc	aac	ccg	tgg	ttc	240
Thr	Gln	Leu	Ile	Ala	Val	Leu	Ile	Asp	Asp	Tyr	Ser	Asn	Pro	Trp	Phe	
	65				70					75					80	
atc	gac	ctg	att	caa	agc	ctc	agc	gat	gtg	ctc	acc	ccc	aag	ggg	tac	288
Ile	Asp	Leu	Ile	Gln	Ser	Leu	Ser	Asp	Val	Leu	Thr	Pro	Lys	Gly	Tyr	
				85					90					95		
cga	ctg	tcc	gtc	att	gac	tca	tta	acc	tct	caa	gcc	ggc	acc	gat	ccc	336
Arg	Leu	Ser	Val	Ile	Asp	Ser	Leu	Thr	Ser	Gln	Ala	Gly	Thr	Asp	Pro	
			100					105					110			
att	acc	agt	gca	cta	tca	atg	cgc	ccc	gat	gga	atc	atc	atc	gcc	caa	384
Ile	Thr	Ser	Ala	Leu	Ser	Met	Arg	Pro	Asp	Gly	Ile	Ile	Ile	Ala	Gln	
		115					120					125				
gac	atc	ccc	gat	ttc	act	gtc	ccc	gat	tcc	cta	ccc	cca	ttt	gtc	atc	432
Asp	Ile	Pro	Asp	Phe	Thr	Val	Pro	Asp	Ser	Leu	Pro	Pro	Phe	Val	Ile	
	130					135					140					
gca	ggc	acc	aga	atc	acc	caa	gcc	agc	acc	cat	gat	tca	gtg	gcc	aac	480
Ala	Gly	Thr	Arg	Ile	Thr	Gln	Ala	Ser	Thr	His	Asp	Ser	Val	Ala	Asn	
	145				150					155					160	
gat	gac	ttc	cgg	ggc	gca	gaa	ata	gcc	aca	aaa	cac	ctc	atc	gat	ctt	528
Asp	Asp	Phe	Arg	Gly	Ala	Glu	Ile	Ala	Thr	Lys	His	Leu	Ile	Asp	Leu	
				165				170						175		
gga	cac	acc	cac	atc	gcc	cac	cta	cgc	gtg	gga	agc	ggc	gct	ggc	tta	576
Gly	His	Thr	His	Ile	Ala	His	Leu	Arg	Val	Gly	Ser	Gly	Ala	Gly	Leu	
			180					185					190			
cga	cgc	ttc	gaa	agc	ttt	gag	gca	acc	atg	cgt	gca	cat	ggc	ctg	gag	624
Arg	Arg	Phe	Glu	Ser	Phe	Glu	Ala	Thr	Met	Arg	Ala	His	Gly	Leu	Glu	
		195					200					205				
ccg	ctt	tcc	aac	gat	tac	ctc	ggc	ccc	gcc	gtt	gag	cac	gcc	ggg	tac	672
Pro	Leu	Ser	Asn	Asp	Tyr	Leu	Gly	Pro	Ala	Val	Glu	His	Ala	Gly	Tyr	
	210					215					220					
acc	gaa	acc	ctc	gca	cta	ctc	aaa	gag	cac	ccg	gag	gtc	acc	gcc	att	720
Thr	Glu	Thr	Leu	Ala	Leu	Leu	Lys	Glu	His	Pro	Glu	Val	Thr	Ala	Ile	
	225				230					235					240	
ttc	tcc	tca	aac	gac	atc	acc	gcc	atc	gga	gca	ctc	ggt	gcc	gcc	cgt	768
Phe	Ser	Ser	Asn	Asp	Ile	Thr	Ala	Ile	Gly	Ala	Leu	Gly	Ala	Ala	Arg	
				245					250					255		
gaa	cta	ggt	tta	cgc	gta	cct	gaa	gat	cta	tca	ata	atc	gga	tat	gac	816
Glu	Leu	Gly	Leu	Arg	Val	Pro	Glu	Asp	Leu	Ser	Ile	Ile	Gly	Tyr	Asp	
			260					265					270			
aac	act	ccc	ctc	gcc	caa	acc	cga	ctg	atc	aac	ctc	acc	acc	atc	gac	864
Asn	Thr	Pro	Leu	Ala	Gln	Thr	Arg	Leu	Ile	Asn	Leu	Thr	Thr	Ile	Asp	
		275					280					285				

gac aac agc atc ggc gtc ggc tac aac gcc gct ctc ttg ttg ctg agc 912
 Asp Asn Ser Ile Gly Val Gly Tyr Asn Ala Ala Leu Leu Leu Leu Ser
 290 295 300

 atg ctt gat ccc gag gca ccc cac ccg gag atc atg cat acg ttg cag 960
 Met Leu Asp Pro Glu Ala Pro His Pro Glu Ile Met His Thr Leu Gln
 305 310 315 320

 ccc tcg ctg att gaa cgg ggc acg tgc gcg cca cgt gga tagctacccc 1009
 Pro Ser Leu Ile Glu Arg Gly Thr Cys Ala Pro Arg Gly
 325 330

 aaataacttg act 1022

<210> 446
 <211> 333
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 446
 Gln Lys Met Ser Thr Ser Arg Pro Thr Ile Tyr Asp Val Ala Lys Ala
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 Asn Val Ser Lys Glu Ser Glu Ala Ala Val Lys Thr Ala Ile Lys Lys
 35 40 45

 Leu Asn Tyr Gln Pro Asn Arg Ala Ala Ser Asp Leu Ala Ala Lys Arg
 50 55 60

 Thr Gln Leu Ile Ala Val Leu Ile Asp Asp Tyr Ser Asn Pro Trp Phe
 65 70 75 80

 Ile Asp Leu Ile Gln Ser Leu Ser Asp Val Leu Thr Pro Lys Gly Tyr
 85 90 95

 Arg Leu Ser Val Ile Asp Ser Leu Thr Ser Gln Ala Gly Thr Asp Pro
 100 105 110

 Ile Thr Ser Ala Leu Ser Met Arg Pro Asp Gly Ile Ile Ile Ala Gln
 115 120 125

 Asp Ile Pro Asp Phe Thr Val Pro Asp Ser Leu Pro Pro Phe Val Ile
 130 135 140

 Ala Gly Thr Arg Ile Thr Gln Ala Ser Thr His Asp Ser Val Ala Asn
 145 150 155 160

 Asp Asp Phe Arg Gly Ala Glu Ile Ala Thr Lys His Leu Ile Asp Leu
 165 170 175

 Gly His Thr His Ile Ala His Leu Arg Val Gly Ser Gly Ala Gly Leu
 180 185 190

 Arg Arg Phe Glu Ser Phe Glu Ala Thr Met Arg Ala His Gly Leu Glu
 195 200 205

Pro Leu Ser Asn Asp Tyr Leu Gly Pro Ala Val Glu His Ala Gly Tyr
 210 215 220
 Thr Glu Thr Leu Ala Leu Leu Lys Glu His Pro Glu Val Thr Ala Ile
 225 230 235 240
 Phe Ser Ser Asn Asp Ile Thr Ala Ile Gly Ala Leu Gly Ala Ala Arg
 245 250 255
 Glu Leu Gly Leu Arg Val Pro Glu Asp Leu Ser Ile Ile Gly Tyr Asp
 260 265 270
 Asn Thr Pro Leu Ala Gln Thr Arg Leu Ile Asn Leu Thr Thr Ile Asp
 275 280 285
 Asp Asn Ser Ile Gly Val Gly Tyr Asn Ala Ala Leu Leu Leu Leu Ser
 290 295 300
 Met Leu Asp Pro Glu Ala Pro His Pro Glu Ile Met His Thr Leu Gln
 305 310 315 320
 Pro Ser Leu Ile Glu Arg Gly Thr Cys Ala Pro Arg Gly
 325 330

<210> 447
 <211> 523
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(523)
 <223> RXN02827

<220>
 <223> All occurrences of n = any nucleotide

<220>
 <223> All occurrences of Xaa = any amino acid

<400> 447
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 gcgggtagga agaagcagcc gtgtcgcata tgcttacttt atg tat gag cag cag 115
 Met Tyr Glu Gln Gln
 1 5
 aag atc ctt aac gaa gtc agt gaa aaa cgt ctt cag gca atc aaa gat 163
 Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu Gln Ala Ile Lys Asp
 10 15 20
 ttt aca gaa ctg gga tct gga ttc aag att gcg atg cgg gat ctt tcc 211
 Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala Met Arg Asp Leu Ser
 25 30 35
 att cgc ggt gca ggt aat ctc tta ggt gct cag cag cat gga ttt att 259
 Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln Gln His Gly Phe Ile
 40 45 50
 gat gca gtc ggt ttc gat atg tat tct caa atg cta agc gaa gct gtt 307

Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met Leu Ser Glu Ala Val
 55 60 65
 tnt cgt aaa caa gga aag aat agt caa gtg gag aag ncc nct gtt gag 355
 Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu Lys Xaa Xaa Val Glu
 70 75 80 85
 atc gac cnc ggt gtc gat gcg tat cta cct gaa aca tac gtg gca gat 403
 Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu Thr Tyr Val Ala Asp
 90 95 100
 can cgg cag aaa atc gag atc tat aaa cga att cgt gaa ctt gat tcg 451
 Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile Arg Glu Leu Asp Ser
 105 110 115
 caa gaa atg cta gat gaa cta gaa gat gat ctg ctc gac cgt ttt gga 499
 Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu Leu Asp Arg Phe Gly
 120 125 130
 gaa can cca gaa gaa gta gca cat 523
 Glu Xaa Pro Glu Glu Val Ala His
 135 140

<210> 448

<211> 141

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 448

Met Tyr Glu Gln Gln Lys Ile Leu Asn Glu Val Ser Glu Lys Arg Leu
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 Gln Ala Ile Lys Asp Phe Thr Glu Leu Gly Ser Gly Phe Lys Ile Ala
 20 25 30
 Met Arg Asp Leu Ser Ile Arg Gly Ala Gly Asn Leu Leu Gly Ala Gln
 35 40 45
 Gln His Gly Phe Ile Asp Ala Val Gly Phe Asp Met Tyr Ser Gln Met
 50 55 60
 Leu Ser Glu Ala Val Xaa Arg Lys Gln Gly Lys Asn Ser Gln Val Glu
 65 70 75 80
 Lys Xaa Xaa Val Glu Ile Asp Xaa Gly Val Asp Ala Tyr Leu Pro Glu
 85 90 95
 Thr Tyr Val Ala Asp Xaa Arg Gln Lys Ile Glu Ile Tyr Lys Arg Ile
 100 105 110
 Arg Glu Leu Asp Ser Gln Glu Met Leu Asp Glu Leu Glu Asp Asp Leu
 115 120 125
 Leu Asp Arg Phe Gly Glu Xaa Pro Glu Glu Val Ala His
 130 135 140

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<210> 450
<211> 147
<212> PRT
<213> Corynebacterium glutamicum
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<400> 450

Met Ser Glu Asn Tyr Ser Lys Ile Val Val Gly Thr Asp Gly Ser Lys
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Ser Ser Leu Leu Ala Val Glu Arg Ala Ala Arg Ile Ala Ala Ala Phe
 20 25 30

Asp Ala Thr Leu Ile Ile Gly Cys Ala Tyr Tyr Glu Ser Lys Glu Asp
 35 40 45

Ala Ser Glu Thr Leu Arg Gln Asp Ser Val Thr Ile Leu Gly Asp Asp
 50 55 60

Pro Ala Arg Glu Asn Leu Asp Lys Ala Ala Asp Ala Ala Arg Ala Val
 65 70 75 80

Gly Ala Thr Ser Ile Glu Thr Glu Val Arg Thr Gly Thr Pro Val Glu
 85 90 95

Ala Leu Met Ala Ile Val Asn Asp His Gln Ala Asp Leu Leu Val Val
 100 105 110

Gly Asn Arg Gly Ile Asn Tyr Leu Thr Gly Arg Leu Leu Gly Ser Val
 115 120 125

Pro Ala Asp Val Ala Arg Gln Ser Asp Cys Asp Val Met Ile Val His
 130 135 140

Thr Val Ser
 145

<210> 451

<211> 1272

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1249)

<223> RXN01671

<400> 451

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tttttgtacc cgaatttgta cccgaattta aggaatcgct atg aat cat gtt gtt 115
 Met Asn His Val Val
 1 5

aat ttt gct tca cat ttg gaa gac gca gcc ctg aag caa gcc gaa gct 163
 Asn Phe Ala Ser His Leu Glu Asp Ala Ala Leu Lys Gln Ala Glu Ala
 10 15 20

act gcc acc atg ccg ttt att tac ccg cat gtg gcg ttg atg cct gat 211
 Thr Ala Thr Met Pro Phe Ile Tyr Pro His Val Ala Leu Met Pro Asp
 25 30 35

gct cac ttt ggg ctg ggt tcg tcg gtg gga acg gtg ttc ggc acc aag 259
 Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr Val Phe Gly Thr Lys
 40 45 50

ggc ggc atc att ccg ggc gct gtg ggc gtg gat ata ggc tgc gga atg	307
Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp Ile Gly Cys Gly Met	
55 60 65	
ata gga gtg tgt acc aat tac acg gcc tct gac ctg gag gga cgt gat	355
Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp Leu Glu Gly Arg Asp	
70 75 80 85	
ttg gtg acg ctt cgg gat tac atc gag cgg gtg att ccg ttg tct cct	403
Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val Ile Pro Leu Ser Pro	
90 95 100	
gga aat tac aat tcc acc acc ttg aag gaa acc ggc aag gtg aag gtc	451
Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr Ala Lys Val Lys Val	
105 110 115	
ggc gag ttg gag gaa ctc ggc gag cgc gat ggc gta gat ttg tcg cac	499
Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly Val Asp Leu Ser His	
120 125 130	
tct ccg acg tgg aag cgc cag ttg ggc tcg ctt ggc gga ggc aat cac	547
Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu Gly Gly Gly Asn His	
135 140 145	
ttc att gag ttg tgt ctt gat gag ttg gat cgc gtg tgg atg ttt ttg	595
Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg Val Trp Met Phe Leu	
150 155 160 165	
cac tct ggc tcc cgc ggc gtg ggc aac aag att gcc cag aag cac atc	643
His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile Ala Gln Lys His Ile	
170 175 180	
aag atc ggc cag gcc gag tgt aag aat gag gag ctt ccc gat aag gat	691
Lys Ile Ala Gln Ala Glu Cys Lys Asn Glu Glu Leu Pro Asp Lys Asp	
185 190 195	
ctt ggc tac ttg acc gag ggc act gag gag ttt gag tct tac atc aag	739
Leu Ala Tyr Leu Thr Glu Gly Thr Glu Glu Phe Glu Ser Tyr Ile Lys	
200 205 210	
gaa ctg aat tgg ggc cag cgt ttt ggc ttc ctc aac agg gaa gaa atg	787
Glu Leu Asn Trp Ala Gln Arg Phe Ala Phe Leu Asn Arg Glu Glu Met	
215 220 225	
atg gac aga ttc gca cgc gag ctg ggc ttt ttc gtc gac aag cag ctt	835
Met Asp Arg Phe Ala Arg Glu Leu Gly Phe Phe Val Asp Lys Gln Leu	
230 235 240 245	
gaa gag gtc gag cgc atc aac tgc cac cat aac tac acg gtc cag gag	883
Glu Glu Val Glu Arg Ile Asn Cys His His Asn Tyr Thr Val Gln Glu	
250 255 260	
gag cac tac ggc gag acc att tgg ctc acc cgt aag ggc gcc gtg ttg	931
Glu His Tyr Gly Glu Thr Ile Trp Leu Thr Arg Lys Gly Ala Val Leu	
265 270 275	
ggc gac gaa ggc acg ccg ggc ttg att ccg ggc tcg atg ggc acc ggc	979
Ala Asp Glu Gly Thr Pro Ala Leu Ile Pro Gly Ser Met Gly Thr Ala	
280 285 290	
tcg tac gtg ggc agt ggc aag ggc aac gcc gag gca ctg cgc tcg ggc	1027

Ser Tyr Val Gly Ser Gly Lys Gly Asn Ala Glu Ala Leu Arg Ser Ala
 295 300 305
 ccg cat ggg gcg ggc cgg agg atg tcg cgc aac cag gct aaa aag cgc 1075
 Pro His Gly Ala Gly Arg Arg Met Ser Arg Asn Gln Ala Lys Lys Arg 325
 310 315 320
 ttc tcg acg gcc gac ctg gat tct cgg atg gcg ggc atc gtc tac cgg 1123
 Phe Ser Thr Ala Asp Leu Asp Ser Arg Met Ala Gly Ile Val Tyr Arg 340
 330 335
 ccc ggc aag gag tgg atc gat gaa att ccc gac gct tac aaa gac atc 1171
 Pro Gly Lys Glu Trp Ile Asp Glu Ile Pro Asp Ala Tyr Lys Asp Ile 355
 345 350
 gat cag gtg atg gcc gat gct gcc gat ttg gtg aca att cgc cat aaa 1219
 Asp Gln Val Met Ala Asp Ala Ala Asp Leu Val Thr Ile Arg His Lys 370
 360 365
 ttg cgc cag atc gtc aac gtg aaa ggc acc taaagcgcac tacggtaaag tgc 1272
 Leu Arg Gln Ile Val Asn Val Lys Gly Thr 380
 375 380

<210> 452

<211> 383

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 452

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 20 25 30
 Ala Leu Met Pro Asp Ala His Phe Gly Leu Gly Ser Ser Val Gly Thr
 35 40 45
 Val Phe Gly Thr Lys Gly Ala Ile Ile Pro Ala Ala Val Gly Val Asp
 50 55 60
 Ile Gly Cys Gly Met Ile Gly Val Cys Thr Asn Tyr Thr Ala Ser Asp
 65 70 75 80
 Leu Glu Gly Arg Asp Leu Val Thr Leu Arg Asp Tyr Ile Glu Arg Val
 85 90 95
 Ile Pro Leu Ser Pro Gly Asn Tyr Asn Ser Thr Thr Leu Lys Glu Thr
 100 105 110
 Ala Lys Val Lys Val Ala Glu Leu Glu Glu Leu Ala Glu Arg Asp Gly
 115 120 125
 Val Asp Leu Ser His Ser Pro Thr Trp Lys Arg Gln Leu Gly Ser Leu
 130 135 140
 Gly Gly Gly Asn His Phe Ile Glu Leu Cys Leu Asp Glu Leu Asp Arg
 145 150 155 160
 Val Trp Met Phe Leu His Ser Gly Ser Arg Gly Val Gly Asn Lys Ile

165										170					175				
Ala	Gln	Lys	His	Ile	Lys	Ile	Ala	Gln	Ala	Glu	Cys	Lys	Asn	Glu	Glu				
			180					185					190						
Leu	Pro	Asp	Lys	Asp	Leu	Ala	Tyr	Leu	Thr	Glu	Gly	Thr	Glu	Glu	Phe				
		195					200					205							
Glu	Ser	Tyr	Ile	Lys	Glu	Leu	Asn	Trp	Ala	Gln	Arg	Phe	Ala	Phe	Leu				
	210					215					220								
Asn	Arg	Glu	Glu	Met	Met	Asp	Arg	Phe	Ala	Arg	Glu	Leu	Gly	Phe	Phe				
225				230					235						240				
Val	Asp	Lys	Gln	Leu	Glu	Glu	Val	Glu	Arg	Ile	Asn	Cys	His	His	Asn				
			245					250					255						
Tyr	Thr	Val	Gln	Glu	Glu	His	Tyr	Gly	Glu	Thr	Ile	Trp	Leu	Thr	Arg				
		260						265					270						
Lys	Gly	Ala	Val	Leu	Ala	Asp	Glu	Gly	Thr	Pro	Ala	Leu	Ile	Pro	Gly				
	275						280					285							
Ser	Met	Gly	Thr	Ala	Ser	Tyr	Val	Gly	Ser	Gly	Lys	Gly	Asn	Ala	Glu				
	290					295					300								
Ala	Leu	Arg	Ser	Ala	Pro	His	Gly	Ala	Gly	Arg	Arg	Met	Ser	Arg	Asn				
305					310				315						320				
Gln	Ala	Lys	Lys	Arg	Phe	Ser	Thr	Ala	Asp	Leu	Asp	Ser	Arg	Met	Ala				
			325					330					335						
Gly	Ile	Val	Tyr	Arg	Pro	Gly	Lys	Glu	Trp	Ile	Asp	Glu	Ile	Pro	Asp				
		340					345					350							
Ala	Tyr	Lys	Asp	Ile	Asp	Gln	Val	Met	Ala	Asp	Ala	Ala	Asp	Leu	Val				
	355					360					365								
Thr	Ile	Arg	His	Lys	Leu	Arg	Gln	Ile	Val	Asn	Val	Lys	Gly	Thr					
	370					375					380								

<210> 453

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS00671

<400> 453

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taccgacgtc	aaatagcgg	cgctactcaa	ggagagttca	atg	ctc	att	tca	cag	115
				Met	Leu	Ile	Ser	Gln	
				1				5	

cgc	cca	acc	atc	acc	gag	gaa	ttt	gtt	aat	aac	gca	cgt	tcc	cgg	ttt	163
Arg	Pro	Thr	Ile	Thr	Glu	Glu	Phe	Val	Asn	Asn	Ala	Arg	Ser	Arg	Phe	

				10					15					20		
gtc	atc	gag	cca	ctg	gag	cca	ggt	ttt	ggc	tac	acc	ctc	ggt	aac	tcc	211
Val	Ile	Glu	Pro	Leu	Glu	Pro	Gly	Phe	Gly	Tyr	Thr	Leu	Gly	Asn	Ser	
				25					30					35		
ctg	cgc	cgt	acc	ctg	ctg	tcc	tcc	att	cct	gga	gca	gca	gta	acc	agc	259
Leu	Arg	Arg	Thr	Leu	Leu	Ser	Ser	Ile	Pro	Gly	Ala	Ala	Val	Thr	Ser	
				40					45					50		
gtc	aag	att	gac	ggt	gta	ctc	cac	gag	ttc	acc	acc	atc	agc	ggt	gtt	307
Val	Lys	Ile	Asp	Gly	Val	Leu	His	Glu	Phe	Thr	Thr	Ile	Ser	Gly	Val	
				55					60					65		
aag	gaa	gat	gtc	tct	gac	atc	atc	ttg	aac	atc	aag	gga	ttg	gtt	ttg	355
Lys	Glu	Asp	Val	Ser	Asp	Ile	Ile	Leu	Asn	Ile	Lys	Gly	Leu	Val	Leu	
				70					75					80		
tct	tct	gat	tcc	gat	gag	cca	gtt	gtt	atg	cag	ctg	gtc	aag	gaa	ggc	403
Ser	Ser	Asp	Ser	Asp	Glu	Pro	Val	Val	Met	Gln	Leu	Val	Lys	Glu	Gly	
				90					95					100		
cca	gga	gtt	gta	act	gca	ggt	gac	att	cag	cca	cca	gca	ggc	gtg	gag	451
Pro	Gly	Val	Val	Thr	Ala	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Gly	Val	Glu	
				105					110					115		
atc	cac	aac	ccg	gat	ctg	cac	att	gca	acc	ctg	aac	gag	acc	gcc	aag	499
Ile	His	Asn	Pro	Asp	Leu	His	Ile	Ala	Thr	Leu	Asn	Glu	Thr	Ala	Lys	
				120					125					130		
att	gag	atc	gag	ctc	atc	gtc	gag	cgt	gga	cgt	ggc	tac	gtt	ccc	gca	547
Ile	Glu	Ile	Glu	Leu	Ile	Val	Glu	Arg	Gly	Arg	Gly	Tyr	Val	Pro	Ala	
				135					140					145		
act	gtt	act	gca	acc	ggt	gga	gag	atc	ggc	cgc	att	ccg	gtc	gat	cag	595
Thr	Val	Thr	Ala	Thr	Gly	Gly	Glu	Ile	Gly	Arg	Ile	Pro	Val	Asp	Gln	
				150					155					160		
atc	tac	tcc	cca	gta	ctg	aag	gtc	agc	tac	aag	gtt	gaa	gct	act	cgt	643
Ile	Tyr	Ser	Pro	Val	Leu	Lys	Val	Ser	Tyr	Lys	Val	Glu	Ala	Thr	Arg	
				170					175					180		
gtt	gag	cag	cgc	acc	gac	ttt	gac	aag	ctg	gtc	atc	gac	gtt	gag	acc	691
Val	Glu	Gln	Arg	Thr	Asp	Phe	Asp	Lys	Leu	Val	Ile	Asp	Val	Glu	Thr	
				185					190					195		
aag	aac	tct	att	acc	gca	cgt	gac	gcc	ctg	gcg	tcg	gca	ggt	aag	acc	739
Lys	Asn	Ser	Ile	Thr	Ala	Arg	Asp	Ala	Leu	Ala	Ser	Ala	Gly	Lys	Thr	
				200					205					210		
ctg	gtt	gag	ctg	ttc	ggc	ctc	gca	cgc	gag	ctg	aac	atc	gca	gcc	gag	787
Leu	Val	Glu	Leu	Phe	Gly	Leu	Ala	Arg	Glu	Leu	Asn	Ile	Ala	Ala	Glu	
				215					220					225		
ggc	atc	gag	atc	gga	cca	tct	cct	cag	gag	acc	gag	tac	atc	gct	gcc	835
Gly	Ile	Glu	Ile	Gly	Pro	Ser	Pro	Gln	Glu	Thr	Glu	Tyr	Ile	Ala	Ala	
				230					235					240		
tac	agc	atg	cca	atc	gag	gat	ctg	gac	ttc	tct	gtc	cgt	tcc	tac	aac	883
Tyr	Ser	Met	Pro	Ile	Glu	Asp	Leu	Asp	Phe	Ser	Val	Arg	Ser	Tyr	Asn	
				250					255					260		

tgc ctc aag cgc gaa gac atc cac acc gtg ggt gaa ctc gca gag cgc 931
 Cys Leu Lys Arg Glu Asp Ile His Thr Val Gly Glu Leu Ala Glu Arg
 265 270 275

 gct gag tcc gat ttg ctg gat atc cgc aac ttc gga cag aag tcg atc 979
 Ala Glu Ser Asp Leu Leu Asp Ile Arg Asn Phe Gly Gln Lys Ser Ile
 280 285 290

 aac gag gta aag atc aag ctt gct ggc ctg ggt ctg acc ctg aag gat 1027
 Asn Glu Val Lys Ile Lys Leu Ala Gly Leu Gly Leu Thr Leu Lys Asp
 295 300 305

 gct cct gaa gac ttc gat cct tca act ctt gaa ggt tat gac gcc gaa 1075
 Ala Pro Glu Asp Phe Asp Pro Ser Thr Leu Glu Gly Tyr Asp Ala Glu
 310 315 320 325

 act ggt ggc tac atc gat gtc gag gcg gaa gat tcc gag taagtcgcat 1124
 Thr Gly Gly Tyr Ile Asp Val Glu Ala Glu Asp Ser Glu
 330 335

 ggtccaattc atg 1137

<210> 454
 <211> 338
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 454
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 Ala Arg Ser Arg Phe Val Ile Glu Pro Leu Glu Pro Gly Phe Gly Tyr
 20 25 30

 Thr Leu Gly Asn Ser Leu Arg Arg Thr Leu Leu Ser Ser Ile Pro Gly
 35 40 45

 Ala Ala Val Thr Ser Val Lys Ile Asp Gly Val Leu His Glu Phe Thr
 50 55 60

 Thr Ile Ser Gly Val Lys Glu Asp Val Ser Asp Ile Ile Leu Asn Ile
 65 70 75 80

 Lys Gly Leu Val Leu Ser Ser Asp Ser Asp Glu Pro Val Val Met Gln
 85 90 95

 Leu Val Lys Glu Gly Pro Gly Val Val Thr Ala Gly Asp Ile Gln Pro
 100 105 110

 Pro Ala Gly Val Glu Ile His Asn Pro Asp Leu His Ile Ala Thr Leu
 115 120 125

 Asn Glu Thr Ala Lys Ile Glu Ile Glu Leu Ile Val Glu Arg Gly Arg
 130 135 140

 Gly Tyr Val Pro Ala Thr Val Thr Ala Thr Gly Gly Glu Ile Gly Arg
 145 150 155 160

 Ile Pro Val Asp Gln Ile Tyr Ser Pro Val Leu Lys Val Ser Tyr Lys

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<210> 455
<211> 1077
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1054)
<223> RXS02760
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40 45 50	
gaa gaa gag acc cta gat gct cca gaa gaa gcc gca gaa gaa gct cct	307
Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala Ala Glu Glu Ala Pro	
55 60 65	
gct gct gca gag tcc gaa gct cca gta gaa gag gac gaa gag gct gac	355
Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu Asp Glu Glu Ala Asp	
70 75 80 85	
agc ctt gct cag gcg gct gct gca ctt ggt gac acc gat gag cag gac	403
Ser Leu Ala Gln Ala Ala Ala Leu Gly Asp Thr Asp Glu Gln Asp	
90 95 100	
gcg gat gca gag tac aag gct cgt ctg cgt aag ttc act cgt gag ctg	451
Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys Phe Thr Arg Glu Leu	
105 110 115	
aag aag cag cct ggt gtt tgg tac atc att cag tgc tac tcc ggc tac	499
Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln Cys Tyr Ser Gly Tyr	
120 125 130	
gag aac aag gtg aag gcg aac ctt gac atg cgt gct cag acc ctt gag	547
Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg Ala Gln Thr Leu Glu	
135 140 145	
gtt gag gat gac atc ttt gag gtt gtt gtt cct atc gag cag gtc act	595
Val Glu Asp Asp Ile Phe Glu Val Val Val Pro Ile Glu Gln Val Thr	
150 155 160 165	
gag atc cgt gat ggt aag cgc aag ctg gtt aag cgt aag ttg ctg ccg	643
Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys Arg Lys Leu Leu Pro	
170 175 180	
ggc tac gtt ttg gtc cgc atg gac atg aat gac cgc gtg tgg tct gtt	691
Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp Arg Val Trp Ser Val	
185 190 195	
gtt cgc gat aca cct ggt gtg acc agc ttt gtg ggt aac gag ggc aat	739
Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val Gly Asn Glu Gly Asn	
200 205 210	
gca act cct gtg aag cac cgc gat gtt gcg aag ttc ttg atg cct cag	787
Ala Thr Pro Val Lys His Arg Asp Val Ala Lys Phe Leu Met Pro Gln	
215 220 225	
gag cag gct gtt gtc acc ggt gag gct gct gct gcg gct gcc gag ggt	835
Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala Ala Ala Ala Glu Gly	
230 235 240 245	
gag cag gtt gtg gct atg cct acc gat acc aag aag cct cag gtt gct	883
Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys Lys Pro Gln Val Ala	
250 255 260	
gtg gac ttc act gtt ggt gag gct gtg acc att ctg act ggt gct ttc	931
Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile Leu Thr Gly Ala Phe	
265 270 275	
gct tct gtt tct gca acg att tct tct atc gat cct gag ctg cag aag	979

Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp Pro Glu Leu Gln Lys
 280 285 290

ctg gaa gtt ttg gtg tcc atc ttt ggt cgt gaa act cct gtt gat ctc 1027
 Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu Thr Pro Val Asp Leu
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 Ser Phe Asp Gln Val Glu Lys Val Ser
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<211> 318

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<213> Corynebacterium glutamicum

<400> 456

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Phe Gly Ala Ser Phe Ser Asp Glu Phe Ala Asp Asp Asp Phe Asp Ala
 20 25 30

Glu Ala Asp Val Glu Ala Asp Ala Ala Ala Glu Ala Ser Ala Leu Glu
 35 40 45

Ala Glu Gln Asp Leu Glu Glu Glu Thr Leu Asp Ala Pro Glu Glu Ala
 50 55 60

Ala Glu Glu Ala Pro Ala Ala Ala Glu Ser Glu Ala Pro Val Glu Glu
 65 70 75 80

Asp Glu Glu Ala Asp Ser Leu Ala Gln Ala Ala Ala Ala Leu Gly Asp
 85 90 95

Thr Asp Glu Gln Asp Ala Asp Ala Glu Tyr Lys Ala Arg Leu Arg Lys
 100 105 110

Phe Thr Arg Glu Leu Lys Lys Gln Pro Gly Val Trp Tyr Ile Ile Gln
 115 120 125

Cys Tyr Ser Gly Tyr Glu Asn Lys Val Lys Ala Asn Leu Asp Met Arg
 130 135 140

Ala Gln Thr Leu Glu Val Glu Asp Asp Ile Phe Glu Val Val Val Pro
 145 150 155 160

Ile Glu Gln Val Thr Glu Ile Arg Asp Gly Lys Arg Lys Leu Val Lys
 165 170 175

Arg Lys Leu Leu Pro Gly Tyr Val Leu Val Arg Met Asp Met Asn Asp
 180 185 190

Arg Val Trp Ser Val Val Arg Asp Thr Pro Gly Val Thr Ser Phe Val
 195 200 205

Gly Asn Glu Gly Asn Ala Thr Pro Val Lys His Arg Asp Val Ala Lys
 210 215 220

Phe Leu Met Pro Gln Glu Gln Ala Val Val Thr Gly Glu Ala Ala Ala

225		230		235		240
Ala Ala Ala Glu Gly Glu Gln Val Val Ala Met Pro Thr Asp Thr Lys						
	245			250		255
Lys Pro Gln Val Ala Val Asp Phe Thr Val Gly Glu Ala Val Thr Ile						
	260			265		270
Leu Thr Gly Ala Phe Ala Ser Val Ser Ala Thr Ile Ser Ser Ile Asp						
	275			280		285
Pro Glu Leu Gln Lys Leu Glu Val Leu Val Ser Ile Phe Gly Arg Glu						
	290			295		300
Thr Pro Val Asp Leu Ser Phe Asp Gln Val Glu Lys Val Ser						
305		310		315		

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<211> 662

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(648)

<223> RXS02830

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cgc ggg ctg gcg ctg aca ggg gcg ggc gat cag ctt ttg tcg cag gcg	96
Arg Gly Leu Ala Leu Thr Gly Ala Gly Asp Gln Leu Leu Ser Gln Ala	
20 25 30	
cgc cgc ctg atc gcc ctg aac gac gag gta tac gcc cgc ttg aac gcc	144
Arg Arg Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala	
35 40 45	
ggt gcc tac gag ggc gag gtg acg ctg ggc gtg cct caa gac gtg atc	192
Gly Ala Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile	
50 55 60	
tac ccc gtc atc ccg cgc gtc ttg cag caa ttc gcc cgc gat ttt ccc	240
Tyr Pro Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro	
65 70 75 80	
cgc gtg caa att cac ctg atc tcg aac ttc acg ctg atg ctg aaa gaa	288
Arg Val Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu	
85 90 95	
cag ttc cgc cgc ggc gaa atc gac gtg atg ctg acg acc gag gac gag	336
Gln Phe Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu	
100 105 110	
ctg ggc gag ggc ggc gag acg ctg gcc cag cgc gag ctg atc tgg gtc	384
Leu Gly Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val	
115 120 125	

ggc gca ccg ggc ggg tcg gcg tgg acc cgc agg ccg ctg ccc ttg gcg 432
 Gly Ala Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala
 130 135 140

ttt gaa cgc gcc tgc att ttc cgg tct ttc gtg cag cgc cgc ttg gat 480
 Phe Glu Arg Ala Cys Ile Phe Arg Ser Phe Val Gln Arg Arg Leu Asp
 145 150 155 160

gcc aac agc atc gat tgg cag atg gtg gtc agc agc gaa tcc aca cgg 528
 Ala Asn Ser Ile Asp Trp Gln Met Val Val Ser Ser Glu Ser Thr Arg
 165 170 175

aca att gaa gcg acc gtc agt gcc gat ctg gcg gtg cat acc tat atc 576
 Thr Ile Glu Ala Thr Val Ser Ala Asp Leu Ala Val His Thr Tyr Ile
 180 185 190

gag ggg gcc gag ccg gcg cac ctc gag cgt att gcc aca acg gcg ccc 624
 Glu Gly Ala Glu Pro Ala His Leu Glu Arg Ile Ala Thr Thr Ala Pro
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 Cys Arg Asn Tyr Val Phe Gln His
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<210> 458

<211> 216

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<213> *Corynebacterium glutamicum*

<400> 458

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Arg Arg Leu Ile Ala Leu Asn Asp Glu Val Tyr Ala Arg Leu Asn Ala
 35 40 45

Gly Ala Tyr Glu Gly Glu Val Thr Leu Gly Val Pro Gln Asp Val Ile
 50 55 60

Tyr Pro Val Ile Pro Arg Val Leu Gln Gln Phe Ala Arg Asp Phe Pro
 65 70 75 80

Arg Val Gln Ile His Leu Ile Ser Asn Phe Thr Leu Met Leu Lys Glu
 85 90 95

Gln Phe Arg Arg Gly Glu Ile Asp Val Met Leu Thr Thr Glu Asp Glu
 100 105 110

Leu Gly Glu Gly Gly Glu Thr Leu Ala Gln Arg Glu Leu Ile Trp Val
 115 120 125

Gly Ala Pro Gly Gly Ser Ala Trp Thr Arg Arg Pro Leu Pro Leu Ala
 130 135 140

Phe Glu Arg Ala Cys Ile Phe Arg Ser Phe Val Gln Arg Arg Leu Asp
 145 150 155 160

Ala Asn Ser Ile Asp Trp Gln Met Val Val Ser Ser Glu Ser Thr Arg
 165 170 175

Thr Ile Glu Ala Thr Val Ser Ala Asp Leu Ala Val His Thr Tyr Ile
 180 185 190

Glu Gly Ala Glu Pro Ala His Leu Glu Arg Ile Ala Thr Thr Ala Pro
 195 200 205

Cys Arg Asn Tyr Val Phe Gln His
 210 215

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 <213> Corynebacterium glutamicum

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 Met Thr Ala Pro Ser
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acg cag gat ctc gca acg act gaa cgt gag gta gat ccc ggc agc aga 163
 Thr Gln Asp Leu Ala Thr Thr Glu Arg Glu Val Asp Pro Gly Ser Arg
 10 15 20

agg ggc caa acc aac gac aat ccc tcg cag gac ctt gtt cgc gtt tac 211
 Arg Gly Gln Thr Asn Asp Asn Pro Ser Gln Asp Leu Val Arg Val Tyr
 25 30 35

ctc aac ggc atc ggc aaa act gcc ttg ctt acc gcg gag gat gaa gtt 259
 Leu Asn Gly Ile Gly Lys Thr Ala Leu Leu Thr Ala Glu Asp Glu Val
 40 45 50

gag ctc gca cag acc att gag gtt ggc ctt tat gca gag cac ctt ctg 307
 Glu Leu Ala Gln Thr Ile Glu Val Gly Leu Tyr Ala Glu His Leu Leu
 55 60 65

aaa aac tct gaa gag cca ctc acc cgc gcc atg aag cgc gat cta aag 355
 Lys Asn Ser Glu Glu Pro Leu Thr Arg Ala Met Lys Arg Asp Leu Lys
 70 75 80 85

gtt ctt gcc aag gac ggc aag aag gct cgt tcc cac ctc ctc gag gca 403
 Val Leu Ala Lys Asp Gly Lys Lys Ala Arg Ser His Leu Leu Glu Ala
 90 95 100

aac ctg cgc ctg gtg gtg tcc ctt gct aag cgc tac acc ggc cgc ggc 451
 Asn Leu Arg Leu Val Val Ser Leu Ala Lys Arg Tyr Thr Gly Arg Gly
 105 110 115

atg cca ctg ctg gat ctt atc cag gag ggc aac ctc gga ctg atc cgc 499
 Met Pro Leu Leu Asp Leu Ile Gln Glu Gly Asn Leu Gly Leu Ile Arg
 120 125 130

gcg atg gaa aag ttt gat tac tcc aag ggc ttt aag ttc tcc acc tac 547
Ala Met Glu Lys Phe Asp Tyr Ser Lys Gly Phe Lys Phe Ser Thr Tyr
135 140 145

gca acc tgg tgg atc cgc cag gca atc acc cgc ggc atg gca gat cag 595
Ala Thr Trp Trp Ile Arg Gln Ala Ile Thr Arg Gly Met Ala Asp Gln
150 155 160 165

tcc cgc acc atc cgc ctc cca gtc cac ctt gtg gag cag gtg aac aag 643
Ser Arg Thr Ile Arg Leu Pro Val His Leu Val Glu Gln Val Asn Lys
170 175 180

ctt tcc cgc atc aag cgc gag ttg tac cag cac ttg ggc cgt gaa gcc 691
Leu Ser Arg Ile Lys Arg Glu Leu Tyr Gln His Leu Gly Arg Glu Ala
185 190 195

acc aat gag gaa ctc gca gaa gag tcc ggc att gaa gag tcc aag att 739
Thr Asn Glu Glu Leu Ala Glu Glu Ser Gly Ile Glu Glu Ser Lys Ile
200 205 210

gaa atg ctg ctt cgt cag tct cgc gat cca gtg agc ttg gac atg cca 787
Glu Met Leu Leu Arg Gln Ser Arg Asp Pro Val Ser Leu Asp Met Pro
215 220 225

gtc ggc gcc gat gaa gaa gct cct ttg ggt gac ttc att gag gat tct 835
Val Gly Ala Asp Glu Glu Ala Pro Leu Gly Asp Phe Ile Glu Asp Ser
230 235 240 245

gag gcc acc gat gca gaa tcc gca gtg gtt gct tcc atg cgc cac tcc 883
Glu Ala Thr Asp Ala Glu Ser Ala Val Val Ala Ser Met Arg His Ser
250 255 260

gat atc cgc gcg gtc ctt aac act ctc gag cca cgc gag cag gat gtc 931
Asp Ile Arg Ala Val Leu Asn Thr Leu Glu Pro Arg Glu Gln Asp Val
265 270 275

atc cgt ttg cgc tac ggc ctc gat gac ggt gtg cca cgc acc ctt gat 979
Ile Arg Leu Arg Tyr Gly Leu Asp Asp Gly Val Pro Arg Thr Leu Asp
280 285 290

cag att ggt cgc cgc ttc gga ctg tcc cgt gag cgc gtc cgc cag ata 1027
Gln Ile Gly Arg Arg Phe Gly Leu Ser Arg Glu Arg Val Arg Gln Ile
295 300 305

gag cgt gaa gtc atg agt aag ctc cgc gat gga gag cgc gca tca cgt 1075
Glu Arg Glu Val Met Ser Lys Leu Arg Asp Gly Glu Arg Ala Ser Arg
310 315 320 325

ctt cgt gag tac gcc cag taaaagcgtg aactaacaat cgaagcgtcg 1123
Leu Arg Glu Tyr Ala Gln
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<211> 331

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

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		Thr	Asn
		25	Asp
			Asn
			Pro
			Ser
			30
Leu	Val	Arg	Val
	35	Tyr	Leu
		Asn	Gly
		40	Ile
			Gly
			Lys
			Thr
			45
Ala	Glu	Asp	Glu
	50	Val	Glu
		Leu	Ala
		55	Gln
			Thr
			Ile
			Glu
			60
Ala	Glu	His	Leu
	65	Leu	Lys
		70	Asn
			Ser
			Glu
			Glu
			75
			Pro
			Leu
			Thr
			Arg
			Ala
			Met
			80
Lys	Arg	Asp	Leu
		85	Lys
			Val
			Leu
			Ala
			Lys
			90
			Asp
			Gly
			Lys
			Lys
			Ala
			Arg
			95
His	Leu	Leu	Glu
			100
			Ala
			Asn
			Leu
			Arg
			105
			Leu
			Val
			Val
			Ser
			Leu
			Ala
			Lys
			Arg
			110
Tyr	Thr	Gly	Arg
		115	Gly
			Met
			Pro
			Leu
			120
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			Asp
			Leu
			Ile
			Gln
			125
			Glu
			Gly
			Asn
Leu	Gly	Leu	Ile
	130	Arg	Ala
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			135
			Glu
			Lys
			Phe
			Asp
			Tyr
			140
			Ser
			Lys
			Gly
			Phe
Lys	Phe	Ser	Thr
	145	Tyr	Ala
			150
			Thr
			Trp
			Trp
			Ile
			Arg
			Gln
			Ala
			Ile
			Thr
			Arg
			160
Gly	Met	Ala	Asp
			Gln
			165
			Ser
			Arg
			Thr
			Ile
			Arg
			170
			Leu
			Pro
			Val
			His
			Leu
			Val
			175
Glu	Gln	Val	Asn
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			Lys
			Leu
			Ser
			Arg
			Ile
			185
			Lys
			Arg
			Glu
			Leu
			Tyr
			Gln
			His
			190
Leu	Gly	Arg	Glu
			195
			Ala
			Thr
			Asn
			Glu
			200
			Glu
			Leu
			Ala
			Glu
			205
Glu	Glu	Ser	Lys
			210
			Ile
			Glu
			Met
			215
			Leu
			Leu
			Arg
			Gln
			220
			Ser
			Arg
			Asp
			Pro
			Val
Ser	Leu	Asp	Met
			225
			Pro
			Val
			Gly
			Ala
			Asp
			Glu
			230
			Ala
			Asp
			Glu
			235
			Ala
			Pro
			Leu
			Gly
			240
Phe	Ile	Glu	Asp
			245
			Ser
			Glu
			Ala
			Thr
			Asp
			Ala
			250
			Glu
			Ser
			Ala
			Val
			Val
			Ala
			255
Ser	Met	Arg	His
			260
			Ser
			Asp
			Ile
			Arg
			Ala
			265
			Val
			Leu
			Asn
			Thr
			Leu
			Glu
			Pro
			270
Arg	Glu	Gln	Asp
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			Val
			Ile
			Arg
			Leu
			280
			Arg
			Tyr
			Gly
			Leu
			Asp
			285
			Asp
			Gly
			Val
Pro	Arg	Thr	Leu
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			Asp
			Gln
			Ile
			Gly
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			Arg
			Arg
			Phe
			Gly
			300
			Leu
			Ser
			Arg
			Glu
Arg	Val	Arg	Gln
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			Ile
			Glu
			Arg
			Glu
			Val
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			315
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			Leu
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			Asp
			Gly
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			Ala
			Gln
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Val Val Arg Tyr Val 5																
aaa ttt tcc cgc act gct aac aga gga gtc cac atc agc gct gaa gct 163																
Lys Phe Ser Arg Thr Ala Asn Arg Gly Val His Ile Ser Ala Glu Ala 20																
cgc att aat gag cgc atc cga gtt ccc gaa gtc cgc ctt gtc gga cct 211																
Arg Ile Asn Glu Arg Ile Arg Val Pro Glu Val Arg Leu Val Gly Pro 35																
aac ggt gag caa gta ggc atc gtc cgt atc gaa gat gcc cgc aag ctc 259																
Asn Gly Glu Gln Val Gly Ile Val Arg Ile Glu Asp Ala Arg Lys Leu 50																
gca ttc gac gca gac cta gac ctg gtc gag gtc gca ccc aac gcc aaa 307																
Ala Phe Asp Ala Asp Leu Asp Leu Val Glu Val Ala Pro Asn Ala Lys 65																
cct cca gtc tgc aag atc atg gac tac gga aag ttc aag tac gaa gcg 355																
Pro Pro Val Cys Lys Ile Met Asp Tyr Gly Lys Phe Lys Tyr Glu Ala 85																
gcc caa aag gct cgt gag tca cgc aag aat cag cag cag acc gtg gtc 403																
Ala Gln Lys Ala Arg Glu Ser Arg Lys Asn Gln Gln Gln Thr Val Val 100																
aaa gag caa aag ctt cgt ccc aag atc gat gat cat gat tat gag acg 451																
Lys Glu Gln Lys Leu Arg Pro Lys Ile Asp Asp His Asp Tyr Glu Thr 115																
aag aag aac aat gtg atc cga ttc ctt gaa aag gga tca aag gtc aaa 499																
Lys Lys Asn Asn Val Ile Arg Phe Leu Glu Lys Gly Ser Lys Val Lys 120																
gtc acg atc atg ttc cgt ggt cgt gag cag gct cgc cca gag ctt ggc 547																
Val Thr Ile Met Phe Arg Gly Arg Glu Gln Ala Arg Pro Glu Leu Gly 145																
tac agg ctc ctc gag cga ctg gca aac gat gtc gta gat ttt ggc atc 595																
Tyr Arg Leu Leu Glu Arg Leu Ala Asn Asp Val Val Asp Phe Gly Ile 165																
gtg gaa acccgc gca aag cag gac gga cga aac atg aca atg gtt ctc 643																
Val Glu Thr Arg Ala Lys Gln Asp Gly Arg Asn Met Thr Met Val Leu																

170 175 180 690

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 Gly Pro Val Arg Lys Gly Lys Lys
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<210> 462
 <211> 189
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 462

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			20					25					30		
Arg	Leu	Val	Gly	Pro	Asn	Gly	Glu	Gln	Val	Gly	Ile	Val	Arg	Ile	Glu
		35					40					45			
Asp	Ala	Arg	Lys	Leu	Ala	Phe	Asp	Ala	Asp	Leu	Asp	Leu	Val	Glu	Val
	50					55						60			
Ala	Pro	Asn	Ala	Lys	Pro	Pro	Val	Cys	Lys	Ile	Met	Asp	Tyr	Gly	Lys
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Phe	Lys	Tyr	Glu	Ala	Ala	Gln	Lys	Ala	Arg	Glu	Ser	Arg	Lys	Asn	Gln
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Gln	Gln	Thr	Val	Val	Lys	Glu	Gln	Lys	Leu	Arg	Pro	Lys	Ile	Asp	Asp
			100					105					110		
His	Asp	Tyr	Glu	Thr	Lys	Lys	Asn	Asn	Val	Ile	Arg	Phe	Leu	Glu	Lys
		115					120					125			
Gly	Ser	Lys	Val	Lys	Val	Thr	Ile	Met	Phe	Arg	Gly	Arg	Glu	Gln	Ala
		130				135					140				
Arg	Pro	Glu	Leu	Gly	Tyr	Arg	Leu	Leu	Glu	Arg	Leu	Ala	Asn	Asp	Val
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Val	Asp	Phe	Gly	Ile	Val	Glu	Thr	Arg	Ala	Lys	Gln	Asp	Gly	Arg	Asn
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Val Pro Gly Lys Leu																5
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Arg Val His Glu Leu Ala Lys Gln Leu Gly Ile Thr Ser Lys Glu Leu																20
ctt gcc acc ctt aag gat aaa ggc gag ttt gtt aaa acc gca tca tcc																211
Leu Ala Thr Leu Lys Asp Lys Gly Glu Phe Val Lys Thr Ala Ser Ser																35
aca att gaa ccc cca gtt gtg aag agg atg cag gag cac tac ggt tcg																259
Thr Ile Glu Pro Pro Val Val Lys Arg Met Gln Glu His Tyr Gly Ser																40
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Ser Gly Ser Asp Lys Ser Asp Thr Ala Ala Lys Pro Ala Ala Ala Lys																55
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Pro Ala Ala Pro Lys Pro Ala Ala Ser Ala Ala Pro Lys Pro Gly Ala																70
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Pro Ala Lys Pro Ala Ala Pro Ala Ala Lys Pro Ala Pro Ala Ala Pro																90
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Ser Ala Ala Ser Ala Ala Lys Pro Gly Ala Ala Pro Lys Pro Gly Val																105
cag gca aag cct gca gca gcc gct aag cca ggc gct cca gca aag cca																499
Gln Ala Lys Pro Ala Ala Ala Ala Lys Pro Pro Gly Ala Pro Ala Lys Pro																120
gca gca cct gca gct cct tct gcc gct aag tca ggt tca gct tca aag																547
Ala Ala Pro Ala Ala Pro Ser Ala Ala Lys Ser Gly Ser Ala Ser Lys																135
cct gca gca gca gct aag cca gca ttt tct ggc cca act cca ggc gat																595
Pro Ala Ala Ala Ala Lys Pro Ala Phe Ser Gly Pro Thr Pro Gly Asp																150
gca tct aag aag gca gag cca gca gct aag cca ggc gcg gaa gca cct																643
Ala Ser Lys Lys Ala Glu Pro Ala Ala Lys Pro Gly Ala Glu Ala Pro																170
cgc cca ggc ggc atg cca cgt cca atg ggc aag cct gct cca aag cca																691
Arg Pro Gly Met Pro Arg Pro Met Gly Lys Pro Ala Pro Lys Pro																185
ggc gca cgt gca cca cgt gta gct aac aac cca ttc tcc acc ggt ggt																739
Gly Ala Arg Ala Pro Arg Val Ala Asn Asn Pro Phe Ser Thr Gly Gly																200
ggc gag cgt cca gct cct cgc cca ggt ggc ggc cca cgt cct ggt ggc																787
Gly Glu Arg Pro Ala Pro Arg Pro Gly Gly Gly Pro Arg Pro Gly Gly																215

gga cct cgc cca ggc ggt gga cca cgt cca cag ggc cag ggt cgt cca	835
Gly Pro Arg Pro Gly Gly Gly Pro Arg Pro Gln Gly Gln Gly Arg Pro	
230 235 240 245	
ggt ggc cag cga gat ggt cag cgc gac gga cag cgt gat ggt cag ggt	883
Gly Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln Gly	
250 255 260	
aac cgc ggc ggt cag cgt caa ggc gct ggc gca ggt gga cca cgc cca	931
Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala Gly Gly Pro Arg Pro	
265 270 275	
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Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg Pro Gln Gly Gly Ser	
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Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr Pro Gly Gln Met Pro	
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Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly Gln Ala Gly Gly Gly	
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Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala Phe Gly Arg Pro Gly	
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Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg Gln Lys Arg Asn Glu	
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Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly Gly Val Arg Leu Pro	
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Asp Phe Ala Asp Lys Ile Gly Ala Asp Ala Ala Ala Leu Val Gln Ala	
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Pro Val Val Thr Val Met Gly His Val Asp His Gly Lys Thr Arg Leu	
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Ile Thr Gln Gly Ile Gly Ala Tyr Gln Val Lys Val Asn Val Glu Asp	
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Val Val Ala Ala Asp Asp Gly Val Met Pro Gln Thr Val Glu Ala Ile	
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Asp	Gly 935	Lys	Val	Arg	Arg	Asn 940	Ala	Thr	Val	Arg	Ile 945	Ile	Arg	Asp	Gly	
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Arg Asp Gly Gln Gly 260	Asn Arg Gly Gly Gln 265	Arg Gln Gly Ala Gly Ala 270
Gly Gly Pro Arg Pro 275	Gln Gly Gly Pro Arg Pro 280	Gln Gly Gly Ser Arg 285
Pro Gln Gly Gly Ser 290	Ala Gln Gly Ala Gln 295	Gly Ala Pro Ser Gln Glu 300
Arg Gln Gly Gly Gly 305	Arg Arg Pro Ser Pro 310	Ala Met Met Pro Pro Thr 315 320
Pro Gly Gln Met 325	Pro Ala Lys Ala Pro 330	Gly Lys Gly Gly Arg Gly Gly 335
Gln Ala Gly Gly Gly 340	Ala Gly Gly Gly Phe 345	Asn Arg Gly Gly Gly Thr 350
Gly Gly Gly Ala Gly 355	Arg Gly Gly Arg Arg 360	Gly Gly Thr Ala Gly Ala 365
Phe Gly Arg Pro Gly 370	Gly Gly Ala Pro Arg 375	Arg Gly Arg Lys Ser Lys Arg 380
Gln Lys Arg Asn Glu 385	Tyr Glu Ser Met Gln 390	Ala Pro Asn Val Ile Gly 395 400
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Ala Leu Val Gln Ala 435	Leu Phe Asn Leu Gly 440	Glu Met Val Thr Ala Thr 445
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Asp	Ile	Ala	Val	Leu	Val	Val	Ala	Ala	Asp	Asp	Gly	Val	Met	Pro	Gln	580	585	590	
Thr	Val	Glu	Ala	Ile	Asn	His	Ala	Lys	Ala	Ala	Asp	Val	Pro	Ile	Val	595	600	605	
Val	Ala	Val	Asn	Lys	Ile	Asp	Lys	Pro	Glu	Ala	Ser	Pro	Glu	Lys	Ile	610	615	620	
Arg	Gly	Gln	Leu	Thr	Glu	Tyr	Gly	Leu	Ile	Pro	Glu	Glu	Tyr	Gly	Gly	625	630	635	640
Asp	Thr	Ile	Phe	Val	Asp	Ile	Ser	Ala	Lys	Gln	Gly	Leu	Asn	Ile	Asp	645	650	655	
Glu	Leu	Leu	Ala	Ser	Val	Cys	Leu	Thr	Ala	Asp	Ala	Glu	Leu	Asp	Leu	660	665	670	
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Leu	Asp	Arg	Gly	Arg	Gly	Pro	Val	Ala	Thr	Val	Ile	Val	Gln	Arg	Gly	690	695	700	
Thr	Leu	Arg	Val	Gly	Asp	Ser	Ile	Val	Ala	Gly	Asp	Thr	Tyr	Gly	Arg	705	710	715	720
Val	Arg	Arg	Met	Val	Asp	Glu	Tyr	Gly	Arg	Asp	Val	Glu	Glu	Ala	Gly	725	730	735	
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Leu	Asn	Ile	Ile	Asp	Arg	Gly	Val	Gly	Ala	Val	Thr	Gln	Thr	Asn	Val	835	840	845	
Thr	Leu	Ala	Ala	Ala	Ser	Asp	Ala	Val	Ile	Ile	Ala	Phe	Asn	Val	Arg	850	855	860	

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Arg Tyr Tyr Thr Ile Ile Tyr Arg Ala Ile Glu Glu Val Glu Ala Ala
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Leu Lys Gly Met Leu Lys Pro Ile Tyr Glu Glu Arg Val Ile Gly His
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915 920 925

Gly Cys Met Val Glu Asp Gly Lys Val Arg Arg Asn Ala Thr Val Arg
930 935 940

Ile Ile Arg Asp Gly Asn Val Ile Ala Glu Asn Ala Lys Ile Val Ser
945 950 955 960

Leu Arg Arg Glu Lys Asp Asp Ala Thr Glu Val Ser Ala Gly Tyr Glu
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<213> Corynebacterium glutamicum

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Val Pro Gly Lys Leu 5
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Leu Ala Thr Leu Lys Asp Lys Gly Glu Phe Val Lys Thr Ala Ser Ser 35
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Gln Ala Lys Pro Ala Ala Ala Ala Lys Pro Gly Ala Pro Ala Lys Pro	
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 Gly Gln Gly Arg Pro Gly Gly Gln Arg Asp Gly Gln Arg Asp Gly Gln
 245 250 255
 Arg Asp Gly Gln Gly Asn Arg Gly Gly Gln Arg Gln Gly Ala Gly Ala
 260 265 270
 Gly Gly Pro Arg Pro Gln Gly Gly Pro Arg Pro Gln Gly Gly Ser Arg
 275 280 285
 Pro Gln Gly Gly Ser Ala Gln Gly Ala Gln Gly Ala Pro Ser Gln Glu
 290 295 300
 Arg Gln Gly Gly Gly Arg Arg Pro Ser Pro Ala Met Met Pro Pro Thr
 305 310 315 320
 Pro Gly Gln Met Pro Ala Lys Ala Pro Gly Lys Gly Gly Arg Gly Gly
 325 330 335
 Gln Ala Gly Gly Gly Ala Gly Gly Gly Phe Asn Arg Gly Gly Gly Thr
 340 345 350
 Gly Gly Gly Ala Gly Arg Gly Gly Arg Arg Gly Gly Thr Ala Gly Ala
 355 360 365
 Phe Gly Arg Pro Gly Gly Ala Pro Arg Arg Gly Arg Lys Ser Lys Arg
 370 375 380
 Gln Lys Arg Asn Glu Tyr Glu Ser Met Gln Ala Pro Asn Val Ile Gly
 385 390 395 400
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 405 410 415
 Gly Ala Ser Leu Ala Asp Phe Ala Asp
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<210> 467

<211> 1751

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1728)

<223> FRXA01496

<400> 467

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1 5 10 15	
gtc acc gca act gca tcg gtt tct gat gaa acc ttg cag ctg ctc ggt	96
Val Thr Ala Thr Ala Ser Val Ser Asp Glu Thr Leu Gln Leu Leu Gly	
20 25 30	
gag gaa atg aac tac aag gtt cag gtt gtt tcc cca gaa gat gaa gac	144
Glu Glu Met Asn Tyr Lys Val Gln Val Val Ser Pro Glu Asp Glu Asp	
35 40 45	
cgt gag ctg ctc gaa agc ttc gac ctt cag ttc ggt gag gac gaa ggt	192
Arg Glu Leu Leu Glu Ser Phe Asp Leu Gln Phe Gly Glu Asp Glu Gly	
50 55 60	
ggc gag gct gac ctt gct aag cgt cct cca gtg gtt acc gtc atg ggt	240
Gly Glu Ala Asp Leu Ala Lys Arg Pro Pro Val Val Thr Val Met Gly	
65 70 75 80	
cac gtt gac cac ggt aag act cgt ttg ctg gat act atc cgt aag gca	288
His Val Asp His Gly Lys Thr Arg Leu Leu Asp Thr Ile Arg Lys Ala	
85 90 95	
aat gtg ggc tcc gac gaa gcc ggc ggc att acc cag ggc att ggt gca	336
Asn Val Gly Ser Asp Glu Ala Gly Gly Ile Thr Gln Gly Ile Gly Ala	
100 105 110	
tac cag gtc aag gta aat gtc gag gac act gag cgc acg atc acc ttc	384
Tyr Gln Val Lys Val Asn Val Glu Asp Thr Glu Arg Thr Ile Thr Phe	
115 120 125	
ctg gat acc cca ggt cac gag gcc ttc acc gca atg cgt gcc cgt ggt	432
Leu Asp Thr Pro Gly His Glu Ala Phe Thr Ala Met Arg Ala Arg Gly	
130 135 140	
gca aag tcc aca gat atc gcg gtt ctg gtt gtt gca gca gac gac ggc	480
Ala Lys Ser Thr Asp Ile Ala Val Leu Val Val Ala Ala Asp Asp Gly	
145 150 155 160	
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Val Met Pro Gln Thr Val Glu Ala Ile Asn His Ala Lys Ala Ala Asp	
165 170 175	
gta cca atc gtg gtt gca gtg aac aag att gat aag cca gaa gct tct	576
Val Pro Ile Val Val Ala Val Asn Lys Ile Asp Lys Pro Glu Ala Ser	
180 185 190	
cca gag aag atc cgt ggt cag ctg acc gaa tac gga ttg atc cct gaa	624
Pro Glu Lys Ile Arg Gly Gln Leu Thr Glu Tyr Gly Leu Ile Pro Glu	
195 200 205	

gag tac ggt ggc gac acc atc ttc gtt gac atc tct gca aag cag gga	672
Glu Tyr Gly Gly Asp Thr Ile Phe Val Asp Ile Ser Ala Lys Gln Gly	
210 215 220	
ctg aac atc gat gag ctg ctc gct tct gtc tgc ctg acc gca gac gct	720
Leu Asn Ile Asp Glu Leu Leu Ala Ser Val Cys Leu Thr Ala Asp Ala	
225 230 235 240	
gag ctt gac ctt gtt gct aac cca gaa atg gac gca cag ggt gtt gca	768
Glu Leu Asp Leu Val Ala Asn Pro Glu Met Asp Ala Gln Gly Val Ala	
245 250 255	
att gaa gct cac ctc gac cgt ggt cgt gga cca gtg gca acc gtt atc	816
Ile Glu Ala His Leu Asp Arg Gly Arg Gly Pro Val Ala Thr Val Ile	
260 265 270	
gtc cag cgc ggt acc ctg cgc gtc ggt gac tcc atc gtt gca ggc gat	864
Val Gln Arg Gly Thr Leu Arg Val Gly Asp Ser Ile Val Ala Gly Asp	
275 280 285	
acc tac gga cgt gtt cgc cgc atg gtg gac gaa tac gga cgc gac gtt	912
Thr Tyr Gly Arg Val Arg Arg Met Val Asp Glu Tyr Gly Arg Asp Val	
290 295 300	
gaa gag gcc gga cct tcc cgt cct gtt cag gtt cag ggt ctt aac ggt	960
Glu Glu Ala Gly Pro Ser Arg Pro Val Gln Val Gln Gly Leu Asn Gly	
305 310 315 320	
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Val Pro Gly Ala Gly Asp Asn Leu Leu Val Val Glu Asp Asp Arg Ile	
325 330 335	
gca cgt cag att gct aac cag cgc aac gcc cgc aag cgt aac gct ctg	1056
Ala Arg Gln Ile Ala Asn Gln Arg Asn Ala Arg Lys Arg Asn Ala Leu	
340 345 350	
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Ala Ala Arg Ser Arg Lys Arg Val Ser Leu Glu Asp Leu Asp Ser Val	
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ctt aag gaa cat agc acc ctt aac ctc att ctt aag ggc gac aac gca	1152
Leu Lys Glu His Ser Thr Leu Asn Leu Ile Leu Lys Gly Asp Asn Ala	
370 375 380	
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Gly Ser Val Glu Ala Leu Glu Glu Ala Leu Leu Lys Ile Glu Met Asp	
385 390 395 400	
gat gaa gtc cag ctc aac atc atc gac cgc ggt gtg ggt gca gtt acc	1248
Asp Glu Val Gln Leu Asn Ile Ile Asp Arg Gly Val Gly Ala Val Thr	
405 410 415	
cag acc aac gtc acc ctt gca gct gca tcc gac gct gtc atc atc gcc	1296
Gln Thr Asn Val Thr Leu Ala Ala Ala Ser Asp Ala Val Ile Ile Ala	
420 425 430	
ttc aac gtt cgc gct gaa ggt aag gca act gag gaa gca aac gca gaa	1344
Phe Asn Val Arg Ala Glu Gly Lys Ala Thr Glu Glu Ala Asn Ala Glu	
435 440 445	
ggc gtc gat gtt cgt tac tac acg atc atc tac cgt gct atc gaa gag	1392

Gly	Val	Asp	Val	Arg	Tyr	Tyr	Thr	Ile	Ile	Tyr	Arg	Ala	Ile	Glu	Glu		
450						455					460						
gtc	gag	gcg	gcc	ctc	aag	ggc	atg	ctc	aag	cca	atc	tac	gaa	gag	cgc	1440	
Val	Glu	Ala	Ala	Leu	Lys	Gly	Met	Leu	Lys	Pro	Ile	Tyr	Glu	Glu	Arg		
465					470					475					480		
ggt	atc	gga	cat	gct	gag	atc	cgt	gcg	atc	ttc	aag	gct	tcc	tct	gtc	1488	
Val	Ile	Gly	His	Ala	Glu	Ile	Arg	Ala	Ile	Phe	Lys	Ala	Ser	Ser	Val		
				485					490						495		
ggc	ctc	atc	gca	ggc	tgc	atg	gtt	gaa	gac	ggc	aag	gtg	cgc	cga	aac	1536	
Gly	Leu	Ile	Ala	Gly	Cys	Met	Val	Glu	Asp	Gly	Lys	Val	Arg	Arg	Asn		
			500					505					510				
gcc	aca	gtc	cgc	att	att	cgc	gac	ggc	aac	gtc	atc	gcc	gag	aat	gca	1584	
Ala	Thr	Val	Arg	Ile	Ile	Arg	Asp	Gly	Asn	Val	Ile	Ala	Glu	Asn	Ala		
			515				520					525					
aag	atc	gtg	tcc	ctt	cgc	cgt	gag	aag	gac	gat	gcc	acc	gaa	gtc	tct	1632	
Lys	Ile	Val	Ser	Leu	Arg	Arg	Glu	Lys	Asp	Asp	Ala	Thr	Glu	Val	Ser		
	530					535					540						
gca	ggc	tac	gag	tgc	ggc	atg	gtt	ctg	tct	tac	cca	gac	atc	tcc	gtc	1680	
Ala	Gly	Tyr	Glu	Cys	Gly	Met	Val	Leu	Ser	Tyr	Pro	Asp	Ile	Ser	Val		
545					550					555					560		
gac	gac	aag	atc	gag	gtc	tac	gaa	atg	gtt	gag	gtt	cca	cgc	gaa	gct	1728	
Asp	Asp	Lys	Ile	Glu	Val	Tyr	Glu	Met	Val	Glu	Val	Pro	Arg	Glu	Ala		
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<210> 468

<211> 576

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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Val	Thr	Ala	Thr	Ala	Ser	Val	Ser	Asp	Glu	Thr	Leu	Gln	Leu	Leu	Gly
			20					25					30		

Glu	Glu	Met	Asn	Tyr	Lys	Val	Gln	Val	Val	Ser	Pro	Glu	Asp	Glu	Asp
		35					40					45			

Arg	Glu	Leu	Leu	Glu	Ser	Phe	Asp	Leu	Gln	Phe	Gly	Glu	Asp	Glu	Gly
	50					55					60				

Gly	Glu	Ala	Asp	Leu	Ala	Lys	Arg	Pro	Pro	Val	Val	Thr	Val	Met	Gly
65					70					75					80

His	Val	Asp	His	Gly	Lys	Thr	Arg	Leu	Leu	Asp	Thr	Ile	Arg	Lys	Ala
				85					90					95	

Asn	Val	Gly	Ser	Asp	Glu	Ala	Gly	Gly	Ile	Thr	Gln	Gly	Ile	Gly	Ala
			100					105					110		

Tyr Gln Val Lys Val Asn Val Glu Asp Thr Glu Arg Thr Ile Thr Phe
 115 120 125
 Leu Asp Thr Pro Gly His Glu Ala Phe Thr Ala Met Arg Ala Arg Gly
 130 135 140
 Ala Lys Ser Thr Asp Ile Ala Val Leu Val Val Ala Ala Asp Asp Gly
 145 150 155 160
 Val Met Pro Gln Thr Val Glu Ala Ile Asn His Ala Lys Ala Ala Asp
 165 170 175
 Val Pro Ile Val Val Ala Val Asn Lys Ile Asp Lys Pro Glu Ala Ser
 180 185 190
 Pro Glu Lys Ile Arg Gly Gln Leu Thr Glu Tyr Gly Leu Ile Pro Glu
 195 200 205
 Glu Tyr Gly Gly Asp Thr Ile Phe Val Asp Ile Ser Ala Lys Gln Gly
 210 215 220
 Leu Asn Ile Asp Glu Leu Leu Ala Ser Val Cys Leu Thr Ala Asp Ala
 225 230 235 240
 Glu Leu Asp Leu Val Ala Asn Pro Glu Met Asp Ala Gln Gly Val Ala
 245 250 255
 Ile Glu Ala His Leu Asp Arg Gly Arg Gly Pro Val Ala Thr Val Ile
 260 265 270
 Val Gln Arg Gly Thr Leu Arg Val Gly Asp Ser Ile Val Ala Gly Asp
 275 280 285
 Thr Tyr Gly Arg Val Arg Arg Met Val Asp Glu Tyr Gly Arg Asp Val
 290 295 300
 Glu Glu Ala Gly Pro Ser Arg Pro Val Gln Val Gln Gly Leu Asn Gly
 305 310 315 320
 Val Pro Gly Ala Gly Asp Asn Leu Leu Val Val Glu Asp Asp Arg Ile
 325 330 335
 Ala Arg Gln Ile Ala Asn Gln Arg Asn Ala Arg Lys Arg Asn Ala Leu
 340 345 350
 Ala Ala Arg Ser Arg Lys Arg Val Ser Leu Glu Asp Leu Asp Ser Val
 355 360 365
 Leu Lys Glu His Ser Thr Leu Asn Leu Ile Leu Lys Gly Asp Asn Ala
 370 375 380
 Gly Ser Val Glu Ala Leu Glu Glu Ala Leu Leu Lys Ile Glu Met Asp
 385 390 395 400
 Asp Glu Val Gln Leu Asn Ile Ile Asp Arg Gly Val Gly Ala Val Thr
 405 410 415
 Gln Thr Asn Val Thr Leu Ala Ala Ala Ser Asp Ala Val Ile Ile Ala
 420 425 430
 Phe Asn Val Arg Ala Glu Gly Lys Ala Thr Glu Glu Ala Asn Ala Glu

435	440	445
Gly Val Asp Val Arg Tyr Tyr Thr Ile Ile Tyr Arg Ala Ile Glu Glu 450 455 460		
Val Glu Ala Ala Leu Lys Gly Met Leu Lys Pro Ile Tyr Glu Glu Arg 465 470 475 480		
Val Ile Gly His Ala Glu Ile Arg Ala Ile Phe Lys Ala Ser Ser Val 485 490 495		
Gly Leu Ile Ala Gly Cys Met Val Glu Asp Gly Lys Val Arg Arg Asn 500 505 510		
Ala Thr Val Arg Ile Ile Arg Asp Gly Asn Val Ile Ala Glu Asn Ala 515 520 525		
Lys Ile Val Ser Leu Arg Arg Glu Lys Asp Asp Ala Thr Glu Val Ser 530 535 540		
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Asp Asp Lys Ile Glu Val Tyr Glu Met Val Glu Val Pro Arg Glu Ala 565 570 575		

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<211> 339

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(316)

<223> RXA00677

<400> 469

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aaggcctccc gcaggggagt gttctggaaa agcggaggat	atg gct aag gaa ggc	115
	Met Ala Lys Glu Gly	
	1 5	

gct att gaa gtt gag ggt cgc att gtc gaa cct ctg ccg aat gca atg	163
Ala Ile Glu Val Glu Gly Arg Ile Val Glu Pro Leu Pro Asn Ala Met	
10 15 20	

ttc cga gtc gag ctc gac aac gga cac aag gta ctc gcc cac atc agt	211
Phe Arg Val Glu Leu Asp Asn Gly His Lys Val Leu Ala His Ile Ser	
25 30 35	

gga aag atg cgc cag cac tac atc cgt atc ctt cct gag gac cgc gtc	259
Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu Pro Glu Asp Arg Val	
40 45 50	

gtt gta gag ctg tcg ccc tat gat ctg act cgt gga cga atc gtt tac	307
Val Val Glu Leu Ser Pro Tyr Asp Leu Thr Arg Gly Arg Ile Val Tyr	
55 60 65	

cgc tac aag taaaaataag ctttaagcct cca 339

Arg Tyr Lys
70

<210> 470
<211> 72
<212> PRT
<213> Corynebacterium glutamicum

<400> 470
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20 25 30
Leu Ala His Ile Ser Gly Lys Met Arg Gln His Tyr Ile Arg Ile Leu
35 40 45
Pro Glu Asp Arg Val Val Val Glu Leu Ser Pro Tyr Asp Leu Thr Arg
50 55 60
Gly Arg Ile Val Tyr Arg Tyr Lys
65 70

<210> 471
<211> 667
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(667)
<223> RXN01284

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Val Ala Lys Ala Lys
1 5
ttc gag cgt acc aag ccc cac gta aac atc ggc acc atc ggt cac gtt 163
Phe Glu Arg Thr Lys Pro His Val Asn Ile Gly Thr Ile Gly His Val
10 15 20
gac cac ggt aag acc acc acc acc gcg gct atc acc aag gtt ctg gct 211
Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile Thr Lys Val Leu Ala
25 30 35
gac act tac cct gag ctc aac gag gct ttc gcc ttc gac tcc atc gat 259
Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala Phe Asp Ser Ile Asp
40 45 50
aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc cac 307
Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser His
55 60 65
gtt gag tac cag act gaa aag cgc cac tac gca cac gtt gac gct cca 355
Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala Pro

70	75	80	85	
ggc cac gcc gac tac atc aag aac atg att acc ggc gct gct cag atg				403
Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln Met				
	90	95	100	
gac ggc gca atc ctc gtt gtt gct gct acc gac ggc cca atg cct cag				451
Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro Gln				
	105	110	115	
acc cgt gag cac gtt ctt ctt gct cgc cag gtt ggc gtt cct tac atc				499
Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr Ile				
	120	125	130	
ctc gtt gct ctt aac aag tgc gac atg gtt gag gat gag gaa atc atc				547
Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile Ile				
	135	140	145	
gag ctc gtc gag atg gaa gtt cgt gaa ctt ctt gct gag cag gac tac				595
Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ala Glu Gln Asp Tyr				
	150	155	160	165
gac gaa gag gct cca att gtt cac atc tcc gct ctg aag gct ctt gag				643
Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu Glu				
	170	175	180	
ggc gac gag aag tgg ggc aag cag				667
Gly Asp Glu Lys Trp Gly Lys Gln				
	185			

<210> 472

<211> 189

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Val Ala Lys Ala Lys Phe Glu Arg Thr Lys Pro His Val Asn Ile Gly				
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Thr Ile Gly His Val Asp His Gly Lys Thr Thr Thr Thr Ala Ala Ile				
	20	25	30	
Thr Lys Val Leu Ala Asp Thr Tyr Pro Glu Leu Asn Glu Ala Phe Ala				
	35	40	45	
Phe Asp Ser Ile Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr				
	50	55	60	
Ile Asn Ile Ser His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala				
	65	70	75	80
His Val Asp Ala Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr				
	85	90	95	
Gly Ala Ala Gln Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp				
	100	105	110	
Gly Pro Met Pro Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val				
	115	120	125	

Gly Val Pro Tyr Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu
 130 135 140

Asp Glu Glu Ile Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu
 145 150 155 160

Ala Glu Gln Asp Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala
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Leu Lys Ala Leu Glu Gly Asp Glu Lys Trp Gly Lys Gln
 180 185

<210> 473
 <211> 507
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(507)
 <223> FRXA01284

<400> 473
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 Ala Asp Thr Tyr Pro Glu Leu Asn Gln Ala Phe Ala Phe Asp Ser Ile
 20 25 30

gat aag gct cct gag gag aag gag cgt ggc atc acg atc aac atc tcc 144
 Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser
 35 40 45

cac gtt gag tac cag act gaa aag cgc cac tac gca cac gtt gac gct 192
 His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala
 50 55 60

cca ggc cac gcc gac tac atc aag aac atg att acc ggc gct gct cag 240
 Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln
 65 70 75 80

atg gac ggc gca atc ctg gtt gtt gct gct acc gac ggc cca atg cct 288
 Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro
 85 90 95

cag acc cgt gag cac gtt ctt ctt gct cgc cag gtt ggc gtt cct tac 336
 Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr
 100 105 110

atc ctg gtt gct ctt aac aag tgc gac atg gtt gag gat gag gaa atc 384
 Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile
 115 120 125

atc gag ctg gtc gag atg gaa gtt cgt gaa ctt ctt gct gag cag gac 432
 Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ala Glu Gln Asp
 130 135 140

tac gac gaa gag gct cca att gtt cac atc tcc gct ctg aag gct ctt 480

Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu
 145 150 155 160

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 Glu Gly Asp Glu Lys Trp Gly Lys Gln
 165

507

<210> 474
 <211> 169
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 474
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 20 25 30
 Asp Lys Ala Pro Glu Glu Lys Glu Arg Gly Ile Thr Ile Asn Ile Ser
 35 40 45
 His Val Glu Tyr Gln Thr Glu Lys Arg His Tyr Ala His Val Asp Ala
 50 55 60
 Pro Gly His Ala Asp Tyr Ile Lys Asn Met Ile Thr Gly Ala Ala Gln
 65 70 75 80
 Met Asp Gly Ala Ile Leu Val Val Ala Ala Thr Asp Gly Pro Met Pro
 85 90 95
 Gln Thr Arg Glu His Val Leu Leu Ala Arg Gln Val Gly Val Pro Tyr
 100 105 110
 Ile Leu Val Ala Leu Asn Lys Cys Asp Met Val Glu Asp Glu Glu Ile
 115 120 125
 Ile Glu Leu Val Glu Met Glu Val Arg Glu Leu Leu Ala Glu Gln Asp
 130 135 140
 Tyr Asp Glu Glu Ala Pro Ile Val His Ile Ser Ala Leu Lys Ala Leu
 145 150 155 160
 Glu Gly Asp Glu Lys Trp Gly Lys Gln
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<210> 475
 <211> 684
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(661)
 <223> RXA00138

<400> 475
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Val Ala Thr Thr Ala Asp Phe Lys Asn Gly Leu Val Leu Lys Asn Glu
1 5 10 15

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<210> 477
<211> 480
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(457)  
<223> RXA00331
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							Met	Val	Gly	His	Met					
							1				5					
tcg aat gat cac cca tac tcc ccc gca aaa cgc gtc gga aat ttc atc															163	
Ser	Asn	Asp	His	Pro	Tyr	Ser	Pro	Ala	Lys	Arg	Val	Gly	Asn	Phe	Ile	
				10					15					20		
ttc gtc tcc ggc gct ctt tca gta gac aag gac tac caa cca gtc gtc															211	
Phe	Val	Ser	Gly	Ala	Leu	Ser	Val	Asp	Lys	Asp	Tyr	Gln	Pro	Val	Val	
			25					30					35			
ggt cgt aaa gaa gca gtt gat gca gca ctt gaa cgc atg cgt gaa cgc															259	

Gly Arg Lys Glu Ala Val Asp Ala Ala Leu Glu Arg Met Arg Glu Arg
 40 45 50
 ctc gcc acc gct ggt ggt gaa ctc aaa gac gtt gtg aaa ctc act tac 307
 Leu Ala Thr Ala Gly Gly Glu Leu Lys Asp Val Val Lys Leu Thr Tyr
 55 60 65
 ttt gtc acc gac atc agc ctg cgc gaa gaa tgc aac gag caa ttc cga 355
 Phe Val Thr Asp Ile Ser Leu Arg Glu Glu Cys Asn Glu Gln Phe Arg
 70 75 80 85
 gag cat ttc ctc gaa ggc cgc ccg gca cgc tct ttc gtg ggt gca tca 403
 Glu His Phe Leu Glu Gly Arg Pro Ala Arg Ser Phe Val Gly Ala Ser
 90 95 100
 tcg ctt cct tat ggt gca act gtg gaa att gat gcg att gcg atg atc 451
 Ser Leu Pro Tyr Gly Ala Thr Val Glu Ile Asp Ala Ile Ala Met Ile
 105 110 115
 gag gac taaccagagc atttttcgca cga 480
 Glu Asp

<210> 478
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 478
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 20 25 30
 Tyr Gln Pro Val Val Gly Arg Lys Glu Ala Val Asp Ala Ala Leu Glu
 35 40 45
 Arg Met Arg Glu Arg Leu Ala Thr Ala Gly Gly Glu Leu Lys Asp Val
 50 55 60
 Val Lys Leu Thr Tyr Phe Val Thr Asp Ile Ser Leu Arg Glu Glu Cys
 65 70 75 80
 Asn Glu Gln Phe Arg Glu His Phe Leu Glu Gly Arg Pro Ala Arg Ser
 85 90 95
 Phe Val Gly Ala Ser Ser Leu Pro Tyr Gly Ala Thr Val Glu Ile Asp
 100 105 110
 Ala Ile Ala Met Ile Glu Asp
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<210> 479
 <211> 570
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>

<221> CDS

<222> (1)..(570)

<223> RXA02822

<400> 479

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ggt acc gag gtt agc cat ccc gcc cat ggt gcg tgg agc cag ttc aag      48
Gly Thr Glu Val Ser His Pro Ala His Gly Ala Trp Ser Gln Phe Lys
  1                      5                      10                    15

ttt gaa ggt ggc gtg cac cgt gtt cag cgt gtg cct gtt act gaa tct      96
Phe Glu Gly Gly Val His Arg Val Gln Arg Val Pro Val Thr Glu Ser
                      20                      25                    30

cag gga cgc atc cag acc tct gct gct ggt gtc ttg gtt tac cca gaa      144
Gln Gly Arg Ile Gln Thr Ser Ala Ala Gly Val Leu Val Tyr Pro Glu
                      35                      40                    45

cca gat gag gtg gaa aac gtt gag atc gat gag aag gat att cgc gtc      192
Pro Asp Glu Val Glu Asn Val Glu Ile Asp Glu Lys Asp Ile Arg Val
                      50                      55                    60

gat gtg tac cgt tcc tca ggt aag ggt ggt cag ggc gtt aac acc act      240
Asp Val Tyr Arg Ser Ser Gly Lys Gly Gly Gln Gly Val Asn Thr Thr
                      65                      70                    75                    80

gac tcc gct gtg cgt att acc cac ttg cca act ggt ttg gtg gtg acc      288
Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Leu Val Val Thr
                      85                      90                    95

tgt cag aag gag cgc tcc cag att cag aac cgt gcg cgt gcg atg cag      336
Cys Gln Lys Glu Arg Ser Gln Ile Gln Asn Arg Ala Arg Ala Met Gln
                      100                     105                    110

gtt ttg gct gcc cgt tta cag gcg atg aag gaa gag gaa gcg gcg gct      384
Val Leu Ala Ala Arg Leu Gln Ala Met Lys Glu Glu Glu Ala Ala Ala
                      115                     120                    125

gag gct gct acg gga cgt gct gcg cag att cgc acc atg gac cgc tct      432
Glu Ala Ala Thr Gly Arg Ala Ala Gln Ile Arg Thr Met Asp Arg Ser
                      130                     135                    140

gag cgc atc cgt acc tac aac tgg ccg gaa aac cgc atc agc gat cac      480
Glu Arg Ile Arg Thr Tyr Asn Trp Pro Glu Asn Arg Ile Ser Asp His
                      145                     150                    155                    160

cgt att ggt ttt aag gcg aac aac ctt gat tcg gtt ctc gat ggt gaa      528
Arg Ile Gly Phe Lys Ala Asn Asn Leu Asp Ser Val Leu Asp Gly Glu
                      165                     170                    175

ttg gat gat ctg ttc acc gcg ttg cag gct gct gag cgt gca              570
Leu Asp Asp Leu Phe Thr Ala Leu Gln Ala Ala Glu Arg Ala
                      180                     185                    190

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<210> 480

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 480

Gly Thr Glu Val Ser His Pro Ala His Gly Ala Trp Ser Gln Phe Lys

1	5	10	15
Phe Glu Gly Gly Val His Arg Val Gln Arg Val Pro Val Thr Glu Ser	20	25	30
Gln Gly Arg Ile Gln Thr Ser Ala Ala Gly Val Leu Val Tyr Pro Glu	35	40	45
Pro Asp Glu Val Glu Asn Val Glu Ile Asp Glu Lys Asp Ile Arg Val	50	55	60
Asp Val Tyr Arg Ser Ser Gly Lys Gly Gly Gln Gly Val Asn Thr Thr	65	70	75
Asp Ser Ala Val Arg Ile Thr His Leu Pro Thr Gly Leu Val Val Thr	85	90	95
Cys Gln Lys Glu Arg Ser Gln Ile Gln Asn Arg Ala Arg Ala Met Gln	100	105	110
Val Leu Ala Ala Arg Leu Gln Ala Met Lys Glu Glu Glu Ala Ala Ala	115	120	125
Glu Ala Ala Thr Gly Arg Ala Ala Gln Ile Arg Thr Met Asp Arg Ser	130	135	140
Glu Arg Ile Arg Thr Tyr Asn Trp Pro Glu Asn Arg Ile Ser Asp His	145	150	155
Arg Ile Gly Phe Lys Ala Asn Asn Leu Asp Ser Val Leu Asp Gly Glu	165	170	175
Leu Asp Asp Leu Phe Thr Ala Leu Gln Ala Ala Glu Arg Ala	180	185	190

<210> 481

<211> 480

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(457)

<223> RXA00011

<400> 481

gaagttcttc ccgtggtgga aaaagtggaac tccatcgaca tccctgatgc cgatgttcgc 60

gtcgatgtct accgctctc cggcccaggt ggtcagtcca	gtg aac acc acc gac	115
	Val Asn Thr Thr Asp	
	1 5	

tct gcc gtg cgc ctg acc cac atc cca acc ggc atc gtg gtg acc tgc	163
Ser Ala Val Arg Leu Thr His Ile Pro Thr Gly Ile Val Val Thr Cys	
10 15 20	

caa aac gag aaa tca cag atc caa aac aag gca tcc gcg atg cgt gtt	211
Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala Ser Ala Met Arg Val	
25 30 35	

ctc cag gca aaa ctg ctt gag cgt aaa cgc cag gaa gaa cgc gcc gaa 259
 Leu Gln Ala Lys Leu Leu Glu Arg Lys Arg Gln Glu Glu Arg Ala Glu
 40 45 50

atg gat gcc ctc gga gct gga ggc aat gca tcc tgg ggt aac caa atg 307
 Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser Trp Gly Asn Gln Met
 55 60 65

cgt tcc tac gtg ctg cac cct tat caa atg gtg aag gat ctg cgc acc 355
 Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val Lys Asp Leu Arg Thr
 70 75 80 85

aac ttt gaa gtc aac gat ccg caa aaa gtc ctt gac ggc gat atc gat 403
 Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu Asp Gly Asp Ile Asp
 90 95 100

ggc ctt ttg gaa gca ggt att cgc tgg cga atg gct gag agc cag tcg 451
 Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met Ala Glu Ser Gln Ser
 105 110 115

gcg gaa taaaggttg ttttctggca gaa 480
 Ala Glu

<210> 482
 <211> 119
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 482
 Val Asn Thr Thr Asp Ser Ala Val Arg Leu Thr His Ile Pro Thr Gly
 1 5 10 15

Ile Val Val Thr Cys Gln Asn Glu Lys Ser Gln Ile Gln Asn Lys Ala
 20 25 30

Ser Ala Met Arg Val Leu Gln Ala Lys Leu Leu Glu Arg Lys Arg Gln
 35 40 45

Glu Glu Arg Ala Glu Met Asp Ala Leu Gly Ala Gly Gly Asn Ala Ser
 50 55 60

Trp Gly Asn Gln Met Arg Ser Tyr Val Leu His Pro Tyr Gln Met Val
 65 70 75 80

Lys Asp Leu Arg Thr Asn Phe Glu Val Asn Asp Pro Gln Lys Val Leu
 85 90 95

Asp Gly Asp Ile Asp Gly Leu Leu Glu Ala Gly Ile Arg Trp Arg Met
 100 105 110

Ala Glu Ser Gln Ser Ala Glu
 115

<210> 483
 <211> 999
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(976)

<223> RXA00012

<400> 483

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ctggattagt catgccttcc attgtgcatg ccgtcggcca agtgtgctga ataaggtggc 60

gttctaagaa tcacaatcgg tgcgggtaat atgtgcaatc atg cgt ccc gaa ttt 115
                                         Met Arg Pro Glu Phe
                                         1           5

tct gca gaa ctc tcc gag cta gac agc acg ctg aca acc att gaa aaa 163
Ser Ala Glu Leu Ser Glu Leu Asp Ser Thr Leu Thr Thr Ile Glu Lys
                        10                      15                      20

gtg ctg aac ccg caa gag atg tct gac cga gtc aga gaa ctt gaa gct 211
Val Leu Asn Pro Gln Glu Met Ser Asp Arg Val Arg Glu Leu Glu Ala
                        25                      30                      35

caa gca gct gac ccg tct ctg tgg gat gac cct gac cat gca cag caa 259
Gln Ala Ala Asp Pro Ser Leu Trp Asp Asp Pro Asp His Ala Gln Gln
                        40                      45                      50

gtc acc tct gag ctg tcc cac gtc cag gcg gag ctg cgc aaa att acc 307
Val Thr Ser Glu Leu Ser His Val Gln Ala Glu Leu Arg Lys Ile Thr
                        55                      60                      65

gat ctg cgc cag cgc atc gaa gat ctg ccc atc atg gtg gaa ctc gca 355
Asp Leu Arg Gln Arg Ile Glu Asp Leu Pro Ile Met Val Glu Leu Ala
                        70                      75                      80                      85

gag gaa gaa gac ggc gat acc tcc atc gcg gaa gaa gaa ctc gcc gat 403
Glu Glu Glu Asp Gly Asp Thr Ser Ile Ala Glu Glu Glu Leu Ala Asp
                        90                      95                      100

ctg cgt tct ctg atc gat gcg ttg gaa gta aag acc atg ctg tcg ggt 451
Leu Arg Ser Leu Ile Asp Ala Leu Glu Val Lys Thr Met Leu Ser Gly
                        105                      110                      115

gaa tat gat gct cgc gag gca gtg atc aat att cga tcc ggt gcc ggt 499
Glu Tyr Asp Ala Arg Glu Ala Val Ile Asn Ile Arg Ser Gly Ala Gly
                        120                      125                      130

ggg gtc gat gct gcg gac tgg gct gaa atg ctc atg cgc atg tac acc 547
Gly Val Asp Ala Ala Asp Trp Ala Glu Met Leu Met Arg Met Tyr Thr
                        135                      140                      145

cgc tgg gcg gaa aag aac ggc cac aaa gta gat att tac gat att tcc 595
Arg Trp Ala Glu Lys Asn Gly His Lys Val Asp Ile Tyr Asp Ile Ser
                        150                      155                      160                      165

tac gcc gaa gaa gcc ggc atc aaa tcc gcc acc ttc gtg gtc cac ggc 643
Tyr Ala Glu Glu Ala Gly Ile Lys Ser Ala Thr Phe Val Val His Gly
                        170                      175                      180

gac tac atg tac ggc cag ctc tcc gtg gag caa ggc gca cac cgc ctc 691
Asp Tyr Met Tyr Gly Gln Leu Ser Val Glu Gln Gly Ala His Arg Leu
                        185                      190                      195

gtg cgc atc agt cct ttt gat aac cag ggc agg cgc caa acc tcc ttc 739

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Val Arg Ile Ser Pro Phe Asp Asn Gln Gly Arg Arg Gln Thr Ser Phe
 200 205 210

gcc gag gta gaa gtt ctt ccc gtg gtg gaa aaa gtg gac tcc atc gac 787
 Ala Glu Val Glu Val Leu Pro Val Val Glu Lys Val Asp Ser Ile Asp
 215 220 225

atc cct gat gcc gat gtt cgc gtc gat gtc tac cgc tcc tcc ggc cca 835
 Ile Pro Asp Ala Asp Val Arg Val Asp Val Tyr Arg Ser Ser Gly Pro
 230 235 240 245

ggt ggt cag tcc agt gaa cac cac cga ctc tgc cgt gcg cct gac cca 883
 Gly Gly Gln Ser Ser Glu His His Arg Leu Cys Arg Ala Pro Asp Pro
 250 255 260

cat ccc aac cgg cat cgt ggt gac ctg cca aaa cga gaa atc aca gat 931
 His Pro Asn Arg His Arg Gly Asp Leu Pro Lys Arg Glu Ile Thr Asp
 265 270 275

cca aaa caa ggc atc cgc gat gcg tgt tct cca ggc aaa act gct 976
 Pro Lys Gln Gly Ile Arg Asp Ala Cys Ser Pro Gly Lys Thr Ala
 280 285 290

tgagcgtaaaa cgccaggaag aac 999

<210> 484

<211> 292

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Arg Pro Glu Phe Ser Ala Glu Leu Ser Glu Leu Asp Ser Thr Leu
 1 5 10 15

Thr Thr Ile Glu Lys Val Leu Asn Pro Gln Glu Met Ser Asp Arg Val
 20 25 30

Arg Glu Leu Glu Ala Gln Ala Ala Asp Pro Ser Leu Trp Asp Asp Pro
 35 40 45

Asp His Ala Gln Gln Val Thr Ser Glu Leu Ser His Val Gln Ala Glu
 50 55 60

Leu Arg Lys Ile Thr Asp Leu Arg Gln Arg Ile Glu Asp Leu Pro Ile
 65 70 75 80

Met Val Glu Leu Ala Glu Glu Glu Asp Gly Asp Thr Ser Ile Ala Glu
 85 90 95

Glu Glu Leu Ala Asp Leu Arg Ser Leu Ile Asp Ala Leu Glu Val Lys
 100 105 110

Thr Met Leu Ser Gly Glu Tyr Asp Ala Arg Glu Ala Val Ile Asn Ile
 115 120 125

Arg Ser Gly Ala Gly Gly Val Asp Ala Ala Asp Trp Ala Glu Met Leu
 130 135 140

Met Arg Met Tyr Thr Arg Trp Ala Glu Lys Asn Gly His Lys Val Asp
 145 150 155 160

<400> 485																
ctg	cga	agc	ttc	tac	acc	cca	gaa	caa	gcc	atc	gaa	cgc	gaa	ggc	gac	48
Leu	Arg	Ser	Phe	Tyr	Thr	Pro	Glu	Gln	Ala	Ile	Glu	Arg	Glu	Gly	Asp	
1				5					10					15		
gtc	tgg	aaa	gcc	gcc	acc	gaa	gaa	gca	gaa	ctc	ctc	gca	gct	gac	ggc	96
Val	Trp	Lys	Ala	Ala	Thr	Glu	Glu	Ala	Glu	Leu	Leu	Ala	Ala	Asp	Gly	
			20					25					30			
gcc	gtc	cac	gac	cag	gaa	ctc	ttc	ctc	aac	tgc	acc	acc	tcc	cca	ctg	144
Ala	Val	His	Asp	Gln	Glu	Leu	Phe	Leu	Asn	Cys	Thr	Thr	Ser	Pro	Leu	
		35					40					45				
atc	ttc	gcc	tcc	gcg	atg	ctc	aac	ttc	ggc	gtc	cac	caa	atc	ctg	gac	192
Ile	Phe	Ala	Ser	Ala	Met	Leu	Asn	Phe	Gly	Val	His	Gln	Ile	Leu	Asp	
	50					55					60					
acc	ctc	tgc	caa	ctc	gca	cca	tcc	ccc	gcc	ggc	cgc	gac	gca	gac	ccc	240
Thr	Leu	Cys	Gln	Leu	Ala	Pro	Ser	Pro	Ala	Gly	Arg	Asp	Ala	Asp	Pro	
65					70					75					80	
aaa	gcc	ctc	gaa	gcc	gcc	acc	tcc	gca	atg	gac	gac	cac	cgc	gac	acc	288

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<210> 486
<211> 247
<212> PRT
<213> Corynebacterium glutamicum
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<400> 486
Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
1 5 10 15
Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
20 25 30
Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
35 40 45
Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
50 55 60

Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220
 Ser Glu Gly Val Val Gln Ile Leu Lys Asn Asp Leu Arg Gly Asp Ala
 225 230 235 240
 Asn Pro Gly His Gly Arg Cys
 245

<210> 487
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(672)
 <223> FRXA01926

<400> 487
 ctg cga agc ttc tac acc cca gaa caa gcc atc gaa cgc gaa ggc gac 48
 Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
 1 5 10 15
 gtc tgg aaa gcc gcc acc gaa gaa gca gaa ctc ctc gca gct gac ggc 96
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 gcc gtc cac gac cag gaa ctc ttc ctc aac tgc acc acc tcc cca ctg 144
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45

atc ttc gcc tcc gcg atg ctc aac ttc ggc gtc cac caa atc ctg gac 192
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp
 50 55 60
 acc ctc tgc caa ctc gca cca tcc ccc gcc ggc cgc gac gca gac ccc 240
 Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro
 65 70 75 80
 aaa gcc ctc gaa gcc gcc acc tcc gca atg gac gac cac cgc gac acc 288
 Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr
 85 90 95
 acc gac gac ttc tcc ggc gtc gtc ttc aaa gtc caa gcc ggc atg gac 336
 Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp
 100 105 110
 aaa aac cac cgc gat acc ctc gcc ttc atg cgc gtc gtc tcc ggc gaa 384
 Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu
 115 120 125
 ttc gac cgc ggc atg caa gtc acc cac tcc caa tcc ggc cgc agc ttc 432
 Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe
 130 135 140
 tcc acc aaa tac gcc ctc acc gtc ttc ggc cgc acc cgc tct acc gtc 480
 Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val
 145 150 155 160
 gaa acc gcc ttc ccc ggc gac atc gtc ggc ctc gtc aac gcc ggc gcc 528
 Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala
 165 170 175
 ctc gca cca ggc gac acc atc ttc gaa ggc cga aaa atc caa tac cca 576
 Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro
 180 185 190
 cca atg cca aaa ttc gcg cca gaa cac ttc cgc atc ctg cgc gcc aaa 624
 Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys
 195 200 205
 tca ctc ggc aaa tac aaa cag ttc cgc aaa gcc ctc gag cag ctg gac 672
 Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp
 210 215 220

<210> 488

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Leu Arg Ser Phe Tyr Thr Pro Glu Gln Ala Ile Glu Arg Glu Gly Asp
 1 5 10 15
 Val Trp Lys Ala Ala Thr Glu Glu Ala Glu Leu Leu Ala Ala Asp Gly
 20 25 30
 Ala Val His Asp Gln Glu Leu Phe Leu Asn Cys Thr Thr Ser Pro Leu
 35 40 45
 Ile Phe Ala Ser Ala Met Leu Asn Phe Gly Val His Gln Ile Leu Asp

50	55	60
Thr Leu Cys Gln Leu Ala Pro Ser Pro Ala Gly Arg Asp Ala Asp Pro 65 70 75 80		
Lys Ala Leu Glu Ala Ala Thr Ser Ala Met Asp Asp His Arg Asp Thr 85 90 95		
Thr Asp Asp Phe Ser Gly Val Val Phe Lys Val Gln Ala Gly Met Asp 100 105 110		
Lys Asn His Arg Asp Thr Leu Ala Phe Met Arg Val Val Ser Gly Glu 115 120 125		
Phe Asp Arg Gly Met Gln Val Thr His Ser Gln Ser Gly Arg Ser Phe 130 135 140		
Ser Thr Lys Tyr Ala Leu Thr Val Phe Gly Arg Thr Arg Ser Thr Val 145 150 155 160		
Glu Thr Ala Phe Pro Gly Asp Ile Val Gly Leu Val Asn Ala Gly Ala 165 170 175		
Leu Ala Pro Gly Asp Thr Ile Phe Glu Gly Arg Lys Ile Gln Tyr Pro 180 185 190		
Pro Met Pro Lys Phe Ala Pro Glu His Phe Arg Ile Leu Arg Ala Lys 195 200 205		
Ser Leu Gly Lys Tyr Lys Gln Phe Arg Lys Ala Leu Glu Gln Leu Asp 210 215 220		

<210> 489

<211> 478

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(478)

<223> RXN02002

<400> 489

aagtggcaaa aaacgtttca agcaggcaac gccggcgctac aacttcgctg agctggggcg 60

attatggccc agcgcccaca acccgctatt cttaataccc	atg agc aac gcc aat	115
	Met Ser Asn Ala Asn	
	1 5	

tcc gac acc acc gcc gcc gag gca cat cgc cgc aga aca ttc gcc gta	163
Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg Thr Phe Ala Val	
10 15 20	

atc gca cac ccc gac gcc ggt aaa tcc acc ctc acc gag gca ttg gcg	211
Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu Thr Glu Ala Leu Ala	
25 30 35	

ctg cat gca cac atc atc tcc gaa gcc ggc gcc acc cac ggc aaa gca	259
Leu His Ala His Ile Ile Ser Glu Ala Gly Ala Thr His Gly Lys Ala	
40 45 50	

ggc cgc aaa gcc acc gtt tcc gac tgg atg gaa atg gaa aaa gac cgc 307
 Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu Met Glu Lys Asp Arg
 55 60 65

ggc atc tcc atc gcc tcc tcc gca ctc caa ttc gag tac gca cca gaa 355
 Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe Glu Tyr Ala Pro Glu
 70 75 80 85

ggc cac gca ggc gag ccc ttc atg atc aac ctc gtg gac acc cca ggc 403
 Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu Val Asp Thr Pro Gly
 90 95 100

cac gcc gac ttc tcc gaa gac acc tac cgc gtc ctc atg gcc gtc gac 451
 His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val Leu Met Ala Val Asp
 105 110 115

gca gca gtc atg ctt atg cac tcc gtc 478
 Ala Ala Val Met Leu Met His Ser Val
 120 125

<210> 490

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

Met Ser Asn Ala Asn Ser Asp Thr Thr Ala Ala Glu Ala His Arg Arg
 1 5 10 15

Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
 20 25 30

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
 35 40 45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
 50 55 60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
 65 70 75 80

Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe Met Ile Asn Leu
 85 90 95

Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp Thr Tyr Arg Val
 100 105 110

Leu Met Ala Val Asp Ala Ala Val Met Leu Met His Ser Val
 115 120 125

<210> 491

<211> 394

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (17)..(394)

<223> FRXA02002

<400> 491

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gctattcttta ataccc atg agc aac gcc aat ccc gac acc acc gcc gcc gag 52
      Met Ser Asn Ala Asn Pro Asp Thr Thr Ala Ala Glu
        1             5             10

gca cat cgc cgc aga aca ttc gcc gta atc gca cac ccc gac gcc ggt 100
Ala His Arg Arg Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly
      15             20             25

aaa tcc acc ctc acc gag gca ttg gcg ctg cat gca cac atc atc tcc 148
Lys Ser Thr Leu Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser
      30             35             40

gaa gcc ggc gcc acc cac ggc aaa gca ggc cgc aaa gcc acc gtt tcc 196
Glu Ala Gly Ala Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser
      45             50             55

gac tgg atg gaa atg gaa aaa gac cgc ggc atc tcc atc gcc tcc tcc 244
Asp Trp Met Glu Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser
      65             70             75

gca ctc caa ttc gag tac gca cca gaa ggc cac gca ggc gag ccc ttc 292
Ala Leu Gln Phe Glu Tyr Ala Pro Glu Gly His Ala Gly Glu Pro Phe
      80             85             90

atg atc aac ctc gtg gac acc cca ggc cac gcc gac ttc tcc gaa gac 340
Met Ile Asn Leu Val Asp Thr Pro Gly His Ala Asp Phe Ser Glu Asp
      95             100            105

acc tac cgc gtc ctc atg gcc gtc gac gca gca gtc atg ctt atg cac 388
Thr Tyr Arg Val Leu Met Ala Val Asp Ala Ala Val Met Leu Met His
      110            115            120

tcc gtc 394
Ser Val
125

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<210> 492

<211> 126

<212> PRT

<213> Corynebacterium glutamicum

<400> 492

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Met Ser Asn Ala Asn Pro Asp Thr Thr Ala Ala Glu Ala His Arg Arg
  1             5             10             15

Arg Thr Phe Ala Val Ile Ala His Pro Asp Ala Gly Lys Ser Thr Leu
      20             25             30

Thr Glu Ala Leu Ala Leu His Ala His Ile Ile Ser Glu Ala Gly Ala
      35             40             45

Thr His Gly Lys Ala Gly Arg Lys Ala Thr Val Ser Asp Trp Met Glu
      50             55             60

Met Glu Lys Asp Arg Gly Ile Ser Ile Ala Ser Ser Ala Leu Gln Phe
      65             70             75             80

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<400> 493															
cgcgaaatggc ttcctctttaa gccccgattg cgtgggggtgc gtgagcctca aactcgagga															60
gggttaaate atctgcggaa agcatgctta gaatgttgcc															115
Met Thr Val Arg Pro															15
atc gtt att cat gga gat cct gtt ctc cac aac cct acc cag ctt gtt															163
Ile Val Ile His Gly Asp Pro Val Leu His Asn Pro Thr Gln Leu Val															20
act gag gat gtc tct gaa ctg cag gaa cta att gca gat atg tac gag															211
Thr Glu Asp Val Ser Glu Leu Gln Glu Leu Ile Ala Asp Met Tyr Glu															35
acg atg gat gtc gcc aat ggt gtg ggt ctt gcg gcc aac cag att ggt															259
Thr Met Asp Val Ala Asn Gly Val Gly Leu Ala Ala Asn Gln Ile Gly															40
gtg tcc aag cgc att ttt gtt tat gac tgt cct gat gat gag ggc gtg															307
Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro Asp Asp Glu Gly Val															55
atg cac aag ggt tgt ttc atc aat cct gtg ttg gaa acc tct gaa atc															355
Met His Lys Gly Cys Phe Ile Asn Pro Val Leu Glu Thr Ser Glu Ile															70
cca gag acc atg cct gcc gat gat ggc tcc gac gag gaa ggc tgc ctg															403
Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp Glu Glu Gly Cys Leu															90
tct gtt cct ggc gag ggc ttc ccc act ggc cgt gct cat tgg gcg aag															451
Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg Ala His Trp Ala Lys															105
gtt act gga ctg aat gaa aag ggc gag gaa gtt tct gtt gag gct gag															499
Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val Ser Val Glu Ala Glu															120
ggg ttc ttg gct cgt tgc ttc cag cat gag gtt ggc cac ctt gat ggt															547
Gly Phe Leu Ala Arg Cys Phe Gln His Glu Val Gly His Leu Asp Gly															

135	140	145	
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Phe Leu Tyr Thr Asp Val Leu Ile Gly Arg Trp Lys Arg Met Ala Lys			
150	155	160	165
aag gct att aag gcc aat ggg tgg act gag cct ggt ttg acc tgg atg			643
Lys Ala Ile Lys Ala Asn Gly Trp Thr Glu Pro Gly Leu Thr Trp Met			
	170	175	180
ccg ggt gaa gat gag gat cct ttc ggg cat gac gcc tat gtc ttc ccc			691
Pro Gly Glu Asp Glu Asp Pro Phe Gly His Asp Ala Tyr Val Phe Pro			
	185	190	195
gtt tcc gca gcc aga aac ctg ccg tcg gcg atc gtg ttg ttg cac gtc			739
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<212> PRT

<213> Corynebacterium glutamicum

<400> 494

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35 40 45

Ala Asn Gln Ile Gly Val Ser Lys Arg Ile Phe Val Tyr Asp Cys Pro
50 55 60

Asp Asp Glu Gly Val Met His Lys Gly Cys Phe Ile Asn Pro Val Leu
65 70 75 80

Glu Thr Ser Glu Ile Pro Glu Thr Met Pro Ala Asp Asp Gly Ser Asp
85 90 95

Glu Glu Gly Cys Leu Ser Val Pro Gly Glu Gly Phe Pro Thr Gly Arg
100 105 110

Ala His Trp Ala Lys Val Thr Gly Leu Asn Glu Lys Gly Glu Glu Val
115 120 125

Ser Val Glu Ala Glu Gly Phe Leu Ala Arg Cys Phe Gln His Glu Val
130 135 140

Gly His Leu Asp Gly Phe Leu Tyr Thr Asp Val Leu Ile Gly Arg Trp
145 150 155 160

Lys Arg Met Ala Lys Lys Ala Ile Lys Ala Asn Gly Trp Thr Glu Pro
165 170 175

Gly Leu Thr Trp Met Pro Gly Glu Asp Glu Asp Pro Phe Gly His Asp
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Ala Tyr Val Phe Pro Val Ser Ala Ala Arg Asn Leu Pro Ser Ala Ile
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Val Leu Leu His Val
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 Met Ala Val Arg Glu
 1 5
 gtc aga tta ttt gga gat ccc gta ctt gtg agt cgg gca gat gag gtc 163
 Val Arg Leu Phe Gly Asp Pro Val Leu Val Ser Arg Ala Asp Glu Val
 10 15 20
 gtg gac ttc gat gaa tca ctg tcc acc ctg atc gat gac atg ttt gac 211
 Val Asp Phe Asp Glu Ser Leu Ser Thr Leu Ile Asp Asp Met Phe Asp
 25 30 35
 acc atg gaa gat gcc ggt ggc gtt ggt cta gca gca aac cag gtg ggt 259
 Thr Met Glu Asp Ala Gly Gly Val Gly Leu Ala Ala Asn Gln Val Gly
 40 45 50
 gtt tta agg cgc gtg ttc gtg ttt gat acc tcc cac cag gag ggt gga 307
 Val Leu Arg Arg Val Phe Val Phe Asp Thr Ser His Gln Glu Gly Gly
 55 60 65
 ttg cgc gga cat gtg atc aac ccg gtg tgg gag cct ctc act gag gac 355
 Leu Arg Gly His Val Ile Asn Pro Val Trp Glu Pro Leu Thr Glu Asp
 70 75 80 85
 acc cag act ggc aaa gag ggc tgt ttg tcc atc cct gat gtc tcg gct 403
 Thr Gln Thr Gly Lys Glu Gly Cys Leu Ser Ile Pro Asp Val Ser Ala
 90 95 100
 gag acc acc cgc tat gaa acg gtt cgg ctg tct ggc cag gac cgc gac 451
 Glu Thr Thr Arg Tyr Glu Thr Val Arg Leu Ser Gly Gln Asp Arg Asp
 105 110 115
 ggc aat cca gtg ggg ttt gtg gcc aat gga ttg ttg gcc agg tgc atc 499
 Gly Asn Pro Val Gly Phe Val Ala Asn Gly Leu Leu Ala Arg Cys Ile
 120 125 130
 caa cac gaa act gat cac ctt gat ggc gtg ctg ttt ttg aag cgc ctt 547
 Gln His Glu Thr Asp His Leu Asp Gly Val Leu Phe Leu Lys Arg Leu
 135 140 145
 gat cca gct gaa cgt aaa gca gcc atg ggc gtt att cgc gcg tct gca 595

Asp Pro Ala Glu Arg Lys Ala Ala Met Gly Val Ile Arg Ala Ser Ala
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 Trp Phe Asn Lys

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 35 40 45
 Ala Asn Gln Val Gly Val Leu Arg Arg Val Phe Val Phe Asp Thr Ser
 50 55 60
 His Gln Glu Gly Gly Leu Arg Gly His Val Ile Asn Pro Val Trp Glu
 65 70 75 80
 Pro Leu Thr Glu Asp Thr Gln Thr Gly Lys Glu Gly Cys Leu Ser Ile
 85 90 95
 Pro Asp Val Ser Ala Glu Thr Thr Arg Tyr Glu Thr Val Arg Leu Ser
 100 105 110
 Gly Gln Asp Arg Asp Gly Asn Pro Val Gly Phe Val Ala Asn Gly Leu
 115 120 125
 Leu Ala Arg Cys Ile Gln His Glu Thr Asp His Leu Asp Gly Val Leu
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 Phe Leu Lys Arg Leu Asp Pro Ala Glu Arg Lys Ala Ala Met Gly Val
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 Ile Arg Ala Ser Ala Trp Phe Asn Lys
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			20					25					30			
Ala	Gly	Asp	Gln	Val	His	Ile	Leu	Arg	Met	Glu	Ala	Phe	Asp	Ser	Asp	
		35					40					45				
Ala	Asn	Ile	Val	Gly	Glu	Arg	Asp	Ile	Glu	Ala	His	Ala	Glu	Gln	Val	
	50					55					60					
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				Met	Thr	Asp	Phe	Lys									
				1				5									
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Leu	Ile	Ser	Asp	Thr	Glu	Trp	Arg	Glu	Arg	Leu	Thr	Pro	Gln	Glu	Phe		
				10					15					20			
cat	gtc	ctc	cgc	gaa	gcc	ggc	acc	gaa	cca	cct	cac	gtc	ggc	gaa	tac	211	
His	Val	Leu	Arg	Glu	Ala	Gly	Thr	Glu	Pro	Pro	His	Val	Gly	Glu	Tyr		
			25					30					35				
acc	aac	acc	acc	acc	gaa	ggc	gtg	tac	tcc	tgt	cgc	gcc	tgt	ggc	gaa	259	
Thr	Asn	Thr	Thr	Thr	Glu	Gly	Val	Tyr	Ser	Cys	Arg	Ala	Cys	Gly	Glu		
			40				45					50					
gag	tta	ttc	cgc	tcc	acc	gag	aag	ttt	gaa	tcc	cac	tgc	ggc	tgg	cct	307	
Glu	Leu	Phe	Arg	Ser	Thr	Glu	Lys	Phe	Glu	Ser	His	Cys	Gly	Trp	Pro		
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Ser	Phe	Phe	Ser	Pro	Leu	Ala	Gly	Asp	Lys	Ile	Ile	Glu	Lys	Glu	Asp		
	70				75					80					85		
ctt	tcc	ctc	ggc	atg	cgt	cgc	gtt	gag	att	ctg	tgc	gct	aac	tgc	ggc	403	
Leu	Ser	Leu	Gly	Met	Arg	Arg	Val	Glu	Ile	Leu	Cys	Ala	Asn	Cys	Gly		
				90					95					100			
tct	cac	atg	ggc	cac	gtc	ttc	gaa	ggc	gaa	ggc	tac	gac	acc	ccc	acc	451	
Ser	His	Met	Gly	His	Val	Phe	Glu	Gly	Glu	Gly	Tyr	Asp	Thr	Pro	Thr		
			105					110					115				
gat	ctt	cgt	tac	tgc	att	aac	tcc	atc	agc	ttg	aag	ctg	gaa	gaa	aag	499	
Asp	Leu	Arg	Tyr	Cys	Ile	Asn	Ser	Ile	Ser	Leu	Lys	Leu	Glu	Glu	Lys		

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 Pro Val Ser
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 His Val Gly Glu Tyr Thr Asn Thr Thr Thr Glu Gly Val Tyr Ser Cys
 35 40 45
 Arg Ala Cys Gly Glu Glu Leu Phe Arg Ser Thr Glu Lys Phe Glu Ser
 50 55 60
 His Cys Gly Trp Pro Ser Phe Phe Ser Pro Leu Ala Gly Asp Lys Ile
 65 70 75 80
 Ile Glu Lys Glu Asp Leu Ser Leu Gly Met Arg Arg Val Glu Ile Leu
 85 90 95
 Cys Ala Asn Cys Gly Ser His Met Gly His Val Phe Glu Gly Glu Gly
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 Tyr Asp Thr Pro Thr Asp Leu Arg Tyr Cys Ile Asn Ser Ile Ser Leu
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 Met Thr Lys Asp Val
 1 5
 cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa 163
 His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu
 10 15 20

ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca	211
Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala	
25 30 35	
cct gag cac tca cag ctg gtc agc tac ctg aac aac gcc atc aag gca	259
Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala	
40 45 50	
cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa	307
Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu	
55 60 65	
gtt atg atc gtc gac ggc ttc acc ggc cgt gtc ctt gcc ggc cgc cga	355
Val Met Ile Val Asp Gly Phe Thr Gly Arg Val Leu Ala Gly Arg Arg	
70 75 80 85	
tac aac gaa ggc atg cac cag gcg atc gaa gcc aaa gag cgc gta gag	403
Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala Lys Glu Arg Val Glu	
90 95 100	
atc aaa aac gag aac cag acc ctg gcg acc gtt acc ctc cag aac tac	451
Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val Thr Leu Gln Asn Tyr	
105 110 115	
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Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr Gly Thr Ala Glu Thr	
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gaa gca gca gag ctc aac cag atc tac aag ctc gac gtc atc gcg atc	547
Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu Asp Val Ile Ala Ile	
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cca acc aac cga cca aac cag cgc gaa gac ttg acc gac ttg gtg tac	595
Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu Thr Asp Leu Val Tyr	
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aaa acc caa gag gct aag ttc gca gca gtc gtc gac gac atc gca gaa	643
Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val Asp Asp Ile Ala Glu	
170 175 180	
cgc acc gaa aag ggc caa cca gtc ctc gtc ggt acc gtc tcc gtc gag	691
Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly Thr Val Ser Val Glu	
185 190 195	
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Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys Arg Gly Ile Lys His	
200 205 210	
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Asn Val Leu Asn Ala Lys His His Glu Gln Glu Ala Gln Ile Val Ala	
215 220 225	
cag gca ggt ctt cca ggc gcc gtc acc gtt gcc acc aac atg gcg ggc	835
Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala Thr Asn Met Ala Gly	
230 235 240 245	
cgt gga acc gac atc gtg ctc ggc gga aac cca gaa atc ctc ctc gac	883
Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro Glu Ile Leu Leu Asp	
250 255 260	

atc	aaa	ctc	cgc	gaa	cgt	gga	ctt	gat	cct	ttc	gaa	gac	gaa	gaa	agc	931
Ile	Lys	Leu	Arg	Glu	Arg	Gly	Leu	Asp	Pro	Phe	Glu	Asp	Glu	Glu	Ser	
			265					270					275			
tac	cag	gaa	gcc	tgg	gac	gct	gaa	ctt	cca	gca	atg	aag	cag	cga	tgc	979
Tyr	Gln	Glu	Ala	Trp	Asp	Ala	Glu	Leu	Pro	Ala	Met	Lys	Gln	Arg	Cys	
		280					285					290				
gaa	gaa	cgt	ggc	gac	aaa	gtc	cgc	gaa	gcc	gga	gga	ctc	tac	gtc	ctt	1027
Glu	Glu	Arg	Gly	Asp	Lys	Val	Arg	Glu	Ala	Gly	Gly	Leu	Tyr	Val	Leu	
		295				300					305					
ggc	acc	gaa	cgc	cac	gaa	tcc	cga	cgc	atc	gac	aac	cag	ctg	cgc	ggt	1075
Gly	Thr	Glu	Arg	His	Glu	Ser	Arg	Arg	Ile	Asp	Asn	Gln	Leu	Arg	Gly	
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cgt	tct	gca	cgt	cag	ggc	gac	cca	gga	tcc	acc	cgc	ttc	tat	ctc	tct	1123
Arg	Ser	Ala	Arg	Gln	Gly	Asp	Pro	Gly	Ser	Thr	Arg	Phe	Tyr	Leu	Ser	
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Met	Arg	Asp	Asp	Leu	Met	Val	Arg	Phe	Val	Gly	Pro	Thr	Met	Glu	Asn	
			345					350					355			
atg	atg	aac	agg	ctc	aac	gtc	cca	gac	gat	gtg	ccc	atc	gaa	tcc	aaa	1219
Met	Met	Asn	Arg	Leu	Asn	Val	Pro	Asp	Asp	Val	Pro	Ile	Glu	Ser	Lys	
		360					365					370				
acc	gtc	acc	aac	tcc	atc	aag	ggc	gcc	caa	gct	cag	gtg	gag	aac	cag	1267
Thr	Val	Thr	Asn	Ser	Ile	Lys	Gly	Ala	Gln	Ala	Gln	Val	Glu	Asn	Gln	
		375				380					385					
aac	ttc	gaa	atg	cgt	aag	aac	gtt	ctg	aag	tac	gac	gaa	gtc	atg	aac	1315
Asn	Phe	Glu	Met	Arg	Lys	Asn	Val	Leu	Lys	Tyr	Asp	Glu	Val	Met	Asn	
390					395					400					405	
gaa	cag	cgc	aag	gtt	atc	tac	agc	gag	cga	cgc	gaa	atc	ctc	gaa	tcc	1363
Glu	Gln	Arg	Lys	Val	Ile	Tyr	Ser	Glu	Arg	Arg	Glu	Ile	Leu	Glu	Ser	
			410					415					420			
gca	gac	atc	tcc	cgc	tac	atc	caa	aac	atg	atc	gaa	gaa	aca	gtc	agc	1411
Ala	Asp	Ile	Ser	Arg	Tyr	Ile	Gln	Asn	Met	Ile	Glu	Glu	Thr	Val	Ser	
			425					430					435			
gca	tac	gtc	gac	ggc	gcc	acc	gcc	aac	ggc	tac	gtc	gaa	gac	tgg	gac	1459
Ala	Tyr	Val	Asp	Gly	Ala	Thr	Ala	Asn	Gly	Tyr	Val	Glu	Asp	Trp	Asp	
		440					445					450				
ctc	gac	aaa	ctc	tgg	aac	gcc	ctc	gaa	gcc	ctc	tac	gac	cca	tcg	atc	1507
Leu	Asp	Lys	Leu	Trp	Asn	Ala	Leu	Glu	Ala	Leu	Tyr	Asp	Pro	Ser	Ile	
	455					460					465					
aac	tgg	acc	gac	ctc	gtc	gaa	ggc	agc	gaa	tac	ggc	aaa	cca	ggg	gag	1555
Asn	Trp	Thr	Asp	Leu	Val	Glu	Gly	Ser	Glu	Tyr	Gly	Lys	Pro	Gly	Glu	
470					475					480					485	
ctg	tcc	gcc	gaa	gat	cta	cgc	acc	gca	ctc	gtc	aac	gac	gcc	cac	gcc	1603
Leu	Ser	Ala	Glu	Asp	Leu	Arg	Thr	Ala	Leu	Val	Asn	Asp	Ala	His	Ala	
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gaa	tac	gca	aaa	ctc	gaa	gaa	gcc	gta	tcc	gca	atc	ggc	ggc	gaa	gca	1651

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 Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met Pro Val Ile Asp Thr
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 Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr Leu Lys Glu Gly Ile
 535 540 545
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 Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu Val Glu Tyr Gln Lys
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 Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser Ser Ser Ser Lys Thr
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<213> Corynebacterium glutamicum

<400> 502

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 35 40 45
 Asn Ala Ile Lys Ala Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile
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 Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
 65 70 75 80
 Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala
 85 90 95
 Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val
 100 105 110
 Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr
 115 120 125
 Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu
 130 135 140

Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu
 145 150 155 160
 Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val
 165 170 175
 Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly
 180 185 190
 Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys
 195 200 205
 Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu
 210 215 220
 Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala
 225 230 235 240
 Thr Asn Met Ala Gly Arg Gly Thr Asp Ile Val Leu Gly Gly Asn Pro
 245 250 255
 Glu Ile Leu Leu Asp Ile Lys Leu Arg Glu Arg Gly Leu Asp Pro Phe
 260 265 270
 Glu Asp Glu Glu Ser Tyr Gln Glu Ala Trp Asp Ala Glu Leu Pro Ala
 275 280 285
 Met Lys Gln Arg Cys Glu Glu Arg Gly Asp Lys Val Arg Glu Ala Gly
 290 295 300
 Gly Leu Tyr Val Leu Gly Thr Glu Arg His Glu Ser Arg Arg Ile Asp
 305 310 315 320
 Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro Gly Ser Thr
 325 330 335
 Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg Phe Val Gly
 340 345 350
 Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro Asp Asp Val
 355 360 365
 Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly Ala Gln Ala
 370 375 380
 Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val Leu Lys Tyr
 385 390 395 400
 Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser Glu Arg Arg
 405 410 415
 Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln Asn Met Ile
 420 425 430
 Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala Asn Gly Tyr
 435 440 445
 Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu Glu Ala Leu
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 Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly Ser Glu Tyr

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Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr Ala Leu Val						
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Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala Val Ser Ala						
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Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met Val Leu Met						
		515		520		525
Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu Met Asp Tyr						
		530		535		540
Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg Asp Pro Leu						
		545		550		555
Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly Met Lys Asp						
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Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser Ala Ser Ser						
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Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu Pro						
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<211> 832

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(832)

<223> FRXA00124

<400> 503

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Met Thr Lys Asp Val	
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cac tac gaa gtc gac gaa cgt aaa aag acc gtc ggt gtg aaa gaa gaa	163
His Tyr Glu Val Asp Glu Arg Lys Lys Thr Val Gly Val Lys Glu Glu	
10 15 20	

ggc gtc gaa tac gtc gaa gac caa ctc ggc atc gac aac ctc tac gca	211
Gly Val Glu Tyr Val Glu Asp Gln Leu Gly Ile Asp Asn Leu Tyr Ala	
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Pro Glu His Ser Gln Leu Val Ser Tyr Leu Asn Asn Ala Ile Lys Ala	
40 45 50	

cag gaa ctg ttc acc cgc gac aag gac tac atc gtc cgc aac ggc gaa	307
Gln Glu Leu Phe Thr Arg Asp Lys Asp Tyr Ile Val Arg Asn Gly Glu	
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70					75					80					85	
tac	aac	gaa	ggc	atg	cac	cag	gcg	atc	gaa	gcc	aaa	gag	cgc	gta	gag	403
Tyr	Asn	Glu	Gly	Met	His	Gln	Ala	Ile	Glu	Ala	Lys	Glu	Arg	Val	Glu	
				90					95					100		
atc	aaa	aac	gag	aac	cag	acc	ctg	gcg	acc	gtt	acc	ctc	cag	aac	tac	451
Ile	Lys	Asn	Glu	Asn	Gln	Thr	Leu	Ala	Thr	Val	Thr	Leu	Gln	Asn	Tyr	
			105					110					115			
ttc	cgc	ctc	tac	acc	aaa	ctc	gcc	ggc	atg	acc	ggg	acc	gca	gag	acc	499
Phe	Arg	Leu	Tyr	Thr	Lys	Leu	Ala	Gly	Met	Thr	Gly	Thr	Ala	Glu	Thr	
		120					125					130				
gaa	gca	gca	gag	ctc	aac	cag	atc	tac	aag	ctc	gac	gtc	atc	gcg	atc	547
Glu	Ala	Ala	Glu	Leu	Asn	Gln	Ile	Tyr	Lys	Leu	Asp	Val	Ile	Ala	Ile	
	135					140					145					
cca	acc	aac	cga	cca	aac	cag	cgc	gaa	gac	ttg	acc	gac	ttg	gtg	tac	595
Pro	Thr	Asn	Arg	Pro	Asn	Gln	Arg	Glu	Asp	Leu	Thr	Asp	Leu	Val	Tyr	
					155					160					165	
aaa	acc	caa	gag	gct	aag	ttc	gca	gca	gtc	gtc	gac	gac	atc	gca	gaa	643
Lys	Thr	Gln	Glu	Ala	Lys	Phe	Ala	Ala	Val	Val	Asp	Asp	Ile	Ala	Glu	
				170					175					180		
cgc	acc	gaa	aag	ggc	caa	cca	gtc	ctc	gtc	ggg	acc	gtc	tcc	gtc	gag	691
Arg	Thr	Glu	Lys	Gly	Gln	Pro	Val	Leu	Val	Gly	Thr	Val	Ser	Val	Glu	
			185					190					195			
cgc	tcc	gaa	tac	ctc	tcc	cag	ctg	ttg	acc	aaa	cga	ggc	atc	aag	cac	739
Arg	Ser	Glu	Tyr	Leu	Ser	Gln	Leu	Leu	Thr	Lys	Arg	Gly	Ile	Lys	His	
		200					205					210				
aac	gtc	ctc	aat	gcg	aag	cac	cac	gag	cag	gaa	gca	cag	atc	gtt	gct	787
Asn	Val	Leu	Asn	Ala	Lys	His	His	Glu	Gln	Glu	Ala	Gln	Ile	Val	Ala	
	215					220					225					
cag	gca	ggt	ctt	cca	ggc	gcc	gtc	acc	gtt	gcc	acc	aac	atg	gcg		832
Gln	Ala	Gly	Leu	Pro	Gly	Ala	Val	Thr	Val	Ala	Thr	Asn	Met	Ala		
	230				235					240						

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<211> 244

<212> PRT

<213> Corynebacterium glutamicum

<400> 504

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Gly	Val	Lys	Glu	Glu	Gly	Val	Glu	Tyr	Val	Glu	Asp	Gln	Leu	Gly	Ile
			20					25					30		

Asp	Asn	Leu	Tyr	Ala	Pro	Glu	His	Ser	Gln	Leu	Val	Ser	Tyr	Leu	Asn
		35					40					45			

Asn	Ala	Ile	Lys	Ala	Gln	Glu	Leu	Phe	Thr	Arg	Asp	Lys	Asp	Tyr	Ile
	50					55					60				

Val Arg Asn Gly Glu Val Met Ile Val Asp Gly Phe Thr Gly Arg Val
 65 70 75 80
 Leu Ala Gly Arg Arg Tyr Asn Glu Gly Met His Gln Ala Ile Glu Ala
 85 90 95
 Lys Glu Arg Val Glu Ile Lys Asn Glu Asn Gln Thr Leu Ala Thr Val
 100 105 110
 Thr Leu Gln Asn Tyr Phe Arg Leu Tyr Thr Lys Leu Ala Gly Met Thr
 115 120 125
 Gly Thr Ala Glu Thr Glu Ala Ala Glu Leu Asn Gln Ile Tyr Lys Leu
 130 135 140
 Asp Val Ile Ala Ile Pro Thr Asn Arg Pro Asn Gln Arg Glu Asp Leu
 145 150 155 160
 Thr Asp Leu Val Tyr Lys Thr Gln Glu Ala Lys Phe Ala Ala Val Val
 165 170 175
 Asp Asp Ile Ala Glu Arg Thr Glu Lys Gly Gln Pro Val Leu Val Gly
 180 185 190
 Thr Val Ser Val Glu Arg Ser Glu Tyr Leu Ser Gln Leu Leu Thr Lys
 195 200 205
 Arg Gly Ile Lys His Asn Val Leu Asn Ala Lys His His Glu Gln Glu
 210 215 220
 Ala Gln Ile Val Ala Gln Ala Gly Leu Pro Gly Ala Val Thr Val Ala
 225 230 235 240
 Thr Asn Met Ala

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA02462

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 Glu Ala Gly Gly Leu Tyr Val Leu Gly Thr Glu Arg His Glu Ser Arg
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 cgc atc gac aac cag ctg cgc ggt cgt tct gca cgt cag ggc gac cca 96
 Arg Ile Asp Asn Gln Leu Arg Gly Arg Ser Ala Arg Gln Gly Asp Pro
 20 25 30
 gga tcc acc cgc ttc tat ctc tct atg cgc gac gac ctg atg gtt cgc 144
 Gly Ser Thr Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg
 35 40 45

ttc gtc ggc cca acc atg gaa aac atg atg aac agg ctc aac gtc cca	192
Phe Val Gly Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro	
50 55 60	
gac gat gtg ccc atc gaa tcc aaa acc gtc acc aac tcc atc aag ggc	240
Asp Asp Val Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly	
65 70 75 80	
gcc caa gct cag gtg gag aac cag aac ttc gaa atg cgt aag aac gtt	288
Ala Gln Ala Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val	
85 90 95	
ctg aag tac gac gaa gtc atg aac gaa cag cgc aag gtt atc tac agc	336
Leu Lys Tyr Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser	
100 105 110	
gag cga cgc gaa atc ctc gaa tcc gca gac atc tcc cgc tac atc caa	384
Glu Arg Arg Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln	
115 120 125	
aac atg atc gaa gaa aca gtc agc gca tac gtc gac ggc gcc acc gcc	432
Asn Met Ile Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala	
130 135 140	
aac ggc tac gtc gaa gac tgg gac ctc gac aaa ctc tgg aac gcc ctc	480
Asn Gly Tyr Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu	
145 150 155 160	
gaa gcc ctc tac gac cca tcg atc aac tgg acc gac ctc gtc gaa ggc	528
Glu Ala Leu Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly	
165 170 175	
agc gaa tac ggc aaa cca ggg gag ctg tcc gcc gaa gat cta cgc acc	576
Ser Glu Tyr Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr	
180 185 190	
gca ctc gtc aac gac gcc cac gcc gaa tac gca aaa ctc gaa gaa gcc	624
Ala Leu Val Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala	
195 200 205	
gta tcc gca atc ggc ggc gaa gca cag atc cgc aac atc gaa cga atg	672
Val Ser Ala Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met	
210 215 220	
gtg ctc atg cca gtc atc gac acc aaa tgg cgc gaa cac ctc tac gaa	720
Val Leu Met Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu	
225 230 235 240	
atg gac tac ctg aaa gaa ggc atc ggc ctg cgc gca atg gca cag cgc	768
Met Asp Tyr Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg	
245 250 255	
gac cca ctg gtc gaa tac caa aag gaa ggc ggc gac atg ttc aac ggc	816
Asp Pro Leu Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly	
260 265 270	
atg aaa gac ggc atc aag gaa gaa acc gtc cgc cag ctc ttc ctc tcc	864
Met Lys Asp Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser	
275 280 285	
gca agc agt tca tca agc aag acg cgg aag tcg ctg act aac tca gaa	912

Ala Ser Ser Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu
 290 295 300

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 Pro
 305

938

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 506
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Gly Ser Thr Arg Phe Tyr Leu Ser Met Arg Asp Asp Leu Met Val Arg
 35 40 45

Phe Val Gly Pro Thr Met Glu Asn Met Met Asn Arg Leu Asn Val Pro
 50 55 60

Asp Asp Val Pro Ile Glu Ser Lys Thr Val Thr Asn Ser Ile Lys Gly
 65 70 75 80

Ala Gln Ala Gln Val Glu Asn Gln Asn Phe Glu Met Arg Lys Asn Val
 85 90 95

Leu Lys Tyr Asp Glu Val Met Asn Glu Gln Arg Lys Val Ile Tyr Ser
 100 105 110

Glu Arg Arg Glu Ile Leu Glu Ser Ala Asp Ile Ser Arg Tyr Ile Gln
 115 120 125

Asn Met Ile Glu Glu Thr Val Ser Ala Tyr Val Asp Gly Ala Thr Ala
 130 135 140

Asn Gly Tyr Val Glu Asp Trp Asp Leu Asp Lys Leu Trp Asn Ala Leu
 145 150 155 160

Glu Ala Leu Tyr Asp Pro Ser Ile Asn Trp Thr Asp Leu Val Glu Gly
 165 170 175

Ser Glu Tyr Gly Lys Pro Gly Glu Leu Ser Ala Glu Asp Leu Arg Thr
 180 185 190

Ala Leu Val Asn Asp Ala His Ala Glu Tyr Ala Lys Leu Glu Glu Ala
 195 200 205

Val Ser Ala Ile Gly Gly Glu Ala Gln Ile Arg Asn Ile Glu Arg Met
 210 215 220

Val Leu Met Pro Val Ile Asp Thr Lys Trp Arg Glu His Leu Tyr Glu
 225 230 235 240

Met Asp Tyr Leu Lys Glu Gly Ile Gly Leu Arg Ala Met Ala Gln Arg
 245 250 255

Asp Pro Leu Val Glu Tyr Gln Lys Glu Gly Gly Asp Met Phe Asn Gly
260 265 270

Met Lys Asp Gly Ile Lys Glu Glu Thr Val Arg Gln Leu Phe Leu Ser
275 280 285

Ala Ser Ser Ser Ser Ser Lys Thr Arg Lys Ser Leu Thr Asn Ser Glu
290 295 300

Pro
305

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<211> 888

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA00125

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gttatcattt ccgtatcgct atttataagg acgactgctc gtg ttt gga ttg tcc 115
Val Phe Gly Leu Ser
1 5

aag gtg ctc cgc gtc ggc gaa ggc cgt gcc gtg aag cga ctt cac aag 163
Lys Val Leu Arg Val Gly Glu Gly Arg Ala Val Lys Arg Leu His Lys
10 15 20

atc gct gac cag gtt atc gcg ctt gaa gat aag ttc gcc aac cta acc 211
Ile Ala Asp Gln Val Ile Ala Leu Glu Asp Lys Phe Ala Asn Leu Thr
25 30 35

gat gag gag ctc aag gca aaa aca gcc gag ttc aaa gaa cgc atc gct 259
Asp Glu Glu Leu Lys Ala Lys Thr Ala Glu Phe Lys Glu Arg Ile Ala
40 45 50

ggc ggt gaa gga ctc gac gaa atc ttc ctc gaa gcg ttc gca aca gcc 307
Gly Gly Glu Gly Leu Asp Glu Ile Phe Leu Glu Ala Phe Ala Thr Ala
55 60 65

cgt gaa gca gct tgg cgt gtg ctc ggc cag aag cac tac cat gta caa 355
Arg Glu Ala Ala Trp Arg Val Leu Gly Gln Lys His Tyr His Val Gln
70 75 80 85

atc atg ggt ggc gca gcg ctg cac ttt ggc aac gtc gcc gaa atg cgc 403
Ile Met Gly Gly Ala Ala Leu His Phe Gly Asn Val Ala Glu Met Arg
90 95 100

acc ggc gaa ggc aaa acc ctc acc tgc gtg ctt cca gca tat ttg aac 451
Thr Gly Glu Gly Lys Thr Leu Thr Cys Val Leu Pro Ala Tyr Leu Asn
105 110 115

gca ctt gaa gga aaa ggc gtc cac gtt gtc acc gtc aat gat tac cta 499
Ala Leu Glu Gly Lys Gly Val His Val Val Thr Val Asn Asp Tyr Leu

120	125	130	
gca aaa cgt gac gca gaa atg atg ggc cgt gtg cac cgc tac tta ggc Ala Lys Arg Asp Ala Glu Met Met Gly Arg Val His Arg Tyr Leu Gly 135 140 145			547
ctc gaa gtg gga gta atc ctc tct gac atg cgc cca gac gag cgc cgc Leu Glu Val Gly Val Ile Leu Ser Asp Met Arg Pro Asp Glu Arg Arg 150 155 160 165			595
gaa gcc tac gct gcc gac att acc tac ggc acc aac aac gaa ctc ggc Glu Ala Tyr Ala Ala Asp Ile Thr Tyr Gly Thr Asn Asn Glu Leu Gly 170 175 180			643
ttc gac tac ctg cgc gac aac atg gca cgc tcc cta agc gac ctc gtg Phe Asp Tyr Leu Arg Asp Asn Met Ala Arg Ser Leu Ser Asp Leu Val 185 190 195			691
cag cgt gga cac aac tac gcc att gtc gac gaa gta gac tcc atc ctc Gln Arg Gly His Asn Tyr Ala Ile Val Asp Glu Val Asp Ser Ile Leu 200 205 210			739
atc gac gaa gcc cgc acc cca ctg att atc tcc ggg acc agt aga cgg Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser Gly Thr Ser Arg Arg 215 220 225			787
cac atc gca gtt cta caa cgt ctt cgc aca gat cgt ccc acg cat gac His Ile Ala Val Leu Gln Arg Leu Arg Thr Asp Arg Pro Thr His Asp 230 235 240 245			835
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<210> 508

<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Val Phe Gly Leu Ser Lys Val Leu Arg Val Gly Glu Gly Arg Ala Val
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Lys Arg Leu His Lys Ile Ala Asp Gln Val Ile Ala Leu Glu Asp Lys
20 25 30

Phe Ala Asn Leu Thr Asp Glu Glu Leu Lys Ala Lys Thr Ala Glu Phe
35 40 45

Lys Glu Arg Ile Ala Gly Gly Glu Gly Leu Asp Glu Ile Phe Leu Glu
50 55 60

Ala Phe Ala Thr Ala Arg Glu Ala Ala Trp Arg Val Leu Gly Gln Lys
65 70 75 80

His Tyr His Val Gln Ile Met Gly Gly Ala Ala Leu His Phe Gly Asn
85 90 95

Val Ala Glu Met Arg Thr Gly Glu Gly Lys Thr Leu Thr Cys Val Leu
100 105 110

Pro Ala Tyr Leu Asn Ala Leu Glu Gly Lys Gly Val His Val Val Thr
 115 120 125

Val Asn Asp Tyr Leu Ala Lys Arg Asp Ala Glu Met Met Gly Arg Val
 130 135 140

His Arg Tyr Leu Gly Leu Glu Val Gly Val Ile Leu Ser Asp Met Arg
 145 150 155 160

Pro Asp Glu Arg Arg Glu Ala Tyr Ala Ala Asp Ile Thr Tyr Gly Thr
 165 170 175

Asn Asn Glu Leu Gly Phe Asp Tyr Leu Arg Asp Asn Met Ala Arg Ser
 180 185 190

Leu Ser Asp Leu Val Gln Arg Gly His Asn Tyr Ala Ile Val Asp Glu
 195 200 205

Val Asp Ser Ile Leu Ile Asp Glu Ala Arg Thr Pro Leu Ile Ile Ser
 210 215 220

Gly Thr Ser Arg Arg His Ile Ala Val Leu Gln Arg Leu Arg Thr Asp
 225 230 235 240

Arg Pro Thr His Asp Gln Gly Arg Ser Leu Arg Ser Arg Arg Thr
 245 250 255

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 <211> 1443
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1420)
 <223> RXA00687

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aaatatgtgg gtttaagtgc tgaggaggcc aggaggataa gtg tcc gcc att att 115
 Val Ser Ala Ile Ile
 1 5

cag gca ttc aag gac gcc gat ctg cgt aag aag att ttc ttc act atc 163
 Gln Ala Phe Lys Asp Ala Asp Leu Arg Lys Lys Ile Phe Phe Thr Ile
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gca atg atc gtt cta tac cgc atc ggt gcg cag atc cct tcc ccg gga 211
 Ala Met Ile Val Leu Tyr Arg Ile Gly Ala Gln Ile Pro Ser Pro Gly
 25 30 35

gtt gac tac gca acg att agt ggt cgt ctg cgt gac ttg act cag gat 259
 Val Asp Tyr Ala Thr Ile Ser Gly Arg Leu Arg Asp Leu Thr Gln Asp
 40 45 50

cag tca agc gtt tat tcg ctg att aac ctg ttt tcc ggt gga gcg ctg 307
 Gln Ser Ser Val Tyr Ser Leu Ile Asn Leu Phe Ser Gly Gly Ala Leu
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ttg cag ctg tcc att ttt gct att ggt atc atg ccg tac atc acg gcg	355
Leu Gln Leu Ser Ile Phe Ala Ile Gly Ile Met Pro Tyr Ile Thr Ala	
70 75 80 85	
tct att atc gtg cag ctg ctg act gtg gtt att cca cac ttt gag gag	403
Ser Ile Ile Val Gln Leu Leu Thr Val Val Ile Pro His Phe Glu Glu	
90 95 100	
ttg aag aag gaa ggc cag tct ggc cag gcc aag atg atg cag tac acc	451
Leu Lys Lys Glu Gly Gln Ser Gly Gln Ala Lys Met Met Gln Tyr Thr	
105 110 115	
agg tac tta acg gtt gct ttg gcg ttg ctg cag tct tca ggc att gtc	499
Arg Tyr Leu Thr Val Ala Leu Ala Leu Leu Gln Ser Ser Gly Ile Val	
120 125 130	
gcg ttg gcg gac cgt gag cag ctg ctt ggc gca ggt att cgt gtg ctg	547
Ala Leu Ala Asp Arg Glu Gln Leu Leu Gly Ala Gly Ile Arg Val Leu	
135 140 145	
tcg gct gat cgc aac ttc ttc gat ctc att gtt ttg gtc atc acc atg	595
Ser Ala Asp Arg Asn Phe Phe Asp Leu Ile Val Leu Val Ile Thr Met	
150 155 160 165	
act gca ggt gcg gtg ctt gtg atg tgg atg ggt gag ctc atc acg gaa	643
Thr Ala Gly Ala Val Leu Val Met Trp Met Gly Glu Leu Ile Thr Glu	
170 175 180	
aag ggc gtg ggc aat ggt atg tcg ttg ctg att ttc gct ggt atc gca	691
Lys Gly Val Gly Asn Gly Met Ser Leu Leu Ile Phe Ala Gly Ile Ala	
185 190 195	
act cgc ctc cca act gat ggc atg aac att ctg ggt aac tcc ggc ggc	739
Thr Arg Leu Pro Thr Asp Gly Met Asn Ile Leu Gly Asn Ser Gly Gly	
200 205 210	
gtg gtt ttc gct gtt gtt ctg gct tcc gtt ctg atc ctg gtc att ggt	787
Val Val Phe Ala Val Val Leu Ala Ser Val Leu Ile Leu Val Ile Gly	
215 220 225	
gtt gta ttc gtt gag cag ggc cag cgt cgt att cca gtg cag tac gca	835
Val Val Phe Val Glu Gln Gly Gln Arg Arg Ile Pro Val Gln Tyr Ala	
230 235 240 245	
aag cgc atg gtg gga cgt cgc cag tac ggt ggt tct tcc act tac ctg	883
Lys Arg Met Val Gly Arg Arg Gln Tyr Gly Gly Ser Ser Thr Tyr Leu	
250 255 260	
cca ttg aag gtc aac caa gct ggt gtt atc cca gtg atc ttc gcg tct	931
Pro Leu Lys Val Asn Gln Ala Gly Val Ile Pro Val Ile Phe Ala Ser	
265 270 275	
tcg ctg att tac atg cca gtg ctg att act cag atc gtg aac tct ggt	979
Ser Leu Ile Tyr Met Pro Val Leu Ile Thr Gln Ile Val Asn Ser Gly	
280 285 290	
tcg ctg gaa gtg tct gat aac tgg tgg cag cgc aac atc att gcg cac	1027
Ser Leu Glu Val Ser Asp Asn Trp Trp Gln Arg Asn Ile Ile Ala His	
295 300 305	

ctg cag acg cct tct tcc tgg cag tac att gtt ttg tac ttt gca ctg 1075
 Leu Gln Thr Pro Ser Ser Trp Gln Tyr Ile Val Leu Tyr Phe Ala Leu 325
 310 315 320

acc atc ttc ttc tct tac ttc tat gtt tcc gtt cag tat gat cca gct 1123
 Thr Ile Phe Phe Ser Tyr Phe Tyr Val Ser Val Gln Tyr Asp Pro Ala 340
 330 335

gag cag gct gaa aac atg aag aag tac ggt gga ttt atc cct ggt att 1171
 Glu Gln Ala Glu Asn Met Lys Lys Tyr Gly Gly Phe Ile Pro Gly Ile 355
 345 350

cgt ccg ggc cgc ccg act gct gag tac ttg gga ttc gtc atg aac cgc 1219
 Arg Pro Gly Arg Pro Thr Ala Glu Tyr Leu Gly Phe Val Met Asn Arg 370
 360 365

ctg ctg ttt gtt ggt tcc ctg tac ctg gct gtc att gct gtg ctg cca 1267
 Leu Leu Phe Val Gly Ser Leu Tyr Leu Ala Val Ile Ala Val Leu Pro 385
 375 380

aac att atg ctg gat cta ggt gtt gac gcc ggt tcg gcc gga gca act 1315
 Asn Ile Met Leu Asp Leu Gly Val Asp Ala Gly Ser Ala Gly Ala Thr 405
 390 395 400

cca ttc ggc gga acc gca atc ttg att ctt gta tct gtt gca ctg acc 1363
 Pro Phe Gly Gly Thr Ala Ile Leu Ile Leu Val Ser Val Ala Leu Thr 420
 410 415

aca gtg aag cag att gag agc cag ctc ctg caa agc aac tac gaa gga 1411
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<211> 440

<212> PRT

<213> Corynebacterium glutamicum

<400> 510

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Ile Pro Ser Pro Gly Val Asp Tyr Ala Thr Ile Ser Gly Arg Leu Arg
 35 40 45

Asp Leu Thr Gln Asp Gln Ser Ser Val Tyr Ser Leu Ile Asn Leu Phe
 50 55 60

Ser Gly Gly Ala Leu Leu Gln Leu Ser Ile Phe Ala Ile Gly Ile Met
 65 70 75 80

Pro Tyr Ile Thr Ala Ser Ile Ile Val Gln Leu Leu Thr Val Val Ile
 85 90 95

Pro His Phe Glu Glu Leu Lys Lys Glu Gly Gln Ser Gly Gln Ala Lys
 100 105 110
 Met Met Gln Tyr Thr Arg Tyr Leu Thr Val Ala Leu Ala Leu Leu Gln
 115 120 125
 Ser Ser Gly Ile Val Ala Leu Ala Asp Arg Glu Gln Leu Leu Gly Ala
 130 135 140
 Gly Ile Arg Val Leu Ser Ala Asp Arg Asn Phe Phe Asp Leu Ile Val
 145 150 155 160
 Leu Val Ile Thr Met Thr Ala Gly Ala Val Leu Val Met Trp Met Gly
 165 170 175
 Glu Leu Ile Thr Glu Lys Gly Val Gly Asn Gly Met Ser Leu Leu Ile
 180 185 190
 Phe Ala Gly Ile Ala Thr Arg Leu Pro Thr Asp Gly Met Asn Ile Leu
 195 200 205
 Gly Asn Ser Gly Gly Val Val Phe Ala Val Val Leu Ala Ser Val Leu
 210 215 220
 Ile Leu Val Ile Gly Val Val Phe Val Glu Gln Gly Gln Arg Arg Ile
 225 230 235 240
 Pro Val Gln Tyr Ala Lys Arg Met Val Gly Arg Arg Gln Tyr Gly Gly
 245 250 255
 Ser Ser Thr Tyr Leu Pro Leu Lys Val Asn Gln Ala Gly Val Ile Pro
 260 265 270
 Val Ile Phe Ala Ser Ser Leu Ile Tyr Met Pro Val Leu Ile Thr Gln
 275 280 285
 Ile Val Asn Ser Gly Ser Leu Glu Val Ser Asp Asn Trp Trp Gln Arg
 290 295 300
 Asn Ile Ile Ala His Leu Gln Thr Pro Ser Ser Trp Gln Tyr Ile Val
 305 310 315 320
 Leu Tyr Phe Ala Leu Thr Ile Phe Phe Ser Tyr Phe Tyr Val Ser Val
 325 330 335
 Gln Tyr Asp Pro Ala Glu Gln Ala Glu Asn Met Lys Lys Tyr Gly Gly
 340 345 350
 Phe Ile Pro Gly Ile Arg Pro Gly Arg Pro Thr Ala Glu Tyr Leu Gly
 355 360 365
 Phe Val Met Asn Arg Leu Leu Phe Val Gly Ser Leu Tyr Leu Ala Val
 370 375 380
 Ile Ala Val Leu Pro Asn Ile Met Leu Asp Leu Gly Val Asp Ala Gly
 385 390 395 400
 Ser Ala Gly Ala Thr Pro Phe Gly Gly Thr Ala Ile Leu Ile Leu Val
 405 410 415
 Ser Val Ala Leu Thr Thr Val Lys Gln Ile Glu Ser Gln Leu Leu Gln

420

425

430

Ser Asn Tyr Glu Gly Leu Leu Lys
 435 440

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 <223> RXA02260

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 Met Ala Leu Thr Leu
 1 5
 caa atc atc ctc gtc gtc gcc agc ctg ctc atg acg gtt ttc gtc ttg 163
 Gln Ile Ile Leu Val Val Ala Ser Leu Leu Met Thr Val Phe Val Leu
 10 15 20
 ctg cac aag ggc aaa ggc ggc gga ctc tcc agc ctc ttc ggt ggc ggt 211
 Leu His Lys Gly Lys Gly Gly Gly Leu Ser Ser Leu Phe Gly Gly Gly
 25 30 35
 gtg cag tcc aat ctt tcg ggc tcc act gtt gtt gaa aag aac ctg gat 259
 Val Gln Ser Asn Leu Ser Gly Ser Thr Val Val Glu Lys Asn Leu Asp
 40 45 50
 cgc gtc acc att ttg gtt gcc gtt atc tgg att gtg tgc att gtc gca 307
 Arg Val Thr Ile Leu Val Ala Val Ile Trp Ile Val Cys Ile Val Ala
 55 60 65
 ctc aac ctc atc cag act tat tca taagacacga gcttaaaaag agc 354
 Leu Asn Leu Ile Gln Thr Tyr Ser
 70 75

<210> 512
 <211> 77
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 512
 Met Ala Leu Thr Leu Gln Ile Ile Leu Val Val Ala Ser Leu Leu Met
 1 5 10 15
 Thr Val Phe Val Leu Leu His Lys Gly Lys Gly Gly Gly Leu Ser Ser
 20 25 30
 Leu Phe Gly Gly Gly Val Gln Ser Asn Leu Ser Gly Ser Thr Val Val
 35 40 45
 Glu Lys Asn Leu Asp Arg Val Thr Ile Leu Val Ala Val Ile Trp Ile
 50 55 60

Val Cys Ile Val Ala Leu Asn Leu Ile Gln Thr Tyr Ser
 65 70 75

<210> 513
 <211> 819
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(796)
 <223> RXN00046

<400> 513
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 acctaaaacg ctgttctcaa cacaggagtt tccttaaata atg gac tta aat act 115
 Met Asp Leu Asn Thr
 1 5
 caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
 Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
 10 15 20
 gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
 Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
 25 30 35
 cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
 His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
 40 45 50
 ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307
 Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
 55 60 65
 gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
 Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
 70 75 80 85
 atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
 Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
 90 95 100
 act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
 Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
 105 110 115
 acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
 Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
 120 125 130
 atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547
 Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
 135 140 145
 ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595
 Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
 150 155 160 165

gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu
 170 175 180

 tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691
 Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro
 185 190 195

 gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739
 Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val
 200 205 210

 ggc acc gca atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787
 Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser
 215 220 225

 ctg ttg cac tagcacttag tccagcgctg cac 819
 Leu Leu His
 230

<210> 514

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 514

Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly
 1 5 10 15

 Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp
 20 25 30

 Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala
 35 40 45

 Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser
 50 55 60

 Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly
 65 70 75 80

 Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val
 85 90 95

 Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro
 100 105 110

 Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp
 115 120 125

 Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu
 130 135 140

 Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly
 145 150 155 160

 Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu
 165 170 175

Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly
 180 185 190

Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala
 195 200 205

Asn Ala Ile Ile Val Gly Thr Ala Ile Thr Asp Pro Gly Phe Ile Thr
 210 215 220

Gly Gln Phe Ala Ser Leu Leu His
 225 230

<210> 515

<211> 819

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(796)

<223> FRXA00046

<400> 515

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acctaaaaacg ctgttctcaa cacaggagtt tccttaaata atg gac tta aat act 115
 Met Asp Leu Asn Thr
 1 5

caa cgc tca aag ctc tac gca cag ctt caa ggc cag ctc att gtt tcc 163
 Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly Gln Leu Ile Val Ser
 10 15 20

gtg caa gct ccc gac ggc cat gcc atg cga gat acc cat acg ctc acc 211
 Val Gln Ala Pro Asp Gly His Ala Met Arg Asp Thr His Thr Leu Thr
 25 30 35

cat gtg gcc gca gcc tgt gtc gat ggc ggt gct cct gcc att cgc tgt 259
 His Val Ala Ala Ala Cys Val Asp Gly Gly Ala Pro Ala Ile Arg Cys
 40 45 50

ggc ggt tac ggc ggt ttg gaa gat atc cgt tca atc tcc aac cgt gtc 307
 Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser Ile Ser Asn Arg Val
 55 60 65

gac gtt ccc gtt ttc gga ctc acc aaa gaa ggc tcc gaa gga gtt tac 355
 Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly Ser Glu Gly Val Tyr
 70 75 80 85

atc acc cca acc agg gat tcc gtt cga gca gtg gca gaa tcc ggc gcc 403
 Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val Ala Glu Ser Gly Ala
 90 95 100

act gta gtc tgc gcg gat gca act ttc cga cct agg cct gac ggc tcc 451
 Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro Arg Pro Asp Gly Ser
 105 110 115

acc ttt gca gag ctg gtc act gtt gcc cac gat tcc gga att ctc atc 499
 Thr Phe Ala Glu Leu Val Thr Val Ala His Asp Ser Gly Ile Leu Ile
 120 125 130

atg gcg gac tgc gca act ccc gaa gaa gtt ctc agt gcg cat aag gct 547
 Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu Ser Ala His Lys Ala
 135 140 145

 ggc gcg gat ttt gtg tcc acc acg ctt gct gga tac acc gaa cac cgc 595
 Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly Tyr Thr Glu His Arg
 150 155 160 165

 gag aaa aca gtc ggt cca gat ttc gat tgc ctc cgc gaa gca cgt gag 643
 Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu Arg Glu Ala Arg Glu
 170 175 180

 tta gtt ccc gat gcg ttc ctc att ggc gaa ggt cgc ttc tcc aac cct 691
 Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly Arg Phe Ser Asn Pro
 185 190 195

 gcg gat gtg gcg cac ggt cgt ctc att ggt gcc aac gcg atc atc gtg 739
 Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala Asn Ala Ile Ile Val
 200 205 210

 ggc acc gga atc act gac cct ggt ttc atc act gga cag ttc gcg tca 787
 Gly Thr Gly Ile Thr Asp Pro Gly Phe Ile Thr Gly Gln Phe Ala Ser
 215 220 225

 ctg ttg cac taacacttag tccaacgctg cac 819
 Leu Leu His
 230

<210> 516

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

Met Asp Leu Asn Thr Gln Arg Ser Lys Leu Tyr Ala Gln Leu Gln Gly
 1 5 10 15

 Gln Leu Ile Val Ser Val Gln Ala Pro Asp Gly His Ala Met Arg Asp
 20 25 30

 Thr His Thr Leu Thr His Val Ala Ala Ala Cys Val Asp Gly Gly Ala
 35 40 45

 Pro Ala Ile Arg Cys Gly Gly Tyr Gly Gly Leu Glu Asp Ile Arg Ser
 50 55 60

 Ile Ser Asn Arg Val Asp Val Pro Val Phe Gly Leu Thr Lys Glu Gly
 65 70 75 80

 Ser Glu Gly Val Tyr Ile Thr Pro Thr Arg Asp Ser Val Arg Ala Val
 85 90 95

 Ala Glu Ser Gly Ala Thr Val Val Cys Ala Asp Ala Thr Phe Arg Pro
 100 105 110

 Arg Pro Asp Gly Ser Thr Phe Ala Glu Leu Val Thr Val Ala His Asp
 115 120 125

 Ser Gly Ile Leu Ile Met Ala Asp Cys Ala Thr Pro Glu Glu Val Leu

130	135	140
Ser Ala His Lys Ala Gly Ala Asp Phe Val Ser Thr Thr Leu Ala Gly		
145	150	155 160
Tyr Thr Glu His Arg Glu Lys Thr Val Gly Pro Asp Phe Asp Cys Leu		
	165	170 175
Arg Glu Ala Arg Glu Leu Val Pro Asp Ala Phe Leu Ile Gly Glu Gly		
	180	185 190
Arg Phe Ser Asn Pro Ala Asp Val Ala His Gly Arg Leu Ile Gly Ala		
	195	200 205
Asn Ala Ile Ile Val Gly Thr Gly Ile Thr Asp Pro Gly Phe Ile Thr		
	210	215 220
Gly Gln Phe Ala Ser Leu Leu His		
225	230	

<210> 517
 <211> 1445
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1422)
 <223> RXA00753

<400> 517	
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Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Val Ala Glu Ile	
1 5 10 15	
cat gag gct atc cgt caa gcc caa gac tct ggt gca cct aat gat gaa	96
His Glu Ala Ile Arg Gln Ala Gln Asp Ser Gly Ala Pro Asn Asp Glu	
20 25 30	
ctt att cct ggt gag atg tgg tca gat aag gtc gag tta ccc tca acg	144
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Ser Thr	
35 40 45	
att gat aaa gca gct gct gat gaa gct gag ata gct att gca cag caa	192
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	
50 55 60	
cag tcc caa ccc cag gcg aga gga cta gcc gct gct gca gcg tgt cag	240
Gln Ser Gln Pro Gln Ala Arg Gly Leu Ala Ala Ala Ala Ala Cys Gln	
65 70 75 80	
aca ttt tgg ccg tca cct tat caa gtt tgt ggt gct atc tta gag cgc	288
Thr Phe Trp Pro Ser Pro Tyr Gln Val Cys Gly Ala Ile Leu Glu Arg	
85 90 95	
tat atc cag cag ggt gcc cag ttt ggg tgg atg ttg ttg ctt act gaa	336
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Leu Leu Thr Glu	
100 105 110	
ggc caa gcg ctt aac cct gat ggt cag gga tat cgt cag cgg ttt atg	384

Gly	Gln	Ala	Leu	Asn	Pro	Asp	Gly	Gln	Gly	Tyr	Arg	Gln	Arg	Phe	Met	
		115					120					125				
aat	ggg	ttt	atc	tat	tgg	cat	cct	tct	act	ggg	gcg	cac	gcg	gtt	aat	432
Asn	Gly	Phe	Ile	Tyr	Trp	His	Pro	Ser	Thr	Gly	Ala	His	Ala	Val	Asn	
	130					135					140					
aat	tac	agt	gca	caa	gtc	tgg	gag	cgt	aac	ggg	tgg	gag	tct	ggg	tgg	480
Asn	Tyr	Ser	Ala	Gln	Val	Trp	Glu	Arg	Asn	Gly	Trp	Glu	Ser	Gly	Trp	
	145				150					155					160	
atg	ggg	tat	ccc	act	ggg	ggg	gaa	gtc	cct	gtg	tct	ggg	tct	aat	ccg	528
Met	Gly	Tyr	Pro	Thr	Gly	Gly	Glu	Val	Pro	Val	Ser	Gly	Ser	Asn	Pro	
				165					170					175		
att	gat	ggg	gag	ttg	agt	ggg	tgg	gtg	caa	acc	ttc	caa	ggg	ggg	cga	576
Ile	Asp	Gly	Glu	Leu	Ser	Gly	Trp	Val	Gln	Thr	Phe	Gln	Gly	Gly	Arg	
			180					185					190			
gtg	tat	cgc	agt	ccg	gta	ttg	gac	ggg	ttc	cag	gtg	gcc	agt	att	aat	624
Val	Tyr	Arg	Ser	Pro	Val	Leu	Asp	Gly	Phe	Gln	Val	Ala	Ser	Ile	Asn	
		195					200					205				
ggg	ctg	atc	ttg	gat	aaa	tgg	ctt	gaa	ttg	ggg	ggg	cct	gat	agt	gac	672
Gly	Leu	Ile	Leu	Asp	Lys	Trp	Leu	Glu	Leu	Gly	Gly	Pro	Asp	Ser	Asp	
	210					215					220					
ctt	ggg	ttt	ccc	att	gcg	gat	gag	gct	gtg	aca	gct	gac	ggg	gtg	ggg	720
Leu	Gly	Phe	Pro	Ile	Ala	Asp	Glu	Ala	Val	Thr	Ala	Asp	Gly	Val	Gly	
	225				230				235					240		
aga	ttt	tct	gtt	ttc	cag	aac	gga	gtt	gtc	tac	tgg	cat	ccg	caa	cac	768
Arg	Phe	Ser	Val	Phe	Gln	Asn	Gly	Val	Val	Tyr	Trp	His	Pro	Gln	His	
				245					250					255		
gga	gct	cac	cct	ata	tta	ggg	aat	ata	tac	agt	atc	tgg	aga	gaa	gaa	816
Gly	Ala	His	Pro	Ile	Leu	Gly	Asn	Ile	Tyr	Ser	Ile	Trp	Arg	Glu	Glu	
			260					265					270			
gga	gct	gag	agt	ggg	gaa	ttc	ggg	tac	cct	atc	ggc	gat	cca	gaa	aag	864
Gly	Ala	Glu	Ser	Gly	Glu	Phe	Gly	Tyr	Pro	Ile	Gly	Asp	Pro	Glu	Lys	
		275					280					285				
tat	aca	gaa	aac	atg	gct	aat	cag	gta	ttc	gaa	aaa	ggc	gaa	ctt	gca	912
Tyr	Thr	Glu	Asn	Met	Ala	Asn	Gln	Val	Phe	Glu	Lys	Gly	Glu	Leu	Ala	
	290					295					300					
gct	aac	cta	tac	ccc	aat	cct	ctt	gag	gct	ttt	att	gag	ttt	tta	ccc	960
Ala	Asn	Leu	Tyr	Pro	Asn	Pro	Leu	Glu	Ala	Phe	Ile	Glu	Phe	Leu	Pro	
	305				310					315					320	
ttt	gct	aat	ctt	gag	gaa	gca	ata	gag	tat	ttt	gag	aac	gga	ttg	tca	1008
Phe	Ala	Asn	Leu	Glu	Glu	Ala	Ile	Glu	Tyr	Phe	Glu	Asn	Gly	Leu	Ser	
				325					330					335		
aat	tct	cgt	gta	gag	gcg	aat	tca	ctt	aac	gcc	aag	aaa	gat	tcg	att	1056
Asn	Ser	Arg	Val	Glu	Ala	Asn	Ser	Leu	Asn	Ala	Lys	Lys	Asp	Ser	Ile	
			340					345					350			
caa	tgt	caa	tcg	caa	tcc	gct	aac	att	cat	gtg	aga	acg	aag	agt	gac	1104
Gln	Cys	Gln	Ser	Gln	Ser	Ala	Asn	Ile	His	Val	Arg	Thr	Lys	Ser	Asp	

355	360	365	
gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat			1152
Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp			
370	375	380	
tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att			1200
Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile			
385	390	395	400
tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa			1248
Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln			
405	410	415	
ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt			1296
Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly			
420	425	430	
tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag			1344
Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln			
435	440	445	
gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aac tac			1392
Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr			
450	455	460	
gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag gag			1445
Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser			
465	470		

<210> 518

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Val Ala Glu Ile	
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His Glu Ala Ile Arg Gln Ala Gln Asp Ser Gly Ala Pro Asn Asp Glu	
20	30
Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Ser Thr	
35	45
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	
50	60
Gln Ser Gln Pro Gln Ala Arg Gly Leu Ala Ala Ala Ala Cys Gln	
65	80
Thr Phe Trp Pro Ser Pro Tyr Gln Val Cys Gly Ala Ile Leu Glu Arg	
85	95
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Leu Leu Thr Glu	
100	110
Gly Gln Ala Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met	
115	125

Asn Gly Phe Ile Tyr Trp His Pro Ser Thr Gly Ala His Ala Val Asn
 130 135 140
 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp
 145 150 155 160
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Ser Gly Ser Asn Pro
 165 170 175
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg
 180 185 190
 Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn
 195 200 205
 Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp
 210 215 220
 Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly
 225 230 235 240
 Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His
 245 250 255
 Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu
 260 265 270
 Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys
 275 280 285
 Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala
 290 295 300
 Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro
 305 310 315 320
 Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser
 325 330 335
 Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile
 340 345 350
 Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp
 355 360 365
 Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp
 370 375 380
 Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile
 385 390 395 400
 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln
 405 410 415
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
 420 425 430
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
 435 440 445
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr

450

455

460

Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
465 470

<210> 519

<211> 826

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(826)

<223> RXN03038

<400> 519

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ccaaacacgt tcaaatccgt taaagtgcct gtttaaaact atg cat tca aag gaa 115
Met His Ser Lys Glu
1 5

gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt 163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val
10 15 20

gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca 211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala
25 30 35

gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac 259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn
40 45 50

tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat 307
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn
55 60 65

ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc 355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala
70 75 80 85

acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat 403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp
90 95 100

ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac 451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp
105 110 115

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499
Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp
120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547
Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg
135 140 145

acc att cct cta gtc tgg gtt gtt cca gaa gac aac acc gtg cct ggc 595
Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val Pro Gly

150	155	160	165	
cca acg gtc tac gca ctc gga ggc ggt gac ggt gga caa ggc ggc cag				643
Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly Gly Gln				
	170	175	180	
aac tgg gtc acc cgc acc gac ctt gag gaa tta acc agt gac aac aac				691
Asn Trp Val Thr Arg Thr Asp Leu Glu Glu Leu Thr Ser Asp Asn Asn				
	185	190	195	
atc aac ctc atc atg ccg atg ctc gga tct ttt agt ttc tac tct gac				739
Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr Ser Asp				
	200	205	210	
tgg gca cgc gaa agc caa tcc atg ggt tgt gcg caa cag tgg gaa aca				787
Trp Ala Arg Glu Ser Gln Ser Met Gly Cys Ala Gln Gln Trp Glu Thr				
	215	220	225	
ttg ctc atg cac gaa ctg cct gag ccg ctt gta gcg gcc				826
Leu Leu Met His Glu Leu Pro Glu Pro Leu Val Ala Ala				
	230	235	240	
<210> 520				
<211> 242				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 520				
Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val				
1	5	10	15	
Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr				
	20	25	30	
Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met				
	35	40	45	
Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro				
	50	55	60	
Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp				
	65	70	75	80
Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu				
	85	90	95	
Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro				
	100	105	110	
Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg				
	115	120	125	
Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser				
	130	135	140	
Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp				
	145	150	155	160
Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly				
	165	170	175	

<400> 521																
gcgcggaaaaa caccaagtaa gccttacagt ccgacagcct catagcggat gggataagtt																60
ccaaacacgt tcaaatccgt taaagtgctt gtttaaaact																
Met His Ser Lys Glu																115
1 5																
gag tta aca gtg cgt aaa gga att tcc cgc gtc ctc tcg gta gcg gtt																163
Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val Leu Ser Val Ala Val																
10 15 20																
gct agt tca atc gga ttc gga act gta ctg aca ggc acc ggc atc gca																211
Ala Ser Ser Ile Gly Phe Gly Thr Val Leu Thr Gly Thr Gly Ile Ala																
25 30 35																
gca gct caa gac tct gca ttt gac tac ggt atg gat cca aac atg aac																259
Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Asn Met Asn																
40 45 50																
tac aac ccg atc gat gac atc aag gat cgt ccc gaa gga ttg tcc aat																307
Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro Glu Gly Leu Ser Asn																
55 60 65																
ctt ccc tac ttc gga agt aaa ttg acc agc tgg ggc tca tca tat gcc																355
Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Tyr Ala																
70 75 80 85																
acc gcc tca tcc ggc gtc gtg acc tcc gcg ctc ccg cag tac acc gat																403
Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu Pro Gln Tyr Thr Asp																
90 95 100																
ccg cgc tac ccc ctc ggc aaa gac gac ctg ccc aag gca acc atc gac																451
Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr Ile Asp																
105 110 115																

atg gag cca gaa gtt ctt gcg cgc ctt gag cga ttc gtc ggc gtt gac 499
 Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg Phe Val Gly Val Asp
 120 125 130

ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg gga cgc 547
 Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met Gly Arg
 135 140 145

acc att cct cta gtc tgg gtt gtt cca aaa gac aac acc gtg cct tgc 595
 Thr Ile Pro Leu Val Trp Val Val Pro Lys Asp Asn Thr Val Pro Cys
 150 155 160 165

cca acg gtc tac gca cta 613
 Pro Thr Val Tyr Ala Leu
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<210> 522

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

Met His Ser Lys Glu Glu Leu Thr Val Arg Lys Gly Ile Ser Arg Val
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 20 25 30

Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met
 35 40 45

Asp Pro Asn Met Asn Tyr Asn Pro Ile Asp Asp Ile Lys Asp Arg Pro
 50 55 60

Glu Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp
 65 70 75 80

Gly Ser Ser Tyr Ala Thr Ala Ser Ser Gly Val Val Thr Ser Ala Leu
 85 90 95

Pro Gln Tyr Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro
 100 105 110

Lys Ala Thr Ile Asp Met Glu Pro Glu Val Leu Ala Arg Leu Glu Arg
 115 120 125

Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser
 130 135 140

Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Lys Asp
 145 150 155 160

Asn Thr Val Pro Cys Pro Thr Val Tyr Ala Leu
 165 170

<210> 523

<211> 1218

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1195)

<223> RXA01274

<400> 523

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                                         Met Lys Leu Leu Arg
                                         1 5

cgc atc gct gca cca gcc atc gcg ctg gga att gcg atg tcc acc att 163
Arg Ile Ala Ala Pro Ala Ile Ala Leu Gly Ile Ala Met Ser Thr Ile
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gtc acg cca tcc acc gca ggc gct gcc gaa gta acc cca gca gac gtt 211
Val Thr Pro Ser Thr Ala Gly Ala Ala Glu Val Thr Pro Ala Asp Val
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gct ggc gat act gca cta tcc acc atc tcc gat agt gct cct gca gat 259
Ala Gly Asp Thr Ala Leu Ser Thr Ile Ser Asp Ser Ala Pro Ala Asp
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gaa gcc tct gca cct cgc tgg cgc gca cac gtc aac gca gca gac gag 307
Glu Ala Ser Ala Pro Arg Trp Arg Ala His Val Asn Ala Ala Asp Glu
                        55 60 65

cgc gtc aaa gaa atg tgg gca tac tcc cct tcc atg gac cgc aat gtg 355
Arg Val Lys Glu Met Trp Ala Tyr Ser Pro Ser Met Asp Arg Asn Val
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cca ctg gta gtt ata act gcc gat gag tcc gca ggt cct cgt cct gtg 403
Pro Leu Val Val Ile Thr Ala Asp Glu Ser Ala Gly Pro Arg Pro Val
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att tac ctt ctt aac ggt ggc gac ggt ggc gaa ggt gcc gct aac tgg 451
Ile Tyr Leu Leu Asn Gly Gly Asp Gly Gly Glu Gly Ala Ala Asn Trp
                        105 110 115

gtt atg cag act gac gtt ctg gat ttc tac cta gaa aag aac gtt aac 499
Val Met Gln Thr Asp Val Leu Asp Phe Tyr Leu Glu Lys Asn Val Asn
                        120 125 130

gtt gtt att cca atg gaa ggc aag ttt tcc tac tac acc gac tgg gta 547
Val Val Ile Pro Met Glu Gly Lys Phe Ser Tyr Tyr Thr Asp Trp Val
                        135 140 145

gaa gag aat gcg tcc ctc ggt ggc aag caa atg tgg gaa acc ttc ctg 595
Glu Glu Asn Ala Ser Leu Gly Gly Lys Gln Met Trp Glu Thr Phe Leu
                        150 155 160 165

gtg aag gaa ctt cca gga cca ttg gaa gaa aag ctc aac act gac ggt 643
Val Lys Glu Leu Pro Gly Pro Leu Glu Glu Lys Leu Asn Thr Asp Gly
                        170 175 180

cag cgt gca att gct ggc atg tcc atg tcc gca act act tcc cta ctc 691
Gln Arg Ala Ile Ala Gly Met Ser Met Ser Ala Thr Thr Ser Leu Leu
                        185 190 195

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ttc cca caa cac ttc cca ggc ttc tac gac gca gca gca tcc ttc tca 739
Phe Pro Gln His Phe Pro Gly Phe Tyr Asp Ala Ala Ala Ser Phe Ser
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gga tgc gca gca acc tca agc ctg ctc cca tgg gaa tac ctc aaa ctc 787
Gly Cys Ala Ala Thr Ser Ser Leu Leu Pro Trp Glu Tyr Leu Lys Leu
215 220 225

acc ctt gac cgc ggc aac gca acc cca gaa caa atg tgg gga cca cgt 835
Thr Leu Asp Arg Gly Asn Ala Thr Pro Glu Gln Met Trp Gly Pro Arg
230 235 240 245

ggt ggc gaa tac aac atc tac aac gac gca ctg atc aac tcc gac aaa 883
Gly Gly Glu Tyr Asn Ile Tyr Asn Asp Ala Leu Ile Asn Ser Asp Lys
250 255 260

cta cgc gga acc gaa cta tac gtc tcc aac gca tcc ggc ctt gct ggt 931
Leu Arg Gly Thr Glu Leu Tyr Val Ser Asn Ala Ser Gly Leu Ala Gly
265 270 275

gaa tgg gaa tcc gtc gac agc cca cgc ttc gaa gga ctc aac caa caa 979
Glu Trp Glu Ser Val Asp Ser Pro Arg Phe Glu Gly Leu Asn Gln Gln
280 285 290

gtt cag tcc atc gca atg gca gaa act gtg gta acc ggc ggc atc atc 1027
Val Gln Ser Ile Ala Met Ala Glu Thr Val Val Thr Gly Gly Ile Ile
295 300 305

gaa gct gca acc aac aag tgc acc cac gac ctc aag gca aaa ctt gac 1075
Glu Ala Ala Thr Asn Lys Cys Thr His Asp Leu Lys Ala Lys Leu Asp
310 315 320 325

tcc gcc ggc atc cca gcc gac tgg aac ctc cgc cca acc ggc acc cac 1123
Ser Ala Gly Ile Pro Ala Asp Trp Asn Leu Arg Pro Thr Gly Thr His
330 335 340

tca tgg ggc tgg tgg caa gat gac ctc cgc gga tct tgg acc acc ttc 1171
Ser Trp Gly Trp Trp Gln Asp Asp Leu Arg Gly Ser Trp Thr Thr Phe
345 350 355

gct cgt gcg ttt gag cta gag gcc tagaaacaga tttaacattg aaa 1218
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360 365

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<210> 524

<211> 365

<212> PRT

<213> Corynebacterium glutamicum

<400> 524

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Met Lys Leu Leu Arg Arg Ile Ala Ala Pro Ala Ile Ala Leu Gly Ile
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Ala Met Ser Thr Ile Val Thr Pro Ser Thr Ala Gly Ala Ala Glu Val
20 25 30

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Thr Pro Ala Asp Val Ala Gly Asp Thr Ala Leu Ser Thr Ile Ser Asp
35 40 45

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Ser Ala Pro Ala Asp Glu Ala Ser Ala Pro Arg Trp Arg Ala His Val
 50 55 60
 Asn Ala Ala Asp Glu Arg Val Lys Glu Met Trp Ala Tyr Ser Pro Ser
 65 70 75 80
 Met Asp Arg Asn Val Pro Leu Val Val Ile Thr Ala Asp Glu Ser Ala
 85 90 95
 Gly Pro Arg Pro Val Ile Tyr Leu Leu Asn Gly Gly Asp Gly Gly Glu
 100 105 110
 Gly Ala Ala Asn Trp Val Met Gln Thr Asp Val Leu Asp Phe Tyr Leu
 115 120 125
 Glu Lys Asn Val Asn Val Val Ile Pro Met Glu Gly Lys Phe Ser Tyr
 130 135 140
 Tyr Thr Asp Trp Val Glu Glu Asn Ala Ser Leu Gly Gly Lys Gln Met
 145 150 155 160
 Trp Glu Thr Phe Leu Val Lys Glu Leu Pro Gly Pro Leu Glu Glu Lys
 165 170 175
 Leu Asn Thr Asp Gly Gln Arg Ala Ile Ala Gly Met Ser Met Ser Ala
 180 185 190
 Thr Thr Ser Leu Leu Phe Pro Gln His Phe Pro Gly Phe Tyr Asp Ala
 195 200 205
 Ala Ala Ser Phe Ser Gly Cys Ala Ala Thr Ser Ser Leu Leu Pro Trp
 210 215 220
 Glu Tyr Leu Lys Leu Thr Leu Asp Arg Gly Asn Ala Thr Pro Glu Gln
 225 230 235 240
 Met Trp Gly Pro Arg Gly Gly Glu Tyr Asn Ile Tyr Asn Asp Ala Leu
 245 250 255
 Ile Asn Ser Asp Lys Leu Arg Gly Thr Glu Leu Tyr Val Ser Asn Ala
 260 265 270
 Ser Gly Leu Ala Gly Glu Trp Glu Ser Val Asp Ser Pro Arg Phe Glu
 275 280 285
 Gly Leu Asn Gln Gln Val Gln Ser Ile Ala Met Ala Glu Thr Val Val
 290 295 300
 Thr Gly Gly Ile Ile Glu Ala Ala Thr Asn Lys Cys Thr His Asp Leu
 305 310 315 320
 Lys Ala Lys Leu Asp Ser Ala Gly Ile Pro Ala Asp Trp Asn Leu Arg
 325 330 335
 Pro Thr Gly Thr His Ser Trp Gly Trp Trp Gln Asp Asp Leu Arg Gly
 340 345 350
 Ser Trp Thr Thr Phe Ala Arg Ala Phe Glu Leu Glu Ala
 355 360 365

<210> 525
 <211> 1141
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1141)
 <223> RXA01449

<400> 525
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 tattttattc attaatattg ttgcgggagg catcatttcc ttg aag ctc ttc ata 115
 Leu Lys Leu Phe Ile
 1 5
 tcc cgc gca ctc atc gcc ggt act gtt tct ttg act ctt ttc tct tca 163
 Ser Arg Ala Leu Ile Ala Gly Thr Val Ser Leu Thr Leu Phe Ser Ser
 10 15 20
 ccg ctc gct tcc gca cag agc tcg gga ctc agt tca gta cta agt tcc 211
 Pro Leu Ala Ser Ala Gln Ser Ser Gly Leu Ser Ser Val Leu Ser Ser
 25 30 35
 gaa gac agc tca gca act aat tca gag cag gac ttt gag aaa agc tcc 259
 Glu Asp Ser Ser Ala Thr Asn Ser Glu Gln Asp Phe Glu Lys Ser Ser
 40 45 50
 gaa tcc gga tct tcc gcc cag gat ttc atc gcg ctt tct act gcc aac 307
 Glu Ser Gly Ser Ser Ala Gln Asp Phe Ile Ala Leu Ser Thr Ala Asn
 55 60 65
 cca gat ctc act ggc ggt tct gtt gaa ggc ttg ctg agt tcg atg tcg 355
 Pro Asp Leu Thr Gly Gly Ser Val Glu Gly Leu Leu Ser Ser Met Ser
 70 75 80 85
 ctg att ggt tcg tcc cag ttg cct ctt gga ggc ccg ctc ttg agt agt 403
 Leu Ile Gly Ser Ser Gln Leu Pro Leu Gly Gly Pro Leu Leu Ser Ser
 90 95 100
 gat tcc aac tat ccg ctc gag aca gac ccc tcg att act gag gca aga 451
 Asp Ser Asn Tyr Pro Leu Glu Thr Asp Pro Ser Ile Thr Glu Ala Arg
 105 110 115
 atc gtc gaa aag cgt gtt tta aat ggt ctt cga ctg gaa aaa tgg tct 499
 Ile Val Glu Lys Arg Val Leu Asn Gly Leu Arg Leu Glu Lys Trp Ser
 120 125 130
 gtt gcg tcg cct tcg atg cag cgc aat gtg gat gtg cag atc atg aag 547
 Val Ala Ser Pro Ser Met Gln Arg Asn Val Asp Val Gln Ile Met Lys
 135 140 145
 tcc gcg gag gcg gac tcc cct gct ccg atg ctg tac atg ctt gat gga 595
 Ser Ala Glu Ala Asp Ser Pro Ala Pro Met Leu Tyr Met Leu Asp Gly
 150 155 160 165
 atc ggc gga aat aag aat tct tct ggt tgg atc aat ggt ggc gag ggt 643
 Ile Gly Gly Asn Lys Asn Ser Ser Gly Trp Ile Asn Gly Gly Glu Gly
 170 175 180

ccg aag gtt ttc gcg gat gaa aat gtg act gta gta atg ccg ttg ggt 691
 Pro Lys Val Phe Ala Asp Glu Asn Val Thr Val Val Met Pro Leu Gly
 185 190 195

gct gct tca tcc atg tac tcg gat tgg ttg gaa gag gac cct gcg cta 739
 Ala Ala Ser Ser Met Tyr Ser Asp Trp Leu Glu Glu Asp Pro Ala Leu
 200 205 210

ggg cgc atc aag tgg gaa act ttt atc gtc gag gag ctc gcg ccc ctg 787
 Gly Arg Ile Lys Trp Glu Thr Phe Ile Val Glu Glu Leu Ala Pro Leu
 215 220 225

ctt gag gct gag gaa gag ctg aac ttc aat ggt cac cgt ggc atc ggc 835
 Leu Glu Ala Glu Glu Glu Leu Asn Phe Asn Gly His Arg Gly Ile Gly
 230 235 240 245

gga tta tcc atg ggt gct act ggt gcg gtt cat tta gct aac tcg aac 883
 Gly Leu Ser Met Gly Ala Thr Gly Ala Val His Leu Ala Asn Ser Asn
 250 255 260

cct gat ctc ttt gat gga gtc att ggc atc tct ggt tgc tac tcc acg 931
 Pro Asp Leu Phe Asp Gly Val Ile Gly Ile Ser Gly Cys Tyr Ser Thr
 265 270 275

ctt gat ccc att gga caa acc acg gtg tca cta att gtt aat tct cgc 979
 Leu Asp Pro Ile Gly Gln Thr Thr Val Ser Leu Ile Val Asn Ser Arg
 280 285 290

ggt ggc aat gta gaa aat atg tgg ggt ccc act ggt tct gaa act tgg 1027
 Gly Gly Asn Val Glu Asn Met Trp Gly Pro Thr Gly Ser Glu Thr Trp
 295 300 305

aaa gct cac gat gtc aca tca aat cct gag ggg ctg cgc gac atg gct 1075
 Lys Ala His Asp Val Thr Ser Asn Pro Glu Gly Leu Arg Asp Met Ala
 310 315 320 325

gtc tat ttg tca gct gcg aac gga gtt gta gat gac atc gat ttg gcg 1123
 Val Tyr Leu Ser Ala Ala Asn Gly Val Val Asp Asp Ile Asp Leu Ala
 330 335 340

gat tcc gag aaa gag cct 1141
 Asp Ser Glu Lys Glu Pro
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<210> 526

<211> 347

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

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Thr Leu Phe Ser Ser Pro Leu Ala Ser Ala Gln Ser Ser Gly Leu Ser
 20 25 30

Ser Val Leu Ser Ser Glu Asp Ser Ser Ala Thr Asn Ser Glu Gln Asp
 35 40 45

Phe Glu Lys Ser Ser Glu Ser Gly Ser Ser Ala Gln Asp Phe Ile Ala

50					55					60					
Leu	Ser	Thr	Ala	Asn	Pro	Asp	Leu	Thr	Gly	Gly	Ser	Val	Glu	Gly	Leu
65					70					75					80
Leu	Ser	Ser	Met	Ser	Leu	Ile	Gly	Ser	Ser	Gln	Leu	Pro	Leu	Gly	Gly
				85					90					95	
Pro	Leu	Leu	Ser	Ser	Asp	Ser	Asn	Tyr	Pro	Leu	Glu	Thr	Asp	Pro	Ser
			100					105					110		
Ile	Thr	Glu	Ala	Arg	Ile	Val	Glu	Lys	Arg	Val	Leu	Asn	Gly	Leu	Arg
		115					120					125			
Leu	Glu	Lys	Trp	Ser	Val	Ala	Ser	Pro	Ser	Met	Gln	Arg	Asn	Val	Asp
130					135					140					
Val	Gln	Ile	Met	Lys	Ser	Ala	Glu	Ala	Asp	Ser	Pro	Ala	Pro	Met	Leu
145				150						155					160
Tyr	Met	Leu	Asp	Gly	Ile	Gly	Gly	Asn	Lys	Asn	Ser	Ser	Gly	Trp	Ile
				165				170						175	
Asn	Gly	Gly	Glu	Gly	Pro	Lys	Val	Phe	Ala	Asp	Glu	Asn	Val	Thr	Val
			180					185					190		
Val	Met	Pro	Leu	Gly	Ala	Ala	Ser	Ser	Met	Tyr	Ser	Asp	Trp	Leu	Glu
		195					200					205			
Glu	Asp	Pro	Ala	Leu	Gly	Arg	Ile	Lys	Trp	Glu	Thr	Phe	Ile	Val	Glu
210					215					220					
Glu	Leu	Ala	Pro	Leu	Leu	Glu	Ala	Glu	Glu	Glu	Leu	Asn	Phe	Asn	Gly
225				230					235					240	
His	Arg	Gly	Ile	Gly	Gly	Leu	Ser	Met	Gly	Ala	Thr	Gly	Ala	Val	His
				245					250					255	
Leu	Ala	Asn	Ser	Asn	Pro	Asp	Leu	Phe	Asp	Gly	Val	Ile	Gly	Ile	Ser
			260					265					270		
Gly	Cys	Tyr	Ser	Thr	Leu	Asp	Pro	Ile	Gly	Gln	Thr	Thr	Val	Ser	Leu
		275					280					285			
Ile	Val	Asn	Ser	Arg	Gly	Gly	Asn	Val	Glu	Asn	Met	Trp	Gly	Pro	Thr
290					295					300					
Gly	Ser	Glu	Thr	Trp	Lys	Ala	His	Asp	Val	Thr	Ser	Asn	Pro	Glu	Gly
305				310					315					320	
Leu	Arg	Asp	Met	Ala	Val	Tyr	Leu	Ser	Ala	Ala	Asn	Gly	Val	Val	Asp
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Asp	Ile	Asp	Leu	Ala	Asp	Ser	Glu	Lys	Glu	Pro					
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<210> 527

<211> 373

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(373)

<223> RXA01798

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                                         1 5

gaa gag tta aca atg cgt aaa gga att tcc cgc atc ctc tcg gta gcg 163
Glu Glu Leu Thr Met Arg Lys Gly Ile Ser Arg Ile Leu Ser Val Ala
                        10 15 20

gtt gct agt tct att gga ttc ggt tcg gtg ttg tct gga acc ggc atc 211
Val Ala Ser Ser Ile Gly Phe Gly Ser Val Leu Ser Gly Thr Gly Ile
                        25 30 35

gca gca gct caa gac tct gca ttt gac tac ggt atg gat cct agc atg 259
Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly Met Asp Pro Ser Met
                        40 45 50

aac tac aac ccg atc gac gac atg aag gat cgt ccc caa ggg tta tcc 307
Asn Tyr Asn Pro Ile Asp Asp Met Lys Asp Arg Pro Gln Gly Leu Ser
                        55 60 65

aac ctt ccc tac ttc gga agc aaa cta acc agc tgg ggc tca tca gat 355
Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser Trp Gly Ser Ser Asp
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gcc acc gcc tca tcc ggc 373
Ala Thr Ala Ser Ser Gly
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<210> 528

<211> 91

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

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Met His Arg Lys Lys Glu Glu Leu Thr Met Arg Lys Gly Ile Ser Arg
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Ile Leu Ser Val Ala Val Ala Ser Ser Ile Gly Phe Gly Ser Val Leu
  20 25 30

Ser Gly Thr Gly Ile Ala Ala Ala Gln Asp Ser Ala Phe Asp Tyr Gly
  35 40 45

Met Asp Pro Ser Met Asn Tyr Asn Pro Ile Asp Asp Met Lys Asp Arg
  50 55 60

Pro Gln Gly Leu Ser Asn Leu Pro Tyr Phe Gly Ser Lys Leu Thr Ser
  65 70 75 80

Trp Gly Ser Ser Asp Ala Thr Ala Ser Ser Gly
  85 90

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<400> 529																
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Met Gly Tyr Pro Ile 5																
ggg 1																
ggg 15																
ggg 20																
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170										175										180										
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Ser	Ser	Ser	Arg	Glu	Leu	Val	Gln	Asp	His	Ser	Lys	Ser	Asp	Leu	Met															
			185					190					195																	
act	ctt	agg	gct	agt	aga	tgt	gcg	ctc	aag	gat	tct	tct	cag	gca	agt	739														
Thr	Leu	Arg	Ala	Ser	Arg	Cys	Ala	Leu	Lys	Asp	Ser	Ser	Gln	Ala	Ser															
		200					205					210																		
ttc	ggg	ggg	gtg	acg	att	cct	agc	cac	tat	gac	tac	tgg	gga	tgt	ctt	787														
Phe	Gly	Gly	Val	Thr	Ile	Pro	Ser	His	Tyr	Asp	Tyr	Trp	Gly	Cys	Leu															
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gac	aag	tcc	gac	cga	ccc	gac	cct	gat	gct	tat	ggg	cgc	cat	gac	tac	835														
Asp	Lys	Ser	Asp	Arg	Pro	Asp	Pro	Asp	Ala	Tyr	Gly	Arg	His	Asp	Tyr															
230					235				240					245																
tgc	act	ctt	tcg	cct	gat	tcg	tat	ggt	ccc	cta	ggg	aag	aag	gct	gag	883														
Cys	Thr	Leu	Ser	Pro	Asp	Ser	Tyr	Gly	Pro	Leu	Gly	Lys	Lys	Ala	Glu															
				250				255						260																
ttt	agt	ggg	gct	tgt	gca	aga	cac	gat	ctg	tgt	atg	gat	gcc	gtt	gat	931														
Phe	Ser	Gly	Ala	Cys	Ala	Arg	His	Asp	Leu	Cys	Met	Asp	Ala	Val	Asp															
			265					270				275																		
gcg	aat	ggc	acg	ggg	tat	gct	ccg	tgc	cac	ccg	gct	ttt	tat	acg	tgg	979														
Ala	Asn	Gly	Thr	Gly	Tyr	Ala	Pro	Cys	His	Pro	Ala	Phe	Tyr	Thr	Trp															
		280					285					290																		
atg	agc	aca	gtt	tgt	act	acc	aac	tat	gct	gag	gat	gct	aat	ttc	aag	1027														
Met	Ser	Thr	Val	Cys	Thr	Thr	Asn	Tyr	Ala	Glu	Asp	Ala	Asn	Phe	Lys															
		295				300					305																			
aag	ggc	tgt	gtg	aat	acc	gcg	aag	gcc	tac	tat	aag	gca	gtc	caa	tta	1075														
Lys	Gly	Cys	Val	Asn	Thr	Ala	Lys	Ala	Tyr	Tyr	Lys	Ala	Val	Gln	Leu															
310					315				320					325																
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Lys	Asn	Pro	Asn																											

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<211> 329

<212> PRT

<213> Corynebacterium glutamicum

<400> 530

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Ile	Asp	Gly	Glu	Ile	Asn	Gly	Trp	Val	Gln	Thr	Phe	Gln	Gly	Gly	Arg
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Val	Tyr	Arg	Thr	Pro	Met	Leu	Glu	Gly	Phe	Gln	Ile	Ala	Ser	Ile	Asn
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Gly	Met	Ile	Leu	Asn	Arg	Trp	Leu	Ala	Ile	Gly	Gly	Pro	Asp	Ser	Ala
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Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Ala Ser Asp Gly Val Gly
 65 70 75 80
 Arg Phe Ser Val Phe Gln Asn Gly Val Leu Tyr Trp His Pro Asn His
 85 90 95
 Gly Ala Trp Glu Met Thr Gly Phe Ile Glu Glu Val Trp Lys Met Arg
 100 105 110
 Gly Gly Leu Asp Ser Gln Trp Gly Tyr Pro Thr Ser Ala Pro Val Leu
 115 120 125
 Asp Ser Asp Ala Pro Val Glu Ile Ala Gln Asn Phe Ser Gly Gly Val
 130 135 140
 Phe Asp Leu Ala Thr Glu Ile Glu Asp Ala Gly Phe Ser Pro Ile Glu
 145 150 155 160
 Asp Lys Glu Met Ser Asn Leu Ile Leu Glu Tyr Phe Gly Tyr Leu Gly
 165 170 175
 Phe Asp Phe Pro Gly Ser Ser Ser Arg Glu Leu Val Gln Asp His Ser
 180 185 190
 Lys Ser Asp Leu Met Thr Leu Arg Ala Ser Arg Cys Ala Leu Lys Asp
 195 200 205
 Ser Ser Gln Ala Ser Phe Gly Gly Val Thr Ile Pro Ser His Tyr Asp
 210 215 220
 Tyr Trp Gly Cys Leu Asp Lys Ser Asp Arg Pro Asp Pro Asp Ala Tyr
 225 230 235 240
 Gly Arg His Asp Tyr Cys Thr Leu Ser Pro Asp Ser Tyr Gly Pro Leu
 245 250 255
 Gly Lys Lys Ala Glu Phe Ser Gly Ala Cys Ala Arg His Asp Leu Cys
 260 265 270
 Met Asp Ala Val Asp Ala Asn Gly Thr Gly Tyr Ala Pro Cys His Pro
 275 280 285
 Ala Phe Tyr Thr Trp Met Ser Thr Val Cys Thr Thr Asn Tyr Ala Glu
 290 295 300
 Asp Ala Asn Phe Lys Lys Gly Cys Val Asn Thr Ala Lys Ala Tyr Tyr
 305 310 315 320
 Lys Ala Val Gln Leu Lys Asn Pro Asn
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<211> 342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(319)

<223> RXA02607

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Met Arg Asp Thr Ala
1 5

ttt cgt tcc atc aag gct aaa gct cag gct aag cgc cgt tcc ctc tgg 163
Phe Arg Ser Ile Lys Ala Lys Ala Gln Ala Lys Arg Arg Ser Leu Trp
10 15 20

att gca gca ggc gct gtc cca acc gca att gcg ttg act atg tcc ctg 211
Ile Ala Ala Gly Ala Val Pro Thr Ala Ile Ala Leu Thr Met Ser Leu
25 30 35

gca cct atg gct tcg gct cag tcc agc aac ctt tcc tct gat gcc gtt 259
Ala Pro Met Ala Ser Ala Gln Ser Ser Asn Leu Ser Ser Asp Ala Val
40 45 50

att ggc agc atc gcg cag ggc gtc acc gat ggc ctg act gac tac ctg 307
Ile Gly Ser Ile Ala Gln Gly Val Thr Asp Gly Leu Thr Asp Tyr Leu
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aag cct cgc gtc tgaagagctt cctgctggtg aag 342
Lys Pro Arg Val
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<211> 73

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

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20 25 30

Leu Thr Met Ser Leu Ala Pro Met Ala Ser Ala Gln Ser Ser Asn Leu
35 40 45

Ser Ser Asp Ala Val Ile Gly Ser Ile Ala Gln Gly Val Thr Asp Gly
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Leu Thr Asp Tyr Leu Lys Pro Arg Val
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<211> 1818

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<213> Corynebacterium glutamicum

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<223> RXA02608

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                               Val Arg Val Ile Ser
                               1           5

gct gag tgg gca acc tcc aag cat gtc att ttg act att cag tct gca 163
Ala Glu Trp Ala Thr Ser Lys His Val Ile Leu Thr Ile Gln Ser Ala
                10                15                20

gca atg cca gag cgc cca atc aag gtg cag ctg ctg ctt ccg cgt gac 211
Ala Met Pro Glu Arg Pro Ile Lys Val Gln Leu Leu Leu Pro Arg Asp
                25                30                35

tgg tac tct tcc ccg aac cgt gag ttc cct gaa atc tgg gca ctt gac 259
Trp Tyr Ser Ser Pro Asn Arg Glu Phe Pro Glu Ile Trp Ala Leu Asp
                40                45                50

ggg ctg cgc gcg att gaa gag cag agt ggt tgg acc att gag acc aac 307
Gly Leu Arg Ala Ile Glu Glu Gln Ser Gly Trp Thr Ile Glu Thr Asn
                55                60                65

att gag cag tac tac gcc gat aag aac gcc att gtt gtg ctc cct gtc 355
Ile Glu Gln Tyr Tyr Ala Asp Lys Asn Ala Ile Val Val Leu Pro Val
                70                75                80                85

ggg ggc gag agc tcc ttc tac tct gac tgg gaa ggg cca aac aac ggc 403
Gly Gly Glu Ser Ser Phe Tyr Ser Asp Trp Glu Gly Pro Asn Asn Gly
                90                95                100

aag aac tac cag tgg gag acc ttc ctg act cag gag ctc gca ccg atc 451
Lys Asn Tyr Gln Trp Glu Thr Phe Leu Thr Gln Glu Leu Ala Pro Ile
                105                110                115

ctg gac aag ggt ttc cgt tct aac acc gat cgc gcc atc acc ggt atc 499
Leu Asp Lys Gly Phe Arg Ser Asn Thr Asp Arg Ala Ile Thr Gly Ile
                120                125                130

tcc atg ggc ggt acc gct gcg gtt aac atc gca acc cac cac cca gac 547
Ser Met Gly Gly Thr Ala Ala Val Asn Ile Ala Thr His His Pro Asp
                135                140                145

atg ttt aag ttc gtc ggt tcc ttc tcc ggc tat ctg gac acc acc tcc 595
Met Phe Lys Phe Val Gly Ser Phe Ser Gly Tyr Leu Asp Thr Thr Ser
                150                155                160                165

gct ggc atg cca atc gct att tcc gca gcc ctg gca gac gcc ggc gga 643
Ala Gly Met Pro Ile Ala Ile Ser Ala Ala Leu Ala Asp Ala Gly Gly
                170                175                180

tac gat gcc aac gca atg tgg gga cca gtc ggt tct gag cgc tgg cag 691
Tyr Asp Ala Asn Ala Met Trp Gly Pro Val Gly Ser Glu Arg Trp Gln
                185                190                195

gaa aac gat cca aag agc aac gta gac aag ctc aag ggc aag acc atc 739
Glu Asn Asp Pro Lys Ser Asn Val Asp Lys Leu Lys Gly Lys Thr Ile
                200                205                210

tac gtt tcc tct ggt aac ggt gca gat gac ttc ggt aag gaa ggc tct 787
Tyr Val Ser Ser Gly Asn Gly Ala Asp Asp Phe Gly Lys Glu Gly Ser

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215	220	225	
gta gct att gga cct gca aac gca gca ggt gtc ggt ctg gaa gtt atc			835
Val Ala Ile Gly Pro Ala Asn Ala Ala Gly Val Gly Leu Glu Val Ile			
230	235	240	245
tcc cgt atg act tcc cag acc ttc gtc gat cgt gca agc cag gct ggc			883
Ser Arg Met Thr Ser Gln Thr Phe Val Asp Arg Ala Ser Gln Ala Gly			
	250	255	260
gtg gaa gtt gtt gct agc ttc cgt cca tcc ggc gtg cac tca tgg gaa			931
Val Glu Val Val Ala Ser Phe Arg Pro Ser Gly Val His Ser Trp Glu			
	265	270	275
tac tgg cag ttc gag atg act cag gcg ttc cct cac atc gct aac gct			979
Tyr Trp Gln Phe Glu Met Thr Gln Ala Phe Pro His Ile Ala Asn Ala			
	280	285	290
ctt ggc atg tcc act gag gac cgt ggc gtt gag tgt gca cct gtc ggc			1027
Leu Gly Met Ser Thr Glu Asp Arg Gly Val Glu Cys Ala Pro Val Gly			
	295	300	305
gca atc gct gac gct gtt gcg gat ggc gcg atg ggc acc tgc ctg acc			1075
Ala Ile Ala Asp Ala Val Ala Asp Gly Ala Met Gly Thr Cys Leu Thr			
310	315	320	325
aac gaa tac gat gtt acc ggc ggt aag gcc cag gac ttc gct aac ggt			1123
Asn Glu Tyr Asp Val Thr Gly Gly Lys Ala Gln Asp Phe Ala Asn Gly			
	330	335	340
cgc gca tac tgg tct gca aac act ggc gct ttc ggc ctg gtt gga cgc			1171
Arg Ala Tyr Trp Ser Ala Asn Thr Gly Ala Phe Gly Leu Val Gly Arg			
	345	350	355
atc aac gct cgt tac tct gag ctg ggt gga cct gcc tcc tgg ttg ggc			1219
Ile Asn Ala Arg Tyr Ser Glu Leu Gly Gly Pro Ala Ser Trp Leu Gly			
	360	365	370
tac cca acc tct tct gag ttg aag aca cca gac gga cgt ggc cgc ttc			1267
Tyr Pro Thr Ser Ser Glu Leu Lys Thr Pro Asp Gly Arg Gly Arg Phe			
	375	380	385
gtc acc ttc gag cac ggc tcc atc tac tgg acc gcc acc act ggt cct			1315
Val Thr Phe Glu His Gly Ser Ile Tyr Trp Thr Ala Thr Thr Gly Pro			
390	395	400	405
tgg gaa atc cca ggc gat atg ctc gcc gca tgg ggc acc cag gac tat			1363
Trp Glu Ile Pro Gly Asp Met Leu Ala Ala Trp Gly Thr Gln Asp Tyr			
	410	415	420
gag aag ggc agc ctc ggc tac cca acc ggc gct gca gtt gaa tac aac			1411
Glu Lys Gly Ser Leu Gly Tyr Pro Thr Gly Ala Ala Val Glu Tyr Asn			
	425	430	435
ggg ggc ctg cgc cag cag ttc gaa ggt ggc tac gta ttc cgt acc tcc			1459
Gly Gly Leu Arg Gln Gln Phe Glu Gly Gly Tyr Val Phe Arg Thr Ser			
	440	445	450
aat aac cag tct tac tgg gtt cgc gga gaa atc tcc aag aag tac gcc			1507
Asn Asn Gln Ser Tyr Trp Val Arg Gly Glu Ile Ser Lys Lys Tyr Ala			
	455	460	465

gaa gac gga atc ttc gct cag ctt ggt ttc cca acc ggc aat gag aag 1555
 Glu Asp Gly Ile Phe Ala Gln Leu Gly Phe Pro Thr Gly Asn Glu Lys
 470 475 480 485

 ttg atc aac ggt ggc gct ttc cag gaa ttc gaa aag ggc aac atc tac 1603
 Leu Ile Asn Gly Gly Ala Phe Gln Glu Phe Glu Lys Gly Asn Ile Tyr
 490 495 500

 tgg tcc gca tcc act ggc gcg cac gtg att ctg cac ggc gac atc ttc 1651
 Trp Ser Ala Ser Thr Gly Ala His Val Ile Leu His Gly Asp Ile Phe
 505 510 515

 gac gca tgg ggt gct aag ggc tgg gag cag ggc gaa tac ggc ttc cca 1699
 Asp Ala Trp Gly Ala Lys Gly Trp Glu Gln Gly Glu Tyr Gly Phe Pro
 520 525 530

 acc tct gac cag acc gca atc acc gcg ggt gga cag acc att gat ttc 1747
 Thr Ser Asp Gln Thr Ala Ile Thr Ala Gly Gly Gln Thr Ile Asp Phe
 535 540 545

 cag aac ggc acc atc cgt cag gtc aat ggc cga att gag gag tct cgc 1795
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<212> PRT

<213> Corynebacterium glutamicum

<400> 534

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 35 40 45

 Ile Trp Ala Leu Asp Gly Leu Arg Ala Ile Glu Glu Gln Ser Gly Trp
 50 55 60

 Thr Ile Glu Thr Asn Ile Glu Gln Tyr Tyr Ala Asp Lys Asn Ala Ile
 65 70 75 80

 Val Val Leu Pro Val Gly Gly Glu Ser Ser Phe Tyr Ser Asp Trp Glu
 85 90 95

 Gly Pro Asn Asn Gly Lys Asn Tyr Gln Trp Glu Thr Phe Leu Thr Gln
 100 105 110

 Glu Leu Ala Pro Ile Leu Asp Lys Gly Phe Arg Ser Asn Thr Asp Arg
 115 120 125

 Ala Ile Thr Gly Ile Ser Met Gly Gly Thr Ala Ala Val Asn Ile Ala
 130 135 140

Thr	His	His	Pro	Asp	Met	Phe	Lys	Phe	Val	Gly	Ser	Phe	Ser	Gly	Tyr	145	150	155	160
Leu	Asp	Thr	Thr	Ser	Ala	Gly	Met	Pro	Ile	Ala	Ile	Ser	Ala	Ala	Leu	165	170	175	
Ala	Asp	Ala	Gly	Gly	Tyr	Asp	Ala	Asn	Ala	Met	Trp	Gly	Pro	Val	Gly	180	185	190	
Ser	Glu	Arg	Trp	Gln	Glu	Asn	Asp	Pro	Lys	Ser	Asn	Val	Asp	Lys	Leu	195	200	205	
Lys	Gly	Lys	Thr	Ile	Tyr	Val	Ser	Ser	Gly	Asn	Gly	Ala	Asp	Asp	Phe	210	215	220	
Gly	Lys	Glu	Gly	Ser	Val	Ala	Ile	Gly	Pro	Ala	Asn	Ala	Ala	Gly	Val	225	230	235	240
Gly	Leu	Glu	Val	Ile	Ser	Arg	Met	Thr	Ser	Gln	Thr	Phe	Val	Asp	Arg	245	250	255	
Ala	Ser	Gln	Ala	Gly	Val	Glu	Val	Val	Ala	Ser	Phe	Arg	Pro	Ser	Gly	260	265	270	
Val	His	Ser	Trp	Glu	Tyr	Trp	Gln	Phe	Glu	Met	Thr	Gln	Ala	Phe	Pro	275	280	285	
His	Ile	Ala	Asn	Ala	Leu	Gly	Met	Ser	Thr	Glu	Asp	Arg	Gly	Val	Glu	290	295	300	
Cys	Ala	Pro	Val	Gly	Ala	Ile	Ala	Asp	Ala	Val	Ala	Asp	Gly	Ala	Met	305	310	315	320
Gly	Thr	Cys	Leu	Thr	Asn	Glu	Tyr	Asp	Val	Thr	Gly	Gly	Lys	Ala	Gln	325	330	335	
Asp	Phe	Ala	Asn	Gly	Arg	Ala	Tyr	Trp	Ser	Ala	Asn	Thr	Gly	Ala	Phe	340	345	350	
Gly	Leu	Val	Gly	Arg	Ile	Asn	Ala	Arg	Tyr	Ser	Glu	Leu	Gly	Gly	Pro	355	360	365	
Ala	Ser	Trp	Leu	Gly	Tyr	Pro	Thr	Ser	Ser	Glu	Leu	Lys	Thr	Pro	Asp	370	375	380	
Gly	Arg	Gly	Arg	Phe	Val	Thr	Phe	Glu	His	Gly	Ser	Ile	Tyr	Trp	Thr	385	390	395	400
Ala	Thr	Thr	Gly	Pro	Trp	Glu	Ile	Pro	Gly	Asp	Met	Leu	Ala	Ala	Trp	405	410	415	
Gly	Thr	Gln	Asp	Tyr	Glu	Lys	Gly	Ser	Leu	Gly	Tyr	Pro	Thr	Gly	Ala	420	425	430	
Ala	Val	Glu	Tyr	Asn	Gly	Gly	Leu	Arg	Gln	Gln	Phe	Glu	Gly	Gly	Tyr	435	440	445	
Val	Phe	Arg	Thr	Ser	Asn	Asn	Gln	Ser	Tyr	Trp	Val	Arg	Gly	Glu	Ile	450	455	460	
Ser	Lys	Lys	Tyr	Ala	Glu	Asp	Gly	Ile	Phe	Ala	Gln	Leu	Gly	Phe	Pro				

465		470		475		480
Thr Gly Asn Glu Lys Leu Ile Asn Gly Gly Ala Phe Gln Glu Phe Glu						
		485		490		495
Lys Gly Asn Ile Tyr Trp Ser Ala Ser Thr Gly Ala His Val Ile Leu						
		500		505		510
His Gly Asp Ile Phe Asp Ala Trp Gly Ala Lys Gly Trp Glu Gln Gly						
		515		520		525
Glu Tyr Gly Phe Pro Thr Ser Asp Gln Thr Ala Ile Thr Ala Gly Gly						
		530		535		540
Gln Thr Ile Asp Phe Gln Asn Gly Thr Ile Arg Gln Val Asn Gly Arg						
		545		550		555
						560
Ile Glu Glu Ser Arg						
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1681)
 <223> RXN03054

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 Met Lys Leu Phe Ser
 1 5
 aag gct gca ggc gtc att gct gca gca ctt ctt gtt gca ggt ggt ata 163
 Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu Val Ala Gly Gly Ile
 10 15 20
 gca cct gtg gca cag ggg caa gct agt cag gtg gtc aca cct gaa gac 211
 Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val Val Thr Pro Glu Asp
 25 30 35
 caa gat gcg tat gtt caa cag ttc cac cac gaa ggg aat acc cca cct 259
 Gln Asp Ala Tyr Val Gln Gln Phe His His Glu Gly Asn Thr Pro Pro
 40 45 50
 gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307
 Val Val Asp Gly Val Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile
 55 60 65
 cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355
 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu
 70 75 80 85
 ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr
 90 95 100

att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa	451
Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln	
105 110 115	
caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag	499
Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Cys Gln	
120 125 130	
acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc	547
Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg	
135 140 145	
tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa	595
Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu	
150 155 160 165	
ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag ccg ttt atg	643
Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met	
170 175 180	
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Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn	
185 190 195	
aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg	739
Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp	
200 205 210	
atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg	787
Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro	
215 220 225	
att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga	835
Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg	
230 235 240 245	
gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat	883
Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn	
250 255 260	
ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac	931
Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp	
265 270 275	
ctt ggt ttt ccc att gcg gat gag gct gtg aca gct gac ggt gtg ggt	979
Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr Ala Asp Gly Val Gly	
280 285 290	
aga ttt tct gtt ttc cag aac gga gtt gtc tac tgg cat ccg caa cac	1027
Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr Trp His Pro Gln His	
295 300 305	
gga gct cac cct ata tta ggg aat ata tac agt atc tgg aga gaa gaa	1075
Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser Ile Trp Arg Glu Glu	
310 315 320 325	
gga gct gag agt ggg gaa ttc ggt tac cct atc ggc gat cca gaa aag	1123
Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile Gly Asp Pro Glu Lys	
330 335 340	

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 Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu Lys Gly Glu Leu Ala
 345 350 355

 gct aac cta tac ccc aat cct ctt gag gct ttt att gag ttt tta ccc 1219
 Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe Ile Glu Phe Leu Pro
 360 365 370

 ttt gct aat ctt gag gaa gca ata gag tat ttt gag aac gga ttg tca 1267
 Phe Ala Asn Leu Glu Glu Ala Ile Glu Tyr Phe Glu Asn Gly Leu Ser
 375 380 385

 aat tct cgt gta gag gcg aat tca ctt aac gcc aag aaa gat tcg att 1315
 Asn Ser Arg Val Glu Ala Asn Ser Leu Asn Ala Lys Lys Asp Ser Ile
 390 395 400 405

 caa tgt caa tcg caa tcc gct aac att cat gtg aga acg aag agt gac 1363
 Gln Cys Gln Ser Gln Ser Ala Asn Ile His Val Arg Thr Lys Ser Asp
 410 415 420

 gga gtc ggg att agg gtt cca aag att ggg ttt aag gct agg atg gat 1411
 Gly Val Gly Ile Arg Val Pro Lys Ile Gly Phe Lys Ala Arg Met Asp
 425 430 435

 tgc gac ctt cct gga act gtc tca gat gta gtg ggg tat gga tgg att 1459
 Cys Asp Leu Pro Gly Thr Val Ser Asp Val Val Gly Tyr Gly Trp Ile
 440 445 450

 tac tac gac tat tgg gga cga tgg gct caa gca gca tat gca caa caa 1507
 Tyr Tyr Asp Tyr Trp Gly Arg Trp Ala Gln Ala Ala Tyr Ala Gln Gln
 455 460 465

 ttc ttc ggt aat agg aat tct gtt gtg caa acc aat tta gag gcg ggt 1555
 Phe Phe Gly Asn Arg Asn Ser Val Val Gln Thr Asn Leu Glu Ala Gly
 470 475 480 485

 tgc agc ggg gag aag aat aca tta ttt tgg ggt act tca tat ttt cag 1603
 Cys Ser Gly Glu Lys Asn Thr Leu Phe Trp Gly Thr Ser Tyr Phe Gln
 490 495 500

 gtg act tat gaa ggt cag ccg tat ttc ggt cag tca gca act aat tac 1651
 Val Thr Tyr Glu Gly Gln Pro Tyr Phe Gly Gln Ser Ala Thr Asn Tyr
 505 510 515

 gct tat ctt ccg tgt acg ata gac cgt agt taacataagg aatggaatag gag 1704
 Ala Tyr Leu Pro Cys Thr Ile Asp Arg Ser
 520 525

<210> 536

<211> 527

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 536

Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu
 1 5 10 15

Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
 20 25 30

Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
 35 40 45
 Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
 50 55 60
 Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
 65 70 75 80
 Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
 85 90 95
 Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
 100 105 110
 Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
 115 120 125
 Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
 130 135 140
 Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met
 145 150 155 160
 Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
 165 170 175
 Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
 180 185 190
 Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
 195 200 205
 Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
 210 215 220
 Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
 225 230 235 240
 Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln
 245 250 255
 Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly
 260 265 270
 Gly Pro Asp Ser Asp Leu Gly Phe Pro Ile Ala Asp Glu Ala Val Thr
 275 280 285
 Ala Asp Gly Val Gly Arg Phe Ser Val Phe Gln Asn Gly Val Val Tyr
 290 295 300
 Trp His Pro Gln His Gly Ala His Pro Ile Leu Gly Asn Ile Tyr Ser
 305 310 315 320
 Ile Trp Arg Glu Glu Gly Ala Glu Ser Gly Glu Phe Gly Tyr Pro Ile
 325 330 335
 Gly Asp Pro Glu Lys Tyr Thr Glu Asn Met Ala Asn Gln Val Phe Glu
 340 345 350
 Lys Gly Glu Leu Ala Ala Asn Leu Tyr Pro Asn Pro Leu Glu Ala Phe

355					360					365					
Ile	Glu	Phe	Leu	Pro	Phe	Ala	Asn	Leu	Glu	Glu	Ala	Ile	Glu	Tyr	Phe
370						375					380				
Glu	Asn	Gly	Leu	Ser	Asn	Ser	Arg	Val	Glu	Ala	Asn	Ser	Leu	Asn	Ala
385					390					395					400
Lys	Lys	Asp	Ser	Ile	Gln	Cys	Gln	Ser	Gln	Ser	Ala	Asn	Ile	His	Val
				405					410					415	
Arg	Thr	Lys	Ser	Asp	Gly	Val	Gly	Ile	Arg	Val	Pro	Lys	Ile	Gly	Phe
			420					425					430		
Lys	Ala	Arg	Met	Asp	Cys	Asp	Leu	Pro	Gly	Thr	Val	Ser	Asp	Val	Val
	435						440					445			
Gly	Tyr	Gly	Trp	Ile	Tyr	Tyr	Asp	Tyr	Trp	Gly	Arg	Trp	Ala	Gln	Ala
450						455					460				
Ala	Tyr	Ala	Gln	Gln	Phe	Phe	Gly	Asn	Arg	Asn	Ser	Val	Val	Gln	Thr
465					470					475					480
Asn	Leu	Glu	Ala	Gly	Cys	Ser	Gly	Glu	Lys	Asn	Thr	Leu	Phe	Trp	Gly
				485					490					495	
Thr	Ser	Tyr	Phe	Gln	Val	Thr	Tyr	Glu	Gly	Gln	Pro	Tyr	Phe	Gly	Gln
			500					505					510		
Ser	Ala	Thr	Asn	Tyr	Ala	Tyr	Leu	Pro	Cys	Thr	Ile	Asp	Arg	Ser	
	515						520					525			

<210> 537

<211> 931

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(931)

<223> FRXA02886

<400> 537

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cagtttggttc	acatcaacta	gtaacgaaag	gatcatgtga	atg	aaa	ctg	ttt	tcc	115
				Met	Lys	Leu	Phe	Ser	
				1				5	

aag	gct	gca	ggc	gtc	att	gct	gca	gca	ctt	ctt	gtt	gca	ggg	ggg	ata	163
Lys	Ala	Ala	Gly	Val	Ile	Ala	Ala	Ala	Leu	Leu	Val	Ala	Gly	Gly	Ile	
				10					15					20		

gca	cct	gtg	gca	cag	ggg	caa	gct	agt	cag	gtg	gtc	aca	cct	gaa	gac	211
Ala	Pro	Val	Ala	Gln	Gly	Gln	Ala	Ser	Gln	Val	Val	Thr	Pro	Glu	Asp	
			25					30					35			

caa	gat	gcg	tat	gtt	caa	cag	ttc	cac	cac	gaa	ggg	aat	acc	cca	cct	259
Gln	Asp	Ala	Tyr	Val	Gln	Gln	Phe	His	His	Glu	Gly	Asn	Thr	Pro	Pro	
			40				45					50				

gtg gta gac ggg gtg ggt ggc tac act gag caa gaa atc gcc gag atc 307
 Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln Glu Ile Ala Glu Ile
 55 60 65
 cac gag gct atc cga caa gcc caa gaa tct ggc gca cct aat gaa gag 355
 His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly Ala Pro Asn Glu Glu
 70 75 80 85
 ctc att ccg ggt gag atg tgg tca gat aag gtg gag ctg cca gta act 403
 Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val Glu Leu Pro Val Thr
 90 95 100
 att gat aaa gca gcc gct gat gag gca gag ata gct att gca cag caa 451
 Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile Ala Ile Ala Gln Gln
 105 110 115
 caa tct cag cca cag acg cga ggc ctt gct gcg gct gcg gcg tgt cag 499
 Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala Ala Ala Ala Cys Gln
 120 125 130
 acg ttt tgg ccg tca cct cat cag gtt tgt ggt gct att tta gag cgc 547
 Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly Ala Ile Leu Glu Arg
 135 140 145
 tat att cag cag ggt gcc cag ttt ggg tgg atg ttg ttt ccg agt gaa 595
 Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met Leu Phe Pro Ser Glu
 150 155 160 165
 ggc caa acg tta aat cct gat ggt cag ggg tat cgt cag cgg ttt atg 643
 Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr Arg Gln Arg Phe Met
 170 175 180
 aat ggg ttt gtt tat tgg cat ccg aca act ggt gcg cat gct gtt aat 691
 Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly Ala His Ala Val Asn
 185 190 195
 aat tac agt gcg cag gtg tgg gag cgt aat ggg tgg gag tct ggg tgg 739
 Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly Trp Glu Ser Gly Trp
 200 205 210
 atg ggt tat ccc act ggt ggt gaa gtc cct gtg aat ggt tcc aat ccg 787
 Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val Asn Gly Ser Asn Pro
 215 220 225
 att gat ggt gag ttg agt ggg tgg gtg caa act ttc caa ggt ggg cga 835
 Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr Phe Gln Gly Gly Arg
 230 235 240 245
 gtg tat cgc agt ccg gta ttg gac ggt ttc cag gtg gcc agt att aat 883
 Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln Val Ala Ser Ile Asn
 250 255 260
 ggg ctg atc ttg gat aaa tgg ctt gaa ttg ggt ggt cct gat agt gac 931
 Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly Gly Pro Asp Ser Asp
 265 270 275

<210> 538

<211> 277

<212> PRT

<213> Corynebacterium glutamicum

<400> 538

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Met Lys Leu Phe Ser Lys Ala Ala Gly Val Ile Ala Ala Ala Leu Leu
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Val Ala Gly Gly Ile Ala Pro Val Ala Gln Gly Gln Ala Ser Gln Val
      20             25             30

Val Thr Pro Glu Asp Gln Asp Ala Tyr Val Gln Gln Phe His His Glu
      35             40             45

Gly Asn Thr Pro Pro Val Val Asp Gly Val Gly Gly Tyr Thr Glu Gln
      50             55             60

Glu Ile Ala Glu Ile His Glu Ala Ile Arg Gln Ala Gln Glu Ser Gly
      65             70             75             80

Ala Pro Asn Glu Glu Leu Ile Pro Gly Glu Met Trp Ser Asp Lys Val
      85             90             95

Glu Leu Pro Val Thr Ile Asp Lys Ala Ala Ala Asp Glu Ala Glu Ile
      100            105            110

Ala Ile Ala Gln Gln Gln Ser Gln Pro Gln Thr Arg Gly Leu Ala Ala
      115            120            125

Ala Ala Ala Cys Gln Thr Phe Trp Pro Ser Pro His Gln Val Cys Gly
      130            135            140

Ala Ile Leu Glu Arg Tyr Ile Gln Gln Gly Ala Gln Phe Gly Trp Met
      145            150            155            160

Leu Phe Pro Ser Glu Gly Gln Thr Leu Asn Pro Asp Gly Gln Gly Tyr
      165            170            175

Arg Gln Arg Phe Met Asn Gly Phe Val Tyr Trp His Pro Thr Thr Gly
      180            185            190

Ala His Ala Val Asn Asn Tyr Ser Ala Gln Val Trp Glu Arg Asn Gly
      195            200            205

Trp Glu Ser Gly Trp Met Gly Tyr Pro Thr Gly Gly Glu Val Pro Val
      210            215            220

Asn Gly Ser Asn Pro Ile Asp Gly Glu Leu Ser Gly Trp Val Gln Thr
      225            230            235            240

Phe Gln Gly Gly Arg Val Tyr Arg Ser Pro Val Leu Asp Gly Phe Gln
      245            250            255

Val Ala Ser Ile Asn Gly Leu Ile Leu Asp Lys Trp Leu Glu Leu Gly
      260            265            270

Gly Pro Asp Ser Asp
      275

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<210> 539

<211> 653

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(630)

<223> RXN03039

<220>

<223> All occurrences of Xaa = any amino acid

<400> 539

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1 5 10 15	
ctg ccc aaa gca acc atc gac atg gag cca gaa gct ctt gcg cgc ctt	96
Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu	
20 25 30	
gag cga ttc gtc ggc gtt gac ggt gat cgc atc cgc caa atc aac gcg	144
Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala	
35 40 45	
tac tcg cca tca atg gga cgc acc att cct cta gtc tgg gtc gtg cca	192
Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro	
50 55 60	
gaa gac aac acc gtg cct ggc cca acg gtc tac gca ctc ggc ggc ggc	240
Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly	
65 70 75 80	
gac ggt ggc caa ggc ggc caa aac tgg gtc acc cgc acc gac ctt gat	288
Asp Gly Gly Gln Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp	
85 90 95	
gag ttg acc agt gaa aac aac atc aac ctc atc atg ccc atg ctc gga	336
Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly	
100 105 110	
tct ttt agt ttc tac gct gac tgg gca ggc gaa agc gaa tcc atg ggt	384
Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly	
115 120 125	
ggt gcg caa cag tgg gaa aca ttc ctc atg cac gaa ctr ccm gag ccg	432
Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro	
130 135 140	
cta gaa gcg gcc atc ggc gca gac ggg caa cgc agc atc gtc ggc atg	480
Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met	
145 150 155 160	
tcc atg tcc ggg gga tcr gtg ctg aac ttt gcg acg cat gac ccc aac	528
Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn	
165 170 175	
ttt tay tcc tck gtc ggc tca ttt tct gga tgt gcc gaa acc aac tcc	576
Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser	
180 185 190	
tgg atg ggr cgc cgn tgg cat cgc agc cac tgc cta caa cgg caa tgt	624
Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys	

195

200

205

cgt gcc tgagcaaatc tttggtgaag tag
 Arg Ala
 210

653

<210> 540

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<220>

<223> All occurrences of Xaa = any amino acid

<400> 540

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Leu Pro Lys Ala Thr Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu
 20 25 30

Glu Arg Phe Val Gly Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala
 35 40 45

Tyr Ser Pro Ser Met Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro
 50 55 60

Glu Asp Asn Thr Val Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly
 65 70 75 80

Asp Gly Gly Gln Gly Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp
 85 90 95

Glu Leu Thr Ser Glu Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly
 100 105 110

Ser Phe Ser Phe Tyr Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly
 115 120 125

Gly Ala Gln Gln Trp Glu Thr Phe Leu Met His Glu Xaa Xaa Glu Pro
 130 135 140

Leu Glu Ala Ala Ile Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met
 145 150 155 160

Ser Met Ser Gly Gly Xaa Val Leu Asn Phe Ala Thr His Asp Pro Asn
 165 170 175

Phe Xaa Ser Xaa Val Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser
 180 185 190

Trp Met Xaa Arg Arg Trp His Arg Ser His Cys Leu Gln Arg Gln Cys
 195 200 205

Arg Ala
 210

<210> 541

<211> 809

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(786)

<223> FRXA02894

<400> 541

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Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile Gly Ala	
1 5 10 15	
gac ggg caa cgc agc atc gtc ggc atg tcc atg tcc ggg gga tca gtg	96
Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly Ser Val	
20 25 30	
ctg aac ttt gcg acg cat gac ccc aac ttt tac tcc tcg gtc ggc tca	144
Leu Asn Phe Ala Thr His Asp Pro Asn Phe Tyr Ser Ser Val Gly Ser	
35 40 45	
ttt tct gga tgt gcc gaa acc aac tcc tgg atg gga cgc cgt ggc atc	192
Phe Ser Gly Cys Ala Glu Thr Asn Ser Trp Met Gly Arg Arg Gly Ile	
50 55 60	
gca gcc acc gcc tac aac ggc aat gtc gtg cct gag caa atc ttt ggt	240
Ala Ala Thr Ala Tyr Asn Gly Asn Val Val Pro Glu Gln Ile Phe Gly	
65 70 75 80	
gaa gta gac agt gat tac tcc cgc tat aac gat cct ttg ctc aac gct	288
Glu Val Asp Ser Asp Tyr Ser Arg Tyr Asn Asp Pro Leu Leu Asn Ala	
85 90 95	
gcg aag ctc gaa gaa caa gac aac ctc tac atc ttc gcc ggt tcc ggt	336
Ala Lys Leu Glu Glu Gln Asp Asn Leu Tyr Ile Phe Ala Gly Ser Gly	
100 105 110	
gtg ttc tct gaa cta gat gtc att ggt gac aac gca ccg att gat gag	384
Val Phe Ser Glu Leu Asp Val Ile Gly Asp Asn Ala Pro Ile Asp Glu	
115 120 125	
gat gcg ttt aaa aac cgc gtt ctg gtc gga ttt gaa atc gaa gct atg	432
Asp Ala Phe Lys Asn Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met	
130 135 140	
tcc aac acc tgc acc cat aat ctt aag gct gcg act gat caa atg ggc	480
Ser Asn Thr Cys Thr His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly	
145 150 155 160	
att gac aac att aac tat gat ttc cga cca acc ggt act cat gct tgg	528
Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp	
165 170 175	
gac tat tgg aat gag gca ctg cac cgt ttc ttc ccg ttg atg atg cag	576
Asp Tyr Trp Asn Glu Ala Leu His Arg Phe Phe Pro Leu Met Met Gln	
180 185 190	
ggc ttc ggg ctt gat ggt ggt ccg atc ccg gtt tat aac cct aac ggt	624
Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro Val Tyr Asn Pro Asn Gly	
195 200 205	

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gtg tcc tct agt gag tct tct tct gag ctg tcg tct gat gtg agt ctt 672
Val Ser Ser Ser Glu Ser Ser Ser Glu Leu Ser Ser Ser Asp Val Ser Leu
210 215 220

ggc acc gtg atc ggt agt gtg gcg gga agc tcc gga tca agt gaa ggc 720
Gly Thr Val Ile Gly Ser Val Ala Gly Ser Ser Gly Ser Ser Glu Gly
225 230 235 240

agc agc gtc cga gag ttc ctt gca gga agt tcc gga tca agc caa tca 768
Ser Ser Val Arg Glu Phe Leu Ala Gly Ser Ser Gly Ser Ser Gln Ser
245 250 255

aca gga agc ttc tac gaa tagctagggc tgcgcaagat tcc 809
Thr Gly Ser Phe Tyr Glu
260

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<210> 542
<211> 262
<212> PRT
<213> Corynebacterium glutamicum

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<400> 542
Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile Gly Ala
1 5 10 15

Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly Ser Val
20 25 30

Leu Asn Phe Ala Thr His Asp Pro Asn Phe Tyr Ser Ser Val Gly Ser
35 40 45

Phe Ser Gly Cys Ala Glu Thr Asn Ser Trp Met Gly Arg Arg Gly Ile
50 55 60

Ala Ala Thr Ala Tyr Asn Gly Asn Val Val Pro Glu Gln Ile Phe Gly
65 70 75 80

Glu Val Asp Ser Asp Tyr Ser Arg Tyr Asn Asp Pro Leu Leu Asn Ala
85 90 95

Ala Lys Leu Glu Glu Gln Asp Asn Leu Tyr Ile Phe Ala Gly Ser Gly
100 105 110

Val Phe Ser Glu Leu Asp Val Ile Gly Asp Asn Ala Pro Ile Asp Glu
115 120 125

Asp Ala Phe Lys Asn Arg Val Leu Val Gly Phe Glu Ile Glu Ala Met
130 135 140

Ser Asn Thr Cys Thr His Asn Leu Lys Ala Ala Thr Asp Gln Met Gly
145 150 155 160

Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro Thr Gly Thr His Ala Trp
165 170 175

Asp Tyr Trp Asn Glu Ala Leu His Arg Phe Phe Pro Leu Met Met Gln
180 185 190

Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro Val Tyr Asn Pro Asn Gly
195 200 205

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Val Ser Ser Ser Glu Ser Ser Ser Glu Leu Ser Ser Asp Val Ser Leu
 210 215 220

Gly Thr Val Ile Gly Ser Val Ala Gly Ser Ser Gly Ser Ser Glu Gly
 225 230 235 240

Ser Ser Val Arg Glu Phe Leu Ala Gly Ser Ser Gly Ser Ser Gln Ser
 245 250 255

Thr Gly Ser Phe Tyr Glu
 260

<210> 543
 <211> 686
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(675)
 <223> FRXA02904

<400> 543
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 1 5 10 15

atc gac atg gag cca gaa gct ctt gcg cgc ctt gag cga ttc gtc ggc 96
 Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu Glu Arg Phe Val Gly
 20 25 30

gtt gac ggt gat cgc atc cgc caa atc aac gcg tac tcg cca tca atg 144
 Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met
 35 40 45

gga cgc acc att cct cta gtc tgg gtc gtg cca gaa gac aac acc gtg 192
 Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val
 50 55 60

cct ggc cca acg gtc tac gca ctc ggc ggc ggc gac ggt ggc caa ggc 240
 Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly
 65 70 75 80

ggc caa aac tgg gtc acc cgc acc gac ctt gat gag ttg acc agt gaa 288
 Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp Glu Leu Thr Ser Glu
 85 90 95

aac aac atc aac ctc atc atg ccc atg ctc gga tct ttt agt ttc tac 336
 Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr
 100 105 110

gct gac tgg gca ggc gaa agc gaa tcc atg ggt ggt gcg caa cag tgg 384
 Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly Gly Ala Gln Gln Trp
 115 120 125

gaa aca ttc ctc atg cac gaa cta ccc gag ccg cta gaa gcg gcc atc 432
 Glu Thr Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile
 130 135 140

ggc gca gac ggg caa cgc agc atc gtc ggc atg tcc atg tcc ggg gga 480
 Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly
 145 150 155 160

tcg gtg ctg aac ttt gcg acg cat gac ccc aac ttt tat tcc tct gtc 528
 Ser Val Leu Asn Phe Ala Thr His Asp Pro Asn Phe Tyr Ser Ser Val
 165 170 175

ggc tca ttt tct gga tgt gcc gaa acc aac tcc tgg atg ggg cgc cgt 576
 Gly Ser Phe Ser Gly Cys Ala Glu Thr Asn Ser Trp Met Gly Arg Arg
 180 185 190

ggc atc gca gcc act gcc tac aac ggc aat gtc gtg cct gag caa atc 624
 Gly Ile Ala Ala Thr Ala Tyr Asn Gly Asn Val Val Pro Glu Gln Ile
 195 200 205

ttt ggt gaa gta gac agt gat tac tct cgc tat aac gat cct agt att 672
 Phe Gly Glu Val Asp Ser Asp Tyr Ser Arg Tyr Asn Asp Pro Ser Ile
 210 215 220

cta tagtgtcacc t 686
 Leu
 225

<210> 544

<211> 225

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

Thr Asp Pro Arg Tyr Pro Leu Gly Lys Asp Asp Leu Pro Lys Ala Thr
 1 5 10 15

Ile Asp Met Glu Pro Glu Ala Leu Ala Arg Leu Glu Arg Phe Val Gly
 20 25 30

Val Asp Gly Asp Arg Ile Arg Gln Ile Asn Ala Tyr Ser Pro Ser Met
 35 40 45

Gly Arg Thr Ile Pro Leu Val Trp Val Val Pro Glu Asp Asn Thr Val
 50 55 60

Pro Gly Pro Thr Val Tyr Ala Leu Gly Gly Gly Asp Gly Gly Gln Gly
 65 70 75 80

Gly Gln Asn Trp Val Thr Arg Thr Asp Leu Asp Glu Leu Thr Ser Glu
 85 90 95

Asn Asn Ile Asn Leu Ile Met Pro Met Leu Gly Ser Phe Ser Phe Tyr
 100 105 110

Ala Asp Trp Ala Gly Glu Ser Glu Ser Met Gly Gly Ala Gln Gln Trp
 115 120 125

Glu Thr Phe Leu Met His Glu Leu Pro Glu Pro Leu Glu Ala Ala Ile
 130 135 140

Gly Ala Asp Gly Gln Arg Ser Ile Val Gly Met Ser Met Ser Gly Gly
 145 150 155 160

Leu
225

gag gtt gtt tac gat cct tcg aag att tcc ctc gag cag ctt gtt gcc 451
Glu Val Val Tyr Asp Pro Ser Lys Ile Ser Leu Glu Gln Leu Val Ala
105 110 115

cgc ggc ctg gaa gca cac gat ccg act cag ggt ttc cgc cag ggt aac 499
 Arg Gly Leu Glu Ala His Asp Pro Thr Gln Gly Phe Arg Gln Gly Asn
 120 125 130

 gat gtg gga acg cag tac cgc tct gct tat tac acc gag aac gaa gag 547
 Asp Val Gly Thr Gln Tyr Arg Ser Ala Tyr Tyr Thr Glu Asn Glu Glu
 135 140 145

 gac gct gcg cgc gta aaa gcc gtg gtc gat gcc tat ggt gag acg ctg 595
 Asp Ala Ala Arg Val Lys Ala Val Val Asp Ala Tyr Gly Glu Thr Leu
 150 155 160 165

 aag cag cac ggt ttt ggt gaa atc acc acg gaa atc ggt gtc att agc 643
 Lys Gln His Gly Phe Gly Glu Ile Thr Thr Glu Ile Gly Val Ile Ser
 170 175 180

 ccg tct gac tac ttc ctc gcc gag gat tac cac cag caa tac ctg gac 691
 Pro Ser Asp Tyr Phe Leu Ala Glu Asp Tyr His Gln Gln Tyr Leu Asp
 185 190 195

 aag aat ccc gat ggc tac tgc cct cat cac tcc acg ggc atc ccg tgc 739
 Lys Asn Pro Asp Gly Tyr Cys Pro His His Ser Thr Gly Ile Pro Cys
 200 205 210

 ggg gta gaa gct taaaagattt ttgcttttcg acg 774
 Gly Val Glu Ala
 215

<210> 546

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 546

Met Ala Trp Phe Phe Ala Pro Glu Pro Val Met Val Thr Ala Asp Glu
 1 5 10 15

 Ala Leu Lys Gly Gly Arg His Pro Val Leu Glu Asn Pro Ala Pro His
 20 25 30

 Thr Val Leu Gly Thr Pro Val Thr Gly Pro Trp Lys Glu Gly Gln Gln
 35 40 45

 Arg Ile Trp Ile Gly Leu Gly Cys Phe Trp Gly Val Glu Gln Met Tyr
 50 55 60

 Trp Gln Met Asp Gly Val Glu Gly Thr Ser Val Gly Tyr Ala Gly Gly
 65 70 75 80

 Phe Thr Pro Asn Pro Thr Tyr Arg Glu Val Cys Ser Gly Arg Thr Gly
 85 90 95

 His Thr Glu Ile Val Glu Val Val Tyr Asp Pro Ser Lys Ile Ser Leu
 100 105 110

 Glu Gln Leu Val Ala Arg Gly Leu Glu Ala His Asp Pro Thr Gln Gly
 115 120 125

 Phe Arg Gln Gly Asn Asp Val Gly Thr Gln Tyr Arg Ser Ala Tyr Tyr
 130 135 140

Thr Glu Asn Glu Glu Asp Ala Ala Arg Val Lys Ala Val Val Asp Ala
 145 150 155 160
 Tyr Gly Glu Thr Leu Lys Gln His Gly Phe Gly Glu Ile Thr Thr Glu
 165 170 175
 Ile Gly Val Ile Ser Pro Ser Asp Tyr Phe Leu Ala Glu Asp Tyr His
 180 185 190
 Gln Gln Tyr Leu Asp Lys Asn Pro Asp Gly Tyr Cys Pro His His Ser
 195 200 205
 Thr Gly Ile Pro Cys Gly Val Glu Ala
 210 215

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(421)
 <223> RXA01431

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attccccagg agtcccgta ttgttaattt aggagaaaacc atg agc aat gtt gtt 115
 Met Ser Asn Val Val
 1 5

gca gta acc gag cag acc ttc aag tcc acc gtc atc gat tcc gac aag 163
 Ala Val Thr Glu Gln Thr Phe Lys Ser Thr Val Ile Asp Ser Asp Lys
 10 15 20

cca gtc atc gtt gac ttc tgg gca gaa tgg tgt ggc ccc tgc aag aag 211
 Pro Val Ile Val Asp Phe Trp Ala Glu Trp Cys Gly Pro Cys Lys Lys
 25 30 35

ctc agc ccc atc att gag gaa atc gca ggc gag tac ggc gac aag gca 259
 Leu Ser Pro Ile Ile Glu Glu Ile Ala Gly Glu Tyr Gly Asp Lys Ala
 40 45 50

gtc gtt gcc agc gtc gac gtc gat gca gag cgt acc ttg ggt gcc atg 307
 Val Val Ala Ser Val Asp Val Asp Ala Glu Arg Thr Leu Gly Ala Met
 55 60 65

ttc cag att atg tcg att cct tct gtt ctc att ttc aaa aat ggt gca 355
 Phe Gln Ile Met Ser Ile Pro Ser Val Leu Ile Phe Lys Asn Gly Ala
 70 75 80 85

aaa gtc gag gaa ttt gtc ggt ctg cgc ccc aag aac gaa att gtg gaa 403
 Lys Val Glu Glu Phe Val Gly Leu Arg Pro Lys Asn Glu Ile Val Glu
 90 95 100

aaa cta gag aag cac ctc tagctggtat tcttactgca gtc 444
 Lys Leu Glu Lys His Leu
 105

<210> 548
 <211> 107
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 548
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 Ile Asp Ser Asp Lys Pro Val Ile Val Asp Phe Trp Ala Glu Trp Cys
 20 25 30
 Gly Pro Cys Lys Lys Leu Ser Pro Ile Ile Glu Glu Ile Ala Gly Glu
 35 40 45
 Tyr Gly Asp Lys Ala Val Val Ala Ser Val Asp Val Asp Ala Glu Arg
 50 55 60
 Thr Leu Gly Ala Met Phe Gln Ile Met Ser Ile Pro Ser Val Leu Ile
 65 70 75 80
 Phe Lys Asn Gly Ala Lys Val Glu Glu Phe Val Gly Leu Arg Pro Lys
 85 90 95
 Asn Glu Ile Val Glu Lys Leu Glu Lys His Leu
 100 105

<210> 549
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1051)
 <223> RXA01432

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 gtgatgctgc actttttacgt ttactacttt gagggaaaca atg tct gaa gaa caa 115
 Met Ser Glu Glu Gln
 1 5
 tct gcc gta gca cca aag att cat gat gtc gcc atc atc ggc tcc ggt 163
 Ser Ala Val Ala Pro Lys Ile His Asp Val Ala Ile Ile Gly Ser Gly
 10 15 20
 cca gct ggc tat acc gca gca gta tat gca gcc cgc gct gac ctc aac 211
 Pro Ala Gly Tyr Thr Ala Ala Val Tyr Ala Ala Arg Ala Asp Leu Asn
 25 30 35
 ccc atc atg ttc gag ggc tat gaa tac ggt gga tct ttg atg acc act 259
 Pro Ile Met Phe Glu Gly Tyr Glu Tyr Gly Gly Ser Leu Met Thr Thr
 40 45 50
 act gac gtg gaa aac ttc cca ggc ttt gaa aag gga atc ctg ggc cca 307
 Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys Gly Ile Leu Gly Pro

55	60	65	
gag ctc atg gaa aac atg cgc gct cag gcc gag cgt ttc ggc acc gac			355
Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu Arg Phe Gly Thr Asp			
70	75	80	85
atg cac atg gag ctt gtc gac cgc gtt gat ctc acc ggc gac atc aag			403
Met His Met Glu Leu Val Asp Arg Val Asp Leu Thr Gly Asp Ile Lys			
	90	95	100
aag ctg tgg gtc ggc gac gat gag tac cac gcg cgt gct gtc atc ttg			451
Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala Arg Ala Val Ile Leu			
	105	110	115
tcc atg ggt tct gca cct cgc tac ttg ggt gtg aag ggc gag cag gaa			499
Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val Lys Gly Glu Gln Glu			
	120	125	130
ctg ctc ggc cgc ggc gtt tct gca tgt gca acc tgc gat ggt ttc ttc			547
Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr Cys Asp Gly Phe Phe			
	135	140	145
ttc cgc gat cag gac atc gcc gtg atc ggt ggt ggc gac tcc gcg atg			595
Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly Gly Asp Ser Ala Met			
150	155	160	165
gag gaa gca acc ttc ctc acc aag ttc gct cgc agt gtc acc atc gtg			643
Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg Ser Val Thr Ile Val			
	170	175	180
cac cgc cgc gaa gag ttc cgc gcc agc gcc atc atg ctg gag cgt gct			691
His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile Met Leu Glu Arg Ala			
	185	190	195
cag aag aac gag aag att cgc ttc gtc acc aac aag act gtc gaa gag			739
Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn Lys Thr Val Glu Glu			
	200	205	210
gtc atc gag gca gac ggc aag gtc agc ggt ctg aag ctc aac gac acc			787
Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu Lys Leu Asn Asp Thr			
	215	220	225
gtc act ggt gaa gat tcc gtc ttg gat gtc acc gcc atg ttc gtt gcc			835
Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr Ala Met Phe Val Ala			
230	235	240	245
atc ggc cat gat cca cgc tct gaa atc ctc gca ggt cag gtc gag gtt			883
Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala Gly Gln Val Glu Val			
	250	255	260
gat cct tcc aac tac gtt ttg gtt cag gag cct tcc acc cgc acc aac			931
Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro Ser Thr Arg Thr Asn			
	265	270	275
ctt gat ggt gtt ttc gct gct ggc gac ctg gtg gac agc cac tac cag			979
Leu Asp Gly Val Phe Ala Ala Gly Asp Leu Val Asp Ser His Tyr Gln			
	280	285	290
cag gcc atc acc gca gct ggt tcc ggt tgc cgc gca gcg atc gat gca			1027
Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Arg Ala Ala Ile Asp Ala			
295	300	305	

gag cat tac cta gct tct ctg gcc taattcacag ttagccttaa acc
 Glu His Tyr Leu Ala Ser Leu Ala
 310 315

1074

<210> 550

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

Met Ser Glu Glu Gln Ser Ala Val Ala Pro Lys Ile His Asp Val Ala
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Ile Ile Gly Ser Gly Pro Ala Gly Tyr Thr Ala Ala Val Tyr Ala Ala
 20 25 30

Arg Ala Asp Leu Asn Pro Ile Met Phe Glu Gly Tyr Glu Tyr Gly Gly
 35 40 45

Ser Leu Met Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Glu Lys
 50 55 60

Gly Ile Leu Gly Pro Glu Leu Met Glu Asn Met Arg Ala Gln Ala Glu
 65 70 75 80

Arg Phe Gly Thr Asp Met His Met Glu Leu Val Asp Arg Val Asp Leu
 85 90 95

Thr Gly Asp Ile Lys Lys Leu Trp Val Gly Asp Asp Glu Tyr His Ala
 100 105 110

Arg Ala Val Ile Leu Ser Met Gly Ser Ala Pro Arg Tyr Leu Gly Val
 115 120 125

Lys Gly Glu Gln Glu Leu Leu Gly Arg Gly Val Ser Ala Cys Ala Thr
 130 135 140

Cys Asp Gly Phe Phe Phe Arg Asp Gln Asp Ile Ala Val Ile Gly Gly
 145 150 155 160

Gly Asp Ser Ala Met Glu Glu Ala Thr Phe Leu Thr Lys Phe Ala Arg
 165 170 175

Ser Val Thr Ile Val His Arg Arg Glu Glu Phe Arg Ala Ser Ala Ile
 180 185 190

Met Leu Glu Arg Ala Gln Lys Asn Glu Lys Ile Arg Phe Val Thr Asn
 195 200 205

Lys Thr Val Glu Glu Val Ile Glu Ala Asp Gly Lys Val Ser Gly Leu
 210 215 220

Lys Leu Asn Asp Thr Val Thr Gly Glu Asp Ser Val Leu Asp Val Thr
 225 230 235 240

Ala Met Phe Val Ala Ile Gly His Asp Pro Arg Ser Glu Ile Leu Ala
 245 250 255

Gly Gln Val Glu Val Asp Pro Ser Asn Tyr Val Leu Val Gln Glu Pro

260	265	270
Ser Thr Arg Thr Asn Leu Asp Gly Val Phe Ala Ala Gly Asp Leu Val		
275	280	285
Asp Ser His Tyr Gln Gln Ala Ile Thr Ala Ala Gly Ser Gly Cys Arg		
290	295	300
Ala Ala Ile Asp Ala Glu His Tyr Leu Ala Ser Leu Ala		
305	310	315

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<211> 495

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(472)

<223> RXN00937

<400> 551

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tctatatata gaccttacaa atcttgaacg gagattctta atg gca acc atc gat	115
Met Ala Thr Ile Asp	
1 5	

gta acc gaa gaa aca ttt gag agc aca gtt acc ggc gac gga att gtc	163
Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr Gly Asp Gly Ile Val	
10 15 20	

ctc gta gac gca tgg gca tcc tgg tgc gga cct tgc cgc cag ttc gcc	211
Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro Cys Arg Gln Phe Ala	
25 30 35	

cca acc tac gag aag gtt tcc gaa acc cac acc gac gca acc ttc gcc	259
Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr Asp Ala Thr Phe Ala	
40 45 50	

aag ctt gat acc gaa gca aac cag ggc ctg gct gca gca ctg cag atc	307
Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala Ala Ala Leu Gln Ile	
55 60 65	

cag tcc atc cca act ctg atg gtt ttc cgc gac ggc atc atg gtc tac	355
Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp Gly Ile Met Val Tyr	
70 75 80 85	

cgc gaa gcc ggc acc atg cca gct cct gca ctg gat gat ctg gtc aac	403
Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu Val Asn	
90 95 100	

cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc gca gag	451
Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val Ala Glu	
105 110 115	

cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt	495
Gln Gln Gly Ser Ala Glu Ala	
120	

<210> 552
 <211> 124
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 552
 Met Ala Thr Ile Asp Val Thr Glu Glu Thr Phe Glu Ser Thr Val Thr
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 Gly Asp Gly Ile Val Leu Val Asp Ala Trp Ala Ser Trp Cys Gly Pro
 20 25 30
 Cys Arg Gln Phe Ala Pro Thr Tyr Glu Lys Val Ser Glu Thr His Thr
 35 40 45
 Asp Ala Thr Phe Ala Lys Leu Asp Thr Glu Ala Asn Gln Gly Leu Ala
 50 55 60
 Ala Ala Leu Gln Ile Gln Ser Ile Pro Thr Leu Met Val Phe Arg Asp
 65 70 75 80
 Gly Ile Met Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu
 85 90 95
 Asp Asp Leu Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg
 100 105 110
 Arg Gln Val Ala Glu Gln Gln Gly Ser Ala Glu Ala
 115 120

<210> 553
 <211> 146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(123)
 <223> FRXA00937

<400> 553
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 Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu
 1 5 10 15
 gtc aac cag gtt aag gca ctc gac atg gat gac gtt cgt cgc cag gtc 96
 Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val
 20 25 30
 gca gag cag cag ggt tct gca gag gca taagcttcca attgtgtttt ggt 146
 Ala Glu Gln Gln Gly Ser Ala Glu Ala
 35 40

<210> 554
 <211> 41
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 554

Val Tyr Arg Glu Ala Gly Thr Met Pro Ala Pro Ala Leu Asp Asp Leu
 1 5 10 15

Val Asn Gln Val Lys Ala Leu Asp Met Asp Asp Val Arg Arg Gln Val
 20 25 30

Ala Glu Gln Gln Gly Ser Ala Glu Ala
 35 40

<210> 555

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(871)

<223> RXA01199

<400> 555

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ttagaaaaag tcattcgaga agaaggcgtg agttttaatc gtg acg tcc ccg cat 115
 Val Thr Ser Pro His
 1 5

aat ttt gtc agt ggt gct att gat ctg ggt gag gtg aaa gcg cgt gcg 163
 Asn Phe Val Ser Gly Ala Ile Asp Leu Gly Glu Val Lys Ala Arg Ala
 10 15 20

gat gcg cgc cag aag gcc cat gag cag ggg ccg gta act cag ggc att 211
 Asp Ala Arg Gln Lys Ala His Glu Gln Gly Pro Val Thr Gln Gly Ile
 25 30 35

gct agt tcc ctt gat gtg acc atg gag aac ctg gag aat gag gtg ctg 259
 Ala Ser Ser Leu Asp Val Thr Met Glu Asn Leu Glu Asn Glu Val Leu
 40 45 50

cgt cgt tcc acg cag gtt ccg gtg att gtt ctc gtg ggt acc ccg cgc 307
 Arg Arg Ser Thr Gln Val Pro Val Ile Val Leu Val Gly Thr Pro Arg
 55 60 65

agc cct gat tcg gag cag ttg aag tcg gat ctg acc acg ctt gct gct 355
 Ser Pro Asp Ser Glu Gln Leu Lys Ser Asp Leu Thr Thr Leu Ala Ala
 70 75 80 85

gaa agt ggc agg aag ttc att ttc ggt tat gtc aat gct gat acc gat 403
 Glu Ser Gly Arg Lys Phe Ile Phe Gly Tyr Val Asn Ala Asp Thr Asp
 90 95 100

gct gat gtg gcc cag gtg ttt ggg gtg cag ggc ttg ccg tcg gtg att 451
 Ala Asp Val Ala Gln Val Phe Gly Val Gln Gly Leu Pro Ser Val Ile
 105 110 115

gct gtg gca gcg gga cgc cct ctg gct gat ttc cag ggc gga cag cca 499
 Ala Val Ala Ala Gly Arg Pro Leu Ala Asp Phe Gln Gly Gly Gln Pro
 120 125 130

gcg gat gca cta aag cag tgg act gat cag gtg gtt cag gct gtg ggt 547

Ala	Asp	Ala	Leu	Lys	Gln	Trp	Thr	Asp	Gln	Val	Val	Gln	Ala	Val	Gly		
135						140					145						
gga	cag	ctg	gaa	gga	ctg	cca	gag	gag	gcc	aca	gac	ggc	gaa	caa	gaa	595	
Gly	Gln	Leu	Glu	Gly	Leu	Pro	Glu	Glu	Ala	Thr	Asp	Gly	Glu	Gln	Glu		
150					155				160						165		
gac	gct	cct	gtg	gaa	gac	ccc	cgc	ttc	gat	gct	gcc	act	gat	gct	cta	643	
Asp	Ala	Pro	Val	Glu	Asp	Pro	Arg	Phe	Asp	Ala	Ala	Thr	Asp	Ala	Leu		
				170					175					180			
aac	cgt	ggc	gct	ttc	gat	gag	gcg	att	gcg	gtt	tat	gag	tcc	att	ttg	691	
Asn	Arg	Gly	Ala	Phe	Asp	Glu	Ala	Ile	Ala	Val	Tyr	Glu	Ser	Ile	Leu		
			185					190					195				
gcg	cag	gag	cca	aac	aac	gct	gat	gcg	aag	caa	gca	ccg	cga	tac	cgc	739	
Ala	Gln	Glu	Pro	Asn	Asn	Ala	Asp	Ala	Lys	Gln	Ala	Pro	Arg	Tyr	Arg		
		200					205					210					
aaa	gct	gtt	ggg	ccg	gct	tgc	cac	cgg	tgg	atc	ctt	cgg	tgg	atg	ttg	787	
Lys	Ala	Val	Gly	Pro	Ala	Cys	His	Arg	Trp	Ile	Leu	Arg	Trp	Met	Leu		
	215					220					225						
tcg	ctg	ctg	cag	atg	ctg	atc	caa	caa	acg	ttg	atc	tgg	cct	aca	caa	835	
Ser	Leu	Leu	Gln	Met	Leu	Ile	Gln	Gln	Thr	Leu	Ile	Trp	Pro	Thr	Gln		
230					235					240					245		
gca	act	gac	gcg	gct	gtt	gtt	gcg	ggt	gat	cct	gag					871	
Ala	Thr	Asp	Ala	Ala	Val	Val	Ala	Gly	Asp	Pro	Glu						
				250					255								

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 <211> 257
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 556																	
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Val	Lys	Ala	Arg	Ala	Asp	Ala	Arg	Gln	Lys	Ala	His	Glu	Gln	Gly	Pro		
			20					25					30				
Val	Thr	Gln	Gly	Ile	Ala	Ser	Ser	Leu	Asp	Val	Thr	Met	Glu	Asn	Leu		
		35					40					45					
Glu	Asn	Glu	Val	Leu	Arg	Arg	Ser	Thr	Gln	Val	Pro	Val	Ile	Val	Leu		
	50					55					60						
Val	Gly	Thr	Pro	Arg	Ser	Pro	Asp	Ser	Glu	Gln	Leu	Lys	Ser	Asp	Leu		
65					70					75					80		
Thr	Thr	Leu	Ala	Ala	Glu	Ser	Gly	Arg	Lys	Phe	Ile	Phe	Gly	Tyr	Val		
				85				90						95			
Asn	Ala	Asp	Thr	Asp	Ala	Asp	Val	Ala	Gln	Val	Phe	Gly	Val	Gln	Gly		
			100					105					110				
Leu	Pro	Ser	Val	Ile	Ala	Val	Ala	Ala	Gly	Arg	Pro	Leu	Ala	Asp	Phe		
		115					120					125					

Gln Gly Gly Gln Pro Ala Asp Ala Leu Lys Gln Trp Thr Asp Gln Val
 130 135 140
 Val Gln Ala Val Gly Gly Gln Leu Glu Gly Leu Pro Glu Glu Ala Thr
 145 150 155 160
 Asp Gly Glu Gln Glu Asp Ala Pro Val Glu Asp Pro Arg Phe Asp Ala
 165 170 175
 Ala Thr Asp Ala Leu Asn Arg Gly Ala Phe Asp Glu Ala Ile Ala Val
 180 185 190
 Tyr Glu Ser Ile Leu Ala Gln Glu Pro Asn Asn Ala Asp Ala Lys Gln
 195 200 205
 Ala Pro Arg Tyr Arg Lys Ala Val Gly Pro Ala Cys His Arg Trp Ile
 210 215 220
 Leu Arg Trp Met Leu Ser Leu Leu Gln Met Leu Ile Gln Gln Thr Leu
 225 230 235 240
 Ile Trp Pro Thr Gln Ala Thr Asp Ala Ala Val Val Ala Gly Asp Pro
 245 250 255
 Glu

<210> 557
 <211> 681
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(658)
 <223> RXA00824

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 aggggagcacc tgctgaaaat ggcaggaatg tagaaaacaa atg aca agc agt gca 115
 Met Thr Ser Ser Ala
 1 5
 aag tgg tcc atc gtt gga gtt gtc gcc atc ctg gct gtg atc gtt gcg 163
 Lys Trp Ser Ile Val Gly Val Val Ala Ile Leu Ala Val Ile Val Ala
 10 15 20
 tta atc ccg cag ctt gtg ggt gga gaa agc gca gag gaa gcg cag ggg 211
 Leu Ile Pro Gln Leu Val Gly Gly Glu Ser Ala Glu Glu Ala Gln Gly
 25 30 35
 gag acg tcg aca agc aaa att acg acg cgt cct gac tgc gtg gcc tct 259
 Glu Thr Ser Thr Ser Lys Ile Thr Thr Arg Pro Asp Cys Val Ala Ser
 40 45 50
 ggc gcg gcg ggt gtg gat ctg ccc tgc ttg ggc ggc gcc aac ggc gtc 307
 Gly Ala Ala Gly Val Asp Leu Pro Cys Leu Gly Gly Ala Asn Gly Val
 55 60 65

ggc aac gag ctg gcc acc gtg gtg aat ctg tgg gcg tgg tgg tgc gaa 355
 Gly Asn Glu Leu Ala Thr Val Val Asn Leu Trp Ala Trp Trp Cys Glu
 70 75 80 85

 ccg tgc cgc gcg gag ctg ccg att ttt gat gaa ttc gcc acc acc cac 403
 Pro Cys Arg Ala Glu Leu Pro Ile Phe Asp Glu Phe Ala Thr Thr His
 90 95 100

 ccc gaa ctc aac gtc att ggc gtg cat gca gac caa aac gca gcc aac 451
 Pro Glu Leu Asn Val Ile Gly Val His Ala Asp Gln Asn Ala Ala Asn
 105 110 115

 ggc gcc gca ctc ctt gag gat ctg ggc gtg aat ctt gca agc tac caa 499
 Gly Ala Ala Leu Leu Glu Asp Leu Gly Val Asn Leu Ala Ser Tyr Gln
 120 125 130

 gac gat tcc aac ctg ttc gca ggc acc ctt ggg ctg ccg ggc gtc gtg 547
 Asp Asp Ser Asn Leu Phe Ala Gly Thr Leu Gly Leu Pro Gly Val Val
 135 140 145

 ccg atc acc atc gtg gtt tct cca gac ggc aat gta gtg gac acc ttc 595
 Pro Ile Thr Ile Val Val Ser Pro Asp Gly Asn Val Val Asp Thr Phe
 150 155 160 165

 ccg cag cct ttc gaa acc atc gat gac ctc gaa acc gct gtg gca ggg 643
 Pro Gln Pro Phe Glu Thr Ile Asp Asp Leu Glu Thr Ala Val Ala Gly
 170 175 180

 gcg ctg cag aat gcg taactaccct gatttaccgc atg 681
 Ala Leu Gln Asn Ala
 185

<210> 558

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Met Thr Ser Ser Ala Lys Trp Ser Ile Val Gly Val Val Ala Ile Leu
 1 5 10 15

 Ala Val Ile Val Ala Leu Ile Pro Gln Leu Val Gly Gly Glu Ser Ala
 20 25 30

 Glu Glu Ala Gln Gly Glu Thr Ser Thr Ser Lys Ile Thr Thr Arg Pro
 35 40 45

 Asp Cys Val Ala Ser Gly Ala Ala Gly Val Asp Leu Pro Cys Leu Gly
 50 55 60

 Gly Ala Asn Gly Val Gly Asn Glu Leu Ala Thr Val Val Asn Leu Trp
 65 70 75 80

 Ala Trp Trp Cys Glu Pro Cys Arg Ala Glu Leu Pro Ile Phe Asp Glu
 85 90 95

 Phe Ala Thr Thr His Pro Glu Leu Asn Val Ile Gly Val His Ala Asp
 100 105 110

Gln Asn Ala Ala Asn Gly Ala Ala Leu Leu Glu Asp Leu Gly Val Asn
 115 120 125

Leu Ala Ser Tyr Gln Asp Asp Ser Asn Leu Phe Ala Gly Thr Leu Gly
 130 135 140

Leu Pro Gly Val Val Pro Ile Thr Ile Val Val Ser Pro Asp Gly Asn
 145 150 155 160

Val Val Asp Thr Phe Pro Gln Pro Phe Glu Thr Ile Asp Asp Leu Glu
 165 170 175

Thr Ala Val Ala Gly Ala Leu Gln Asn Ala
 180 185

<210> 559

<211> 486

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(463)

<223> RXA01841

<400> 559

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 Met Glu Glu Gly Glu
 1 5

gag atc agc ctg tct gat ttt gaa ggc gag gtc gtc gtc ctc aac gct 163
 Glu Ile Ser Leu Ser Asp Phe Glu Gly Glu Val Val Val Leu Asn Ala
 10 15 20

tgg ggc cag tgg tgt gca ccg tgt cgg gcg gaa gtc gat gac ctg cag 211
 Trp Gly Gln Trp Cys Ala Pro Cys Arg Ala Glu Val Asp Asp Leu Gln
 25 30 35

ctt gtc cag gag act ctc gac ccc ctc ggt ggc acg gtg ctg ggc atc 259
 Leu Val Gln Glu Thr Leu Asp Pro Leu Gly Gly Thr Val Leu Gly Ile
 40 45 50

aac gtc cgt gac tac aac cag acc atc gcc cag gac ttc aaa ctc gac 307
 Asn Val Arg Asp Tyr Asn Gln Thr Ile Ala Gln Asp Phe Lys Leu Asp
 55 60 65

aac gcg gtg acc tat ccc tcg atc tac gac ccg ccg ttt cgt atc gct 355
 Asn Ala Val Thr Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Arg Ile Ala
 70 75 80 85

gcg gcc ctg ggt ggg gtg ccg acc tcg gtc atc ccg acc acc att gtc 403
 Ala Ala Leu Gly Gly Val Pro Thr Ser Val Ile Pro Thr Thr Ile Val
 90 95 100

ctg gac cga agc cac cgc ccg gcc gcg gtg ttc ctg agg gag gtc acc 451
 Leu Asp Arg Ser His Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr
 105 110 115

gcg ttg tct ggt tagtcctggg aggtgatgag ctc
 Ala Leu Ser Gly
 120

486

<210> 560
 <211> 121
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 560
 Met Glu Glu Gly Glu Glu Ile Ser Leu Ser Asp Phe Glu Gly Glu Val
 1 5 10 15
 Val Val Leu Asn Ala Trp Gly Gln Trp Cys Ala Pro Cys Arg Ala Glu
 20 25 30
 Val Asp Asp Leu Gln Leu Val Gln Glu Thr Leu Asp Pro Leu Gly Gly
 35 40 45
 Thr Val Leu Gly Ile Asn Val Arg Asp Tyr Asn Gln Thr Ile Ala Gln
 50 55 60
 Asp Phe Lys Leu Asp Asn Ala Val Thr Tyr Pro Ser Ile Tyr Asp Pro
 65 70 75 80
 Pro Phe Arg Ile Ala Ala Ala Leu Gly Gly Val Pro Thr Ser Val Ile
 85 90 95
 Pro Thr Thr Ile Val Leu Asp Arg Ser His Arg Pro Ala Ala Val Phe
 100 105 110
 Leu Arg Glu Val Thr Ala Leu Ser Gly
 115 120

<210> 561
 <211> 1219
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (48)..(1196)
 <223> RXN01863

<400> 561
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 Met Asn Ser
 1
 gtc aaa ttg aag caa cct gtt agc att tac aat gat cca tgg gaa tca 104
 Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro Trp Glu Ser
 5 10 15
 tat aac gat gtt aaa gaa cat ggc caa tta act tta agt aac atc gaa 152
 Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser Asn Ile Glu
 20 25 30 35
 ttt aca act aca aat ctt tgt aat atg cgt tgt agc cac tgt gca gtt 200
 Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His Cys Ala Val

40										45					50					
ggt	tat	act	tta	caa	act	gtc	gac	ccc	gag	cct	tta	gat	atg	gac	tta	248				
Gly	Tyr	Thr	Leu	Gln	Thr	Val	Asp	Pro	Glu	Pro	Leu	Asp	Met	Asp	Leu					
			55					60					65							
att	tat	cgt	aga	ctt	gat	gaa	att	cca	aat	ctg	cga	acg	atg	tca	att	296				
Ile	Tyr	Arg	Arg	Leu	Asp	Glu	Ile	Pro	Asn	Leu	Arg	Thr	Met	Ser	Ile					
		70					75					80								
aca	ggt	ggc	gaa	cca	atg	ttt	tct	aaa	aag	tct	att	aga	aat	gtt	gtt	344				
Thr	Gly	Gly	Glu	Pro	Met	Phe	Ser	Lys	Lys	Ser	Ile	Arg	Asn	Val	Val					
	85					90					95									
aaa	cct	cta	tta	aag	tat	gca	cat	cat	cga	ggt	ata	tat	aca	caa	atg	392				
Lys	Pro	Leu	Leu	Lys	Tyr	Ala	His	His	Arg	Gly	Ile	Tyr	Thr	Gln	Met					
100				105					110						115					
aat	tca	aac	cta	aca	ttg	cct	caa	gat	cgt	tat	tta	gat	att	gct	gaa	440				
Asn	Ser	Asn	Leu	Thr	Leu	Pro	Gln	Asp	Arg	Tyr	Leu	Asp	Ile	Ala	Glu					
			120					125						130						
tat	atc	gat	gtt	atg	cat	atc	tca	cat	aac	tggt	gga	aca	act	gat	gaa	488				
Tyr	Ile	Asp	Val	Met	His	Ile	Ser	His	Asn	Trp	Gly	Thr	Thr	Asp	Glu					
			135					140					145							
ttc	gca	aat	gtt	ggc	ttt	ggc	gca	atg	aag	aag	caa	cca	ccg	tta	aaa	536				
Phe	Ala	Asn	Val	Gly	Phe	Gly	Ala	Met	Lys	Lys	Gln	Pro	Pro	Leu	Lys					
		150					155					160								
gct	aag	tta	aaa	tta	tat	gaa	caa	atg	att	tcg	aat	gca	cgt	aca	tta	584				
Ala	Lys	Leu	Lys	Leu	Tyr	Glu	Gln	Met	Ile	Ser	Asn	Ala	Arg	Thr	Leu					
	165					170				175										
tca	gaa	caa	gga	atg	ttt	gta	tct	gcg	gaa	aca	atg	ctc	aat	caa	agt	632				
Ser	Glu	Gln	Gly	Met	Phe	Val	Ser	Ala	Glu	Thr	Met	Leu	Asn	Gln	Ser					
180				185						190					195					
acg	cta	cca	cat	tta	cga	aaa	ata	cat	caa	gaa	gtc	gtt	cat	gat	atg	680				
Thr	Leu	Pro	His	Leu	Arg	Lys	Ile	His	Gln	Glu	Val	Val	His	Asp	Met					
			200						205					210						
aaa	tgt	agc	aga	cac	gag	att	cac	cct	atg	tat	cca	gct	gac	ttt	gca	728				
Lys	Cys	Ser	Arg	His	Glu	Ile	His	Pro	Met	Tyr	Pro	Ala	Asp	Phe	Ala					
			215					220					225							
agt	caa	tta	aat	gtg	tta	act	cta	gcg	gaa	atg	aaa	aag	aca	att	cat	776				
Ser	Gln	Leu	Asn	Val	Leu	Thr	Leu	Ala	Glu	Met	Lys	Lys	Thr	Ile	His					
		230					235					240								
gat	ata	ttg	gat	ttc	aga	gat	gaa	gat	att	tggt	atg	tta	ttt	ggt	act	824				
Asp	Ile	Leu	Asp	Phe	Arg	Asp	Glu	Asp	Ile	Trp	Met	Leu	Phe	Gly	Thr					
	245					250					255									
ttg	cct	gtg	ttt	cca	tgc	tta	aag	gat	gat	gaa	gat	caa	aag	tta	cta	872				
Leu	Pro	Val	Phe	Pro	Cys	Leu	Lys	Asp	Asp	Glu	Asp	Gln	Lys	Leu	Leu					
260					265					270					275					
tca	cgt	tta	aga	aat	gct	aac	aat	gta	acg	act	aga	aat	gac	ccg	gat	920				
Ser	Arg	Leu	Arg	Asn	Ala	Asn	Asn	Val	Thr	Thr	Arg	Asn	Asp	Pro	Asp					
				280					285					290						

ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta 968
 Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val
 295 300 305

 act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat 1016
 Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp
 310 315 320

 aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa 1064
 Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys
 325 330 335

 tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt 1112
 Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val
 340 345 350 355

 ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag 1160
 Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu
 360 365 370

 cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 1206
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
 375 380

 taattatgcg gag 1219

<210> 562

<211> 383

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

Met Asn Ser Val Lys Leu Lys Gln Pro Val Ser Ile Tyr Asn Asp Pro
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 Trp Glu Ser Tyr Asn Asp Val Lys Glu His Gly Gln Leu Thr Leu Ser
 20 25 30

 Asn Ile Glu Phe Thr Thr Thr Asn Leu Cys Asn Met Arg Cys Ser His
 35 40 45

 Cys Ala Val Gly Tyr Thr Leu Gln Thr Val Asp Pro Glu Pro Leu Asp
 50 55 60

 Met Asp Leu Ile Tyr Arg Arg Leu Asp Glu Ile Pro Asn Leu Arg Thr
 65 70 75 80

 Met Ser Ile Thr Gly Gly Glu Pro Met Phe Ser Lys Lys Ser Ile Arg
 85 90 95

 Asn Val Val Lys Pro Leu Leu Lys Tyr Ala His His Arg Gly Ile Tyr
 100 105 110

 Thr Gln Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp
 115 120 125

 Ile Ala Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr
 130 135 140

Thr Asp Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro
 145 150 155 160
 Pro Leu Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala
 165 170 175
 Arg Thr Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu
 180 185 190
 Asn Gln Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val
 195 200 205
 His Asp Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala
 210 215 220
 Asp Phe Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys
 225 230 235 240
 Thr Ile His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu
 245 250 255
 Phe Gly Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln
 260 265 270
 Lys Leu Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn
 275 280 285
 Asp Pro Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn
 290 295 300
 Val Ile Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile
 305 310 315 320
 Gln Lys Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp
 325 330 335
 Leu Ala Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly
 340 345 350
 Pro Asn Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys
 355 360 365
 Asp Asn Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
 370 375 380

<210> 563

<211> 888

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (59) .. (865)

<223> FRXA01863

<400> 563

ttagaaatgt tgtaaacctc tattaaagta tgcacatcat cgaggtatat atacacaa atg 61
 Met

1

aat tca aac cta aca ttg cct caa gat cgt tat tta gat att gct gaa	109
Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala Glu	
5 10 15	
tat atc gat gtt atg cat atc tca cat aac tgg gga aca act gat gaa	157
Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Asp Glu	
20 25 30	
ttc gca aat gtt ggc ttt ggc gca atg aag aag caa cca ccg tta aaa	205
Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu Lys	
35 40 45	
gct aag tta aaa tta tat gaa caa atg att tcg aat gca cgt aca tta	253
Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr Leu	
50 55 60 65	
tca gaa caa gga atg ttt gta tct gcg gaa aca atg ctc aat caa agt	301
Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln Ser	
70 75 80	
acg cta cca cat tta cga aaa ata cat caa gaa gtc gtt cat gat atg	349
Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp Met	
85 90 95	
aaa tgt agc aga cac gag att cac cct atg tat cca gct gac ttt gca	397
Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe Ala	
100 105 110	
agt caa tta aat gtg tta act cta gcg gaa atg aaa aag aca att cat	445
Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile His	
115 120 125	
gat ata ttg gat ttc aga gat gaa gat att tgg atg tta ttt ggt act	493
Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly Thr	
130 135 140 145	
ttg cct gtg ttt cca tgc tta aag gat gat gaa gat caa aag tta cta	541
Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu Leu	
150 155 160	
tca cgt tta aga aat gct aac aat gta acg act aga aat gac ccg gat	589
Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro Asp	
165 170 175	
ggc cgt agt cgt tta aat gtc aat gta ttt aca ggt aat gta atc gta	637
Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile Val	
180 185 190	
act gat ttc gga gat gaa aca ggt aca att tcg aat ata caa aaa gat	685
Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys Asp	
195 200 205	
aaa tta aca gat gta ttt gat aaa tgg tta tcc tct gat ctt gct aaa	733
Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala Lys	
210 215 220 225	
tca tta aat tgt cat tgt tcc gag ttt agt tgt tta gga cca aat gtt	781
Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn Val	
230 235 240	
ctt gtt aaa aat atg tac tat ccg aat atg gat ttt aaa gat aat gag	829

Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn Glu
 245 250 255

cgt cat atg cac aaa caa cca caa att ata caa ttt taaaaactct 875
 Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
 260 265

taattatgcg gag 888

<210> 564

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

Met Asn Ser Asn Leu Thr Leu Pro Gln Asp Arg Tyr Leu Asp Ile Ala
 1 5 10 15

Glu Tyr Ile Asp Val Met His Ile Ser His Asn Trp Gly Thr Thr Asp
 20 25 30

Glu Phe Ala Asn Val Gly Phe Gly Ala Met Lys Lys Gln Pro Pro Leu
 35 40 45

Lys Ala Lys Leu Lys Leu Tyr Glu Gln Met Ile Ser Asn Ala Arg Thr
 50 55 60

Leu Ser Glu Gln Gly Met Phe Val Ser Ala Glu Thr Met Leu Asn Gln
 65 70 75 80

Ser Thr Leu Pro His Leu Arg Lys Ile His Gln Glu Val Val His Asp
 85 90 95

Met Lys Cys Ser Arg His Glu Ile His Pro Met Tyr Pro Ala Asp Phe
 100 105 110

Ala Ser Gln Leu Asn Val Leu Thr Leu Ala Glu Met Lys Lys Thr Ile
 115 120 125

His Asp Ile Leu Asp Phe Arg Asp Glu Asp Ile Trp Met Leu Phe Gly
 130 135 140

Thr Leu Pro Val Phe Pro Cys Leu Lys Asp Asp Glu Asp Gln Lys Leu
 145 150 155 160

Leu Ser Arg Leu Arg Asn Ala Asn Asn Val Thr Thr Arg Asn Asp Pro
 165 170 175

Asp Gly Arg Ser Arg Leu Asn Val Asn Val Phe Thr Gly Asn Val Ile
 180 185 190

Val Thr Asp Phe Gly Asp Glu Thr Gly Thr Ile Ser Asn Ile Gln Lys
 195 200 205

Asp Lys Leu Thr Asp Val Phe Asp Lys Trp Leu Ser Ser Asp Leu Ala
 210 215 220

Lys Ser Leu Asn Cys His Cys Ser Glu Phe Ser Cys Leu Gly Pro Asn
 225 230 235 240

Val Leu Val Lys Asn Met Tyr Tyr Pro Asn Met Asp Phe Lys Asp Asn
245 250 255

Glu Arg His Met His Lys Gln Pro Gln Ile Ile Gln Phe
260 265

<210> 565

<211> 1047

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1024)

<223> RXA02323

<400> 565

ggaatcattt tcaatagagt cgacgcaagt gtacacttct taatggaaat tgttttcaat 60

aaagtcaagt tttttgacct tcgcttttta ggagcacccc atg tca tct cat gat 115
Met Ser Ser His Asp
1 5

ctc gtt gac gta gtt gtc gtc ggc gcc ggc gct gca ggt ctc gcc gcc 163
Leu Val Asp Val Val Val Val Gly Ala Gly Ala Gly Leu Ala Ala
10 15 20

gct gtc gcg ctc ggc cgc tca ctg cgc agt gtc atc gtc atc gac gct 211
Ala Val Ala Leu Gly Arg Ser Leu Arg Ser Val Ile Val Ile Asp Ala
25 30 35

ggt caa ccc cgt aac agc tat gcg cac gct gct cac aat gtc ctc ggc 259
Gly Gln Pro Arg Asn Ser Tyr Ala His Ala Ala His Asn Val Leu Gly
40 45 50

cag gaa ggc att gcg ccc gcc gag ctg ctg gaa aaa ggc cgc gcc gaa 307
Gln Glu Gly Ile Ala Pro Ala Glu Leu Leu Glu Lys Gly Arg Ala Glu
55 60 65

gcg cgt tcc tat ggc gtc acc att gcg ccc ggg cgc gta gca aaa gtt 355
Ala Arg Ser Tyr Gly Val Thr Ile Ala Pro Gly Arg Val Ala Lys Val
70 75 80 85

gag cgc acc ggt tcc acc ttc gcc ata acg ctt gac gac gcc tcc ctc 403
Glu Arg Thr Gly Ser Thr Phe Ala Ile Thr Leu Asp Asp Ala Ser Leu
90 95 100

ctt cac tct cgg cgc atc att ttg gcc cac ggc gcc gtt gac gat ctg 451
Leu His Ser Arg Arg Ile Ile Leu Ala His Gly Ala Val Asp Asp Leu
105 110 115

cca gag gta gaa gga ctg tca gat ttt tgg gga acc aaa gtg ttg cac 499
Pro Glu Val Glu Gly Leu Ser Asp Phe Trp Gly Thr Lys Val Leu His
120 125 130

tgc gct tac tgc cac ggc ttt gag gcc cgc gat tct gaa atc gtc gtg 547
Cys Ala Tyr Cys His Gly Phe Glu Ala Arg Asp Ser Glu Ile Val Val
135 140 145

gtg ggt acc tcg ccc atg gct gcg cac caa gcg ttg atg ttc tcg cag 595

Val Gly Thr Ser Pro Met Ala Ala His Gln Ala Leu Met Phe Ser Gln
 150 155 160 165
 ttg tcc aaa act gtc agc ttg gtg ggc acg atc gac att gat gaa caa 643
 Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile Asp Ile Asp Glu Gln
 170 175 180
 acc agc gag agc cta gat agt gct gga gta aaa gtg ttg ggc acc aat 691
 Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys Val Leu Gly Thr Asn
 185 190 195
 gcg gtg cgc gta tcc gcc gaa ggt gat ggc ctg tct gtg gaa ctg tcc 739
 Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu Ser Val Glu Leu Ser
 200 205 210
 gaa ggc gat cat tta agc tgc gac aac atc gtg gtg gca tct cgt cca 787
 Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val Val Ala Ser Arg Pro
 215 220 225
 ctg gtg gat ggc acg ctg tac acc caa ctt ggt ggt cag atg gaa gaa 835
 Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly Gly Gln Met Glu Glu
 230 235 240 245
 aac ccg atg ggc agg ttc att cca ggt acc caa acc ggg cgc act cct 883
 Asn Pro Met Gly Arg Phe Ile Pro Gly Thr Gln Thr Gly Arg Thr Pro
 250 255 260
 att gaa ggt gtg tgg gct gcc gga aac gcg caa gct ccc atg gcg atg 931
 Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln Ala Pro Met Ala Met
 265 270 275
 gtc tat ggt tcc gct gct caa ggc gtg atg gct gga gca gag atc aac 979
 Val Tyr Gly Ser Ala Ala Gln Gly Val Met Ala Gly Ala Glu Ile Asn
 280 285 290
 ttt gat ctg atc ctg gaa gat att tcc gtg gca agc gcg cag agc 1024
 Phe Asp Leu Ile Leu Glu Asp Ile Ser Val Ala Ser Ala Gln Ser
 295 300 305
 taaactgcgt gaggttggtg cct 1047

 <210> 566
 <211> 308
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 566
 Met Ser Ser His Asp Leu Val Asp Val Val Val Val Gly Ala Gly Ala
 1 5 10 15
 Ala Gly Leu Ala Ala Ala Val Ala Leu Gly Arg Ser Leu Arg Ser Val
 20 25 30
 Ile Val Ile Asp Ala Gly Gln Pro Arg Asn Ser Tyr Ala His Ala Ala
 35 40 45
 His Asn Val Leu Gly Gln Glu Gly Ile Ala Pro Ala Glu Leu Leu Glu
 50 55 60
 Lys Gly Arg Ala Glu Ala Arg Ser Tyr Gly Val Thr Ile Ala Pro Gly

65	70	75	80
Arg Val Ala Lys Val Glu Arg Thr Gly Ser Thr Phe Ala Ile Thr Leu	85	90	95
Asp Asp Ala Ser Leu Leu His Ser Arg Arg Ile Ile Leu Ala His Gly	100	105	110
Ala Val Asp Asp Leu Pro Glu Val Glu Gly Leu Ser Asp Phe Trp Gly	115	120	125
Thr Lys Val Leu His Cys Ala Tyr Cys His Gly Phe Glu Ala Arg Asp	130	135	140
Ser Glu Ile Val Val Val Gly Thr Ser Pro Met Ala Ala His Gln Ala	145	150	155
Leu Met Phe Ser Gln Leu Ser Lys Thr Val Ser Leu Val Gly Thr Ile	165	170	175
Asp Ile Asp Glu Gln Thr Ser Glu Ser Leu Asp Ser Ala Gly Val Lys	180	185	190
Val Leu Gly Thr Asn Ala Val Arg Val Ser Ala Glu Gly Asp Gly Leu	195	200	205
Ser Val Glu Leu Ser Glu Gly Asp His Leu Ser Cys Asp Asn Ile Val	210	215	220
Val Ala Ser Arg Pro Leu Val Asp Gly Thr Leu Tyr Thr Gln Leu Gly	225	230	235
Gly Gln Met Glu Glu Asn Pro Met Gly Arg Phe Ile Pro Gly Thr Gln	245	250	255
Thr Gly Arg Thr Pro Ile Glu Gly Val Trp Ala Ala Gly Asn Ala Gln	260	265	270
Ala Pro Met Ala Met Val Tyr Gly Ser Ala Ala Gln Gly Val Met Ala	275	280	285
Gly Ala Glu Ile Asn Phe Asp Leu Ile Leu Glu Asp Ile Ser Val Ala	290	295	300
Ser Ala Gln Ser			
305			

<210> 567

<211> 354

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(331)

<223> RXA01072

<400> 567

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                                   Met Ala Ile Thr Val
                                   1      5

tac acc aag cca gct tgc gtc cag tgc aat gcc acc aag aag gcc ctc 163
Tyr Thr Lys Pro Ala Cys Val Gln Cys Asn Ala Thr Lys Lys Ala Leu
              10              15              20

gac cgc gct ggt ctt gag tat gac ctc gtt gat atc agc ctt gat gaa 211
Asp Arg Ala Gly Leu Glu Tyr Asp Leu Val Asp Ile Ser Leu Asp Glu
              25              30              35

gag gca cgt gag tac gtc ctc gca ctt ggc tac ctg cag gca cca gtt 259
Glu Ala Arg Glu Tyr Val Leu Ala Leu Gly Tyr Leu Gln Ala Pro Val
              40              45              50

gtc gtt gca gat ggc tcc cac tgg tcc ggt ttc cgc cca gag cgc atc 307
Val Val Ala Asp Gly Ser His Trp Ser Gly Phe Arg Pro Glu Arg Ile
              55              60              65

cgt gaa atg gca acc gca gct gcc taaactgcac ttcgtggcac gac 354
Arg Glu Met Ala Thr Ala Ala Ala
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<210> 568
 <211> 77
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 568
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Thr Lys Lys Ala Leu Asp Arg Ala Gly Leu Glu Tyr Asp Leu Val Asp
              20              25              30

Ile Ser Leu Asp Glu Glu Ala Arg Glu Tyr Val Leu Ala Leu Gly Tyr
              35              40              45

Leu Gln Ala Pro Val Val Val Ala Asp Gly Ser His Trp Ser Gly Phe
              50              55              60

Arg Pro Glu Arg Ile Arg Glu Met Ala Thr Ala Ala Ala
 65              70              75

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<210> 569
 <211> 684
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(661)
 <223> RXA02436

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<400> 569
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cgttctttcta agaccccaca ttagtaaaaag catggggacat gtg gtt ggc att tcg 115

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	Val 1	Val 1	Gly 1	Ile 1	Ser 5	
ctc gat gta gtt atg atg ggc gtt atg act tct aag acc gca act gcg 163						
Leu Asp Val Val Met Met Gly Val Met Thr Ser Lys Thr Ala Thr Ala						
						10 15 20
att ctg cat aca aat cgc gga gac atc acc atc gac ctg ttc ggc aac 211						
Ile Leu His Thr Asn Arg Gly Asp Ile Thr Ile Asp Leu Phe Gly Asn						
						25 30 35
cac gct cca gag acc gtc gct aac ttc gtt ggc ctg gca cag ggc acc 259						
His Ala Pro Glu Thr Val Ala Asn Phe Val Gly Leu Ala Gln Gly Thr						
						40 45 50
aag gac tac cag tcc gca aac gct cag ggc gac agc gaa ggt ccg ttc 307						
Lys Asp Tyr Gln Ser Ala Asn Ala Gln Gly Asp Ser Glu Gly Pro Phe						
						55 60 65
tac aac gga tct gtc ttc cac cgc gtc atc gac ggt ttc atg atc cag 355						
Tyr Asn Gly Ser Val Phe His Arg Val Ile Asp Gly Phe Met Ile Gln						
						70 75 80 85
ggt gaa gac cca acc ggc acc ggc cgt ggc ggc cct ggc tac acc ttc 403						
Gly Glu Asp Pro Thr Gly Thr Gly Arg Gly Gly Pro Gly Tyr Thr Phe						
						90 95 100
gct gat gaa ttc cac cca gag ctg cgc ttc gac cgc gca tac ctg ctg 451						
Ala Asp Glu Phe His Pro Glu Leu Arg Phe Asp Arg Ala Tyr Leu Leu						
						105 110 115
gca atg gca aat gcg ggc cca ggc acc aac ggt tcc cag ttc ttc atc 499						
Ala Met Ala Asn Ala Gly Pro Gly Thr Asn Gly Ser Gln Phe Phe Ile						
						120 125 130
act gtg acc cca acc cct cac ctg aac aac gct cac acc atc ttc ggt 547						
Thr Val Thr Pro Thr Pro His Leu Asn Asn Ala His Thr Ile Phe Gly						
						135 140 145
gag gtc act gac gct gag tct cag aag gtt gtg gat gca att gca acc 595						
Glu Val Thr Asp Ala Glu Ser Gln Lys Val Val Asp Ala Ile Ala Thr						
						150 155 160 165
acc gca acc gat cgt tac gac cgc cca gct gac gca gtt gtc atc gag 643						
Thr Ala Thr Asp Arg Tyr Asp Arg Pro Ala Asp Ala Val Val Ile Glu						
						170 175 180
tct gta gag atc acc gcg taacagccac ctctacgtac act 684						
Ser Val Glu Ile Thr Ala						
						185

<210> 570

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 570

Val	Val	Gly	Ile	Ser	Leu	Asp	Val	Val	Met	Met	Gly	Val	Met	Thr	Ser
1				5					10					15	

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<210> 571
<211> 900
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(877)
<223> RXN01837
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<400> 571
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ttggacattc tcaaaatcaa gtagcaaggg atcaaactct gtg agt act aat aag 115
                               Val Ser Thr Asn Lys
                               1                               5

gaa cga cgc caa cag gcg ctt tcc cag ctg gag aaa gaa atc aaa agc 163
Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu Lys Glu Ile Lys Ser
                               10                               15                               20

cgg gac cgc aaa gaa aag acc aag cca cta acc gtg gtc ttt gct tcc 211
Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr Val Val Phe Ala Ser
                               25                               30                               35

ctg gct gtc atc ctg gtt gtc gtt ggc ggt atc tgg tac gca gct acc 259
Leu Ala Val Ile Leu Val Val Val Gly Gly Ile Trp Tyr Ala Ala Thr

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40	45	50	
cgc agc acc gaa gac gaa gtc atc acc gct gat gaa aca tcc acc acc			307
Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp Glu Thr Ser Thr Thr			
55	60	65	
gca gag acc cct gac tac cag cca ctg gcg ctg acc cgc acc acc gcg			355
Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu Thr Arg Thr Thr Ala			
70	75	80	85
ctc ggc gac tcc gtg acc tgt gag tac cca gat gct ggc gag gct tcc			403
Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp Ala Gly Glu Ala Ser			
	90	95	100
aag gat gtc tcc aag cct gct act gaa aac gtg cca gca acc ggc acc			451
Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val Pro Ala Thr Gly Thr			
	105	110	115
gtg acc gtc aac ctg acc acc gcc cag ggc aac atc ggc atg gaa ctt			499
Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn Ile Gly Met Glu Leu			
	120	125	130
gat cgc tcc gta tcc cct tgt acc gtc aac gct gtt gag cac atg gct			547
Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala Val Glu His Met Ala			
	135	140	145
tcc gag ggc tac tac aac gat act gtc tgc cac cgc atc acc acc tct			595
Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser			
150	155	160	165
ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc			643
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly			
	170	175	180
ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act			691
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr			
	185	190	195
gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc			739
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala			
	200	205	210
aac gct ggc gct gac acc aac ggg ctc cca gtt ctt cct caa cta cga			787
Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val Leu Pro Gln Leu Arg			
	215	220	225
gga ttc ccc act ggc acc gaa cta cac cta ctt cgg cca gat cac cga			835
Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu Arg Pro Asp His Arg			
230	235	240	245
aga agg cct tgc aac cct cga cgc cat cgc aga agt tgg cac			877
Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg Ser Trp His			
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tgaaggtgga accggcgacg gag			900

<210> 572

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

Val Ser Thr Asn Lys Glu Arg Arg Gln Gln Ala Leu Ser Gln Leu Glu
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Lys Glu Ile Lys Ser Arg Asp Arg Lys Glu Lys Thr Lys Pro Leu Thr
 20 25 30

Val Val Phe Ala Ser Leu Ala Val Ile Leu Val Val Val Gly Gly Ile
 35 40 45

Trp Tyr Ala Ala Thr Arg Ser Thr Glu Asp Glu Val Ile Thr Ala Asp
 50 55 60

Glu Thr Ser Thr Thr Ala Glu Thr Pro Asp Tyr Gln Pro Leu Ala Leu
 65 70 75 80

Thr Arg Thr Thr Ala Leu Gly Asp Ser Val Thr Cys Glu Tyr Pro Asp
 85 90 95

Ala Gly Glu Ala Ser Lys Asp Val Ser Lys Pro Ala Thr Glu Asn Val
 100 105 110

Pro Ala Thr Gly Thr Val Thr Val Asn Leu Thr Thr Ala Gln Gly Asn
 115 120 125

Ile Gly Met Glu Leu Asp Arg Ser Val Ser Pro Cys Thr Val Asn Ala
 130 135 140

Val Glu His Met Ala Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His
 145 150 155 160

Arg Ile Thr Thr Ser Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser
 165 170 175

Ser Thr Gly Ala Gly Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro
 180 185 190

Thr Asp Glu Ala Thr Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly
 195 200 205

Thr Ile Ala Met Ala Asn Ala Gly Ala Asp Thr Asn Gly Leu Pro Val
 210 215 220

Leu Pro Gln Leu Arg Gly Phe Pro Thr Gly Thr Glu Leu His Leu Leu
 225 230 235 240

Arg Pro Asp His Arg Arg Arg Pro Cys Asn Pro Arg Arg His Arg Arg
 245 250 255

Ser Trp His

<210> 573

<211> 416

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(393)

<223> FRXA01837

<400> 573

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Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser	
1 5 10 15	
ggc att tac gtt ctc cag tgc ggc gat cca agc agc acc ggc gca ggc	96
Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly	
20 25 30	
ggc cca ggg ttc agc ttc gcc aac gaa tac cca acc gac gaa gca act	144
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr	
35 40 45	
gac cta acc acc cca gtc atc tac gag cgc ggc acc atc gcc atg gcc	192
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala	
50 55 60	
aac gct ggc gct gac acc aac ggc tcc cag ttc ttc ctc aac tac gag	240
Asn Ala Gly Ala Asp Thr Asn Gly Ser Gln Phe Phe Leu Asn Tyr Glu	
65 70 75 80	
gat tcc cca ctg gca ccg aac tac acc tac ttc ggc cag atc acc gaa	288
Asp Ser Pro Leu Ala Pro Asn Tyr Thr Tyr Phe Gly Gln Ile Thr Glu	
85 90 95	
gaa ggc ctt gca acc ctc gac gcc atc gca gaa gtt ggc act gaa ggt	336
Glu Gly Leu Ala Thr Leu Asp Ala Ile Ala Glu Val Gly Thr Glu Gly	
100 105 110	
gga acc ggc gac gga gca cca gcg caa gag gtt cgc att gaa tcc gca	384
Gly Thr Gly Asp Gly Ala Pro Ala Gln Glu Val Arg Ile Glu Ser Ala	
115 120 125	
gct gtt gcg taagttctaa gccctcttc ttt	416
Ala Val Ala	
130	

<210> 574

<211> 131

<212> PRT

<213> Corynebacterium glutamicum

<400> 574

Ser Glu Gly Tyr Tyr Asn Asp Thr Val Cys His Arg Ile Thr Thr Ser	
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Gly Ile Tyr Val Leu Gln Cys Gly Asp Pro Ser Ser Thr Gly Ala Gly	
20 25 30	
Gly Pro Gly Phe Ser Phe Ala Asn Glu Tyr Pro Thr Asp Glu Ala Thr	
35 40 45	
Asp Leu Thr Thr Pro Val Ile Tyr Glu Arg Gly Thr Ile Ala Met Ala	
50 55 60	
Asn Ala Gly Ala Asp Thr Asn Gly Ser Gln Phe Phe Leu Asn Tyr Glu	
65 70 75 80	

<400> 575																										
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taaaaaaacct gccgggtcaaa agatcactaa cctgaacttc																atg	act	gat	tac	acg						115
																Met	Thr	Asp	Tyr	Thr						
																1				5						
ttc	ctc	gaa	gac	att	gac	acc	ccg	gaa	gcg	ctc	gcg	tgg	gcg	gaa	aaa	163										
Phe	Leu	Glu	Asp	Ile	Asp	Thr	Pro	Glu	Ala	Leu	Ala	Trp	Ala	Glu	Lys											
				10					15					20												
tgg	tcg	ggg	gaa	agc	gtc	gaa	aag	cta	aaa	agc	cca	gcc	aag	gac	gcc	211										
Trp	Ser	Gly	Glu	Ser	Val	Glu	Lys	Leu	Lys	Ser	Pro	Ala	Lys	Asp	Ala											
				25					30					35												
ctg	gaa	gcc	agg	ctg	ctg	gct	gcg	ttg	gac	acc	gat	gat	cgc	att	gcc	259										
Leu	Glu	Ala	Arg	Leu	Leu	Ala	Ala	Leu	Asp	Thr	Asp	Asp	Arg	Ile	Ala											
				40					45					50												
tac	gtg	agc	cgg	cgc	ggt	gag	aag	ctg	tac	aac	ttt	tgg	cgg	gac	gcg	307										
Tyr	Val	Ser	Arg	Arg	Gly	Glu	Lys	Leu	Tyr	Asn	Phe	Trp	Arg	Asp	Ala											
				55					60					65												
cag	cat	ccg	cgt	gga	gtg	tgg	cgc	acg	acc	acg	ttg	gag	tcg	tat	gaa	355										
Gln	His	Pro	Arg	Gly	Val	Trp	Arg	Thr	Thr	Thr	Leu	Glu	Ser	Tyr	Glu											
				70					75					80			85									
agt	gac	cag	ccg	gag	tgg	gac	gtg	ctc	att	gat	gtg	gat	gcg	ttg	gcg	403										
Ser	Asp	Gln	Pro	Glu	Trp	Asp	Val	Leu	Ile	Asp	Val	Asp	Ala	Leu	Ala											
				90					95					100												
gag	gat	gag	ggc	gaa	aac	tgg	gta	tgg	aag	ggc	gcg	gtt	gtg	cgc	tcg	451										
Glu	Asp	Glu	Gly	Glu	Asn	Trp	Val	Trp	Lys	Gly	Ala	Val	Val	Arg	Ser											
				105					110					115												
ccg	gag	ttt	gat	cgg	gcg	ttg	gtg	aag	ttc	tcg	cgg	ggc	ggg	gct	gat	499										
Pro	Glu	Phe	Asp	Arg	Ala	Leu	Val	Lys	Phe	Ser	Arg	Gly	Gly	Ala	Asp											

120					125					130							
gcg	acg	gtg	att	agg	gag	ttt	gat	ctg	gcc	acg	gct	gct	ttc	gtg	gat	547	
Ala	Thr	Val	Ile	Arg	Glu	Phe	Asp	Leu	Ala	Thr	Ala	Ala	Phe	Val	Asp		
135					140					145							
gat	tcg	ccg	ttt	gaa	ttg	aag	gag	gcg	aag	tcc	gat	gtc	acg	tgg	gtt	595	
Asp	Ser	Pro	Phe	Glu	Leu	Lys	Glu	Ala	Lys	Ser	Asp	Val	Thr	Trp	Val		
150					155					160					165		
gat	ctg	gat	acg	ttg	ctg	gtg	ggc	acg	gat	acc	ggc	gag	ggg	tca	ctg	643	
Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr	Gly	Glu	Gly	Ser	Leu		
170					175					180							
acg	gat	tct	ggg	tac	ccg	gcg	cgg	gtg	ctc	acg	tgg	aag	cgt	ggg	act	691	
Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr	Trp	Lys	Arg	Gly	Thr		
185					190					195							
ccg	ctt	gag	cag	gcg	gag	ttg	ttc	ttt	gag	ggg	tcg	cgt	cag	gat	gtg	739	
Pro	Leu	Glu	Gln	Ala	Glu	Leu	Phe	Phe	Glu	Gly	Ser	Arg	Gln	Asp	Val		
200					205					210							
gcg	act	cat	gcg	tgg	cgg	gat	tca	aca	cct	ggt	ttt	gag	cgg	acg	ttt	787	
Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly	Phe	Glu	Arg	Thr	Phe		
215					220					225							
gtg	tca	agg	tcg	ttg	gat	ttc	tat	aat	tcg	gag	acg	tcg	ctg	gaa	acc	835	
Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr		
230					235					240					245		
gag	ggt	ggc	ctg	gtc	aag	ctt	gat	gtg	ccg	acc	gat	tgc	gat	gtc	att	883	
Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile		
250					255					260							
gtg	aag	aag	cag	tgg	att	ttt	gtg	agt	cct	cgg	acg	gat	ttc	gct	ggg	931	
Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly		
265					270					275							
att	cca	gca	ggt	ggc	ttg	gga	gtg	ctg	ctg	tta	aag	gag	ttc	ctt	gag	979	
Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu		
280					285					290							
ggc	ggg	cgc	gat	ttt	cag	cct	gtg	ttt	acg	cct	act	gag	tcg	acg	tcg	1027	
Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro	Thr	Glu	Ser	Thr	Ser		
295					300					305							
ctg	cag	gga	ttg	gcc	acg	aca	aag	aat	ttc	ctg	gtt	tta	acg	ctc	ctt	1075	
Leu	Gln	Gly	Leu	Ala	Thr	Thr	Lys	Asn	Phe	Leu	Val	Leu	Thr	Leu	Leu		
310					315					320					325		
aat	aat	gtc	tcc	aca	gaa	atc	gtc	aca	gtg	ccg	ctc	aat	gat	ccg	aca	1123	
Asn	Asn	Val	Ser	Thr	Glu	Ile	Val	Thr	Val	Pro	Leu	Asn	Asp	Pro	Thr		
330					335					340							
acg	gag	cat	gaa	cac	att	gac	ctc	cca	gag	cat	gtc	acc	gcg	cat	gtg	1171	
Thr	Glu	His	Glu	His	Ile	Asp	Leu	Pro	Glu	His	Val	Thr	Ala	His	Val		
345					350					355							
gtt	gct	acc	tcc	ccg	ttg	gat	ggc	gat	gaa	att	tgg	gtg	cag	gca	gcg	1219	
Val	Ala	Thr	Ser	Pro	Leu	Asp	Gly	Asp	Glu	Ile	Trp	Val	Gln	Ala	Ala		
360					365					370							

agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala 375 380 385	1267
ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln 390 395 400 405	1315
gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro 410 415 420	1363
tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val 425 430 435	1411
cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro 440 445 450	1459
acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala 455 460 465	1507
aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala 470 475 480 485	1555
acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu 490 495 500	1603
gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile 505 510 515	1651
cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln 520 525 530	1699
tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp 535 540 545	1747
atg ttg cgc tat cac acc tgg tca gcg ggt gct tcg tgg atg gcg gag Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala Ser Trp Met Ala Glu 550 555 560 565	1795
tac ggc aac cct gac gat ccg gag gaa cgg gcg gtg att gag cag tac Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala Val Ile Glu Gln Tyr 570 575 580	1843
tcg ccg gtg cag gcg gtg gtg ggc gtc gag aag cga att tat cca ccc Ser Pro Val Gln Ala Val Val Gly Val Glu Lys Arg Ile Tyr Pro Pro 585 590 595	1891
gca ttg gtg acg acc tca acc cgg gac gac cgc gtc cac ccc gcg cac Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg Val His Pro Ala His 600 605 610	1939

gcg cgc ctt ttt gct caa gct ttg ctt gat gcg ggc cag gcc gtg gat 1987
 Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp
 615 620 625

tac tac gaa aac acc gag ggc ggc cat gcc ggc gcg gcg gat aac aag 2035
 Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys
 630 635 640 645

cag acc gcg ttt gtg gaa tgc ctg atc tac acc tgg atc gag aag act 2083
 Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr
 650 655 660

ttg gat cag cag ggt agc att taatacctat gattatgcga agg 2127
 Leu Asp Gln Gln Gly Ser Ile
 665

<210> 576

<211> 668

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu
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 20 25 30

Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
 35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
 50 55 60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65 70 75 80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
 85 90 95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
 100 105 110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
 115 120 125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
 130 135 140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
 145 150 155 160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
 165 170 175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
 180 185 190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
 195 200 205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
 210 215 220
 Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
 225 230 235 240
 Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
 245 250 255
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
 370 375 380
 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
 385 390 395 400
 Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
 405 410 415
 Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
 420 425 430
 Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
 435 440 445
 Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
 450 455 460
 Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
 465 470 475 480
 Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
 485 490 495
 His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
 500 505 510
 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
 515 520 525

Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln
 530 535 540
 Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala
 545 550 555 560
 Ser Trp Met Ala Glu Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala
 565 570 575
 Val Ile Glu Gln Tyr Ser Pro Val Gln Ala Val Val Gly Val Glu Lys
 580 585 590
 Arg Ile Tyr Pro Pro Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg
 595 600 605
 Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala
 610 615 620
 Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly
 625 630 635 640
 Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr
 645 650 655
 Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
 660 665

<210> 577
 <211> 215
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(192)
 <223> FRXA02047

<400> 577
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 ttg ctt gat gcg ggc cag gcc gtg gat tac tac gaa aac acc gag ggc 96
 Leu Leu Asp Ala Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly
 20 25 30
 ggc cat gcc ggc gcg gcg gat aac aag cag acc gcg ttt gtg gaa tcg 144
 Gly His Ala Gly Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser
 35 40 45
 ctg atc tac acc tgg atc gaa aag act ttg gat cag cag ggt agc att 192
 Leu Ile Tyr Thr Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
 50 55 60
 taatacctat gattatgcga agg 215

<210> 578
 <211> 64
 <212> PRT

<213> Corynebacterium glutamicum

<400> 578

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Trp Asp Asp Arg Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala
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Leu Leu Asp Ala Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly
          20           25           30

Gly His Ala Gly Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser
          35           40           45

Leu Ile Tyr Thr Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
 50           55           60

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<210> 579

<211> 477

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> RXA02174

<400> 579

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                               Met Glu Lys Pro Gln
                               1           5

att gag cta ccg gtc ggt cca gca ccg gaa gat ctc gta atc tct gac 163
Ile Glu Leu Pro Val Gly Pro Ala Pro Glu Asp Leu Val Ile Ser Asp
          10           15           20

atc atc gtt ggc gaa gga gca gaa gcc cgc cca ggt gga gaa gtt gag 211
Ile Ile Val Gly Glu Gly Ala Glu Ala Arg Pro Gly Gly Glu Val Glu
          25           30           35

gtc cac tat gtg ggc gtt gac ttt gaa acc ggc gag gag ttt gac tct 259
Val His Tyr Val Gly Val Asp Phe Glu Thr Gly Glu Glu Phe Asp Ser
          40           45           50

tcc tgg gat cgt gga cag acc agc cag ttc cca ctc aac ggc ctc att 307
Ser Trp Asp Arg Gly Gln Thr Ser Gln Phe Pro Leu Asn Gly Leu Ile
          55           60           65

gca ggt tgg caa gag gga att cca ggc atg aag gtc ggc gga cgt cgt 355
Ala Gly Trp Gln Glu Gly Ile Pro Gly Met Lys Val Gly Gly Arg Arg
          70           75           80           85

cag ctg acc att ccg cca gag gct gct tac ggc cct gag ggt tcc ggc 403
Gln Leu Thr Ile Pro Pro Glu Ala Ala Tyr Gly Pro Glu Gly Ser Gly
          90           95           100

cac cca ctg tct ggc cgt acc ctg gtg ttc atc atc gat ttg atc agc 451
His Pro Leu Ser Gly Arg Thr Leu Val Phe Ile Ile Asp Leu Ile Ser
          105           110           115

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Ala

477

<210> 580
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<212> PRT
<213> Corynebacterium glutamicum

<400> 580
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20 25 30
Gly Gly Glu Val Glu Val His Tyr Val Gly Val Asp Phe Glu Thr Gly
35 40 45
Glu Glu Phe Asp Ser Ser Trp Asp Arg Gly Gln Thr Ser Gln Phe Pro
50 55 60
Leu Asn Gly Leu Ile Ala Gly Trp Gln Glu Gly Ile Pro Gly Met Lys
65 70 75 80
Val Gly Gly Arg Arg Gln Leu Thr Ile Pro Pro Glu Ala Ala Tyr Gly
85 90 95
Pro Glu Gly Ser Gly His Pro Leu Ser Gly Arg Thr Leu Val Phe Ile
100 105 110
Ile Asp Leu Ile Ser Ala
115

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<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1447)
<223> RXA00568

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Val Lys Ser Ser Val
1 5
gag aag ctg agc gac acc cgt tca aag atc acc gtt gag gtt cca ttt 163
Glu Lys Leu Ser Asp Thr Arg Ser Lys Ile Thr Val Glu Val Pro Phe
10 15 20
tct gaa ctg aag cca gag atc gac cag gca tac gcc gct cta gcg cag 211
Ser Glu Leu Lys Pro Glu Ile Asp Gln Ala Tyr Ala Ala Leu Ala Gln
25 30 35

caa gtc cag atc cct ggt ttc cgt aag ggc aag gca ccg cgt cag ctt	259
Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys Ala Pro Arg Gln Leu	
40 45 50	
atc gac gca cgc ttc ggc cgt ggt gcg gtt ctg gag cag gtt gtc aac	307
Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu Glu Gln Val Val Asn	
55 60 65	
gac atg ctt cct aac cgc tac gca cag gca atc gaa gct gag ggc atc	355
Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile Glu Ala Glu Gly Ile	
70 75 80 85	
aag gca atc ggc cag cct aac gta gag gtc acc aag atc gaa gac aac	403
Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr Lys Ile Glu Asp Asn	
90 95 100	
gag ctc gtt gag ttc gtc gct gag gtt gac gtt cgc cca gag ttc gag	451
Glu Leu Val Glu Phe Val Ala Glu Val Asp Val Arg Pro Glu Phe Glu	
105 110 115	
ctt cct aag ttc gag gac atc act gtt gag gtc cca gct atc aag gct	499
Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val Pro Ala Ile Lys Ala	
120 125 130	
gac gaa gag gca atc gaa gca gag ctc gag acc ctg cgt gca cgt ttc	547
Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr Leu Arg Ala Arg Phe	
135 140 145	
tcc acc ttg aag gat cac aac cac aag ctg aag aag ggt gag ttc gtc	595
Ser Thr Leu Lys Asp His Asn His Lys Leu Lys Lys Gly Glu Phe Val	
150 155 160 165	
acc atc aac atc acc gca agc att gac ggt gag aag att gaa gag gca	643
Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu Lys Ile Glu Glu Ala	
170 175 180	
acc act gag ggt ctg tcc tac gaa atc gga tct gac gat ctg att gac	691
Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser Asp Asp Leu Ile Asp	
185 190 195	
ggc ctg gac aag gct ctg atc ggc gct aag aag gat gaa acc gta gag	739
Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys Asp Glu Thr Val Glu	
200 205 210	
ttc acc tct gag ctg gca aac ggc gag cac aag ggc aag gaa gct caa	787
Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys Gly Lys Glu Ala Gln	
215 220 225	
atc agc gtt gag atc acc gca acc aag cag cgc gag ctg cct gag ctg	835
Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg Glu Leu Pro Glu Leu	
230 235 240 245	
gat gat gag ttc gca cag ctg gct tct gag ttc gac acc atc gaa gag	883
Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe Asp Thr Ile Glu Glu	
250 255 260	
ctt cgt gag tcc acc gtg tct gac gtt gag gct aag cag aag aac gag	931
Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala Lys Gln Lys Asn Glu	
265 270 275	
cag gct gct gca atc cgc gac gaa gtt ctc gct gcg gct ctt ggc gag	979

Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala Ala Ala Leu Gly Glu
280 285 290

gct gac ttc gct ctg cca cag tcc atc gtt gac gag cag gca cac tcc 1027
Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp Glu Gln Ala His Ser
295 300 305

cag ctg cac cag ctg ctg ggc gag ctt gca cac gac gat gct gca ctg 1075
Gln Leu His Gln Leu Leu Gly Glu Leu Ala His Asp Asp Ala Ala Leu
310 315 320 325

aac tcc ctg ctt gag gct cag ggc acc act cgt gaa gag ttc gac aag 1123
Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg Glu Glu Phe Asp Lys
330 335 340

aag aac gtc gaa gat gct gag aag gct gtt cgc acc cag ctg ttc ctg 1171
Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg Thr Gln Leu Phe Leu
345 350 355

gac acc ctg tct gag gtt gag gag cct gag gtt tcc cag cag gag ctg 1219
Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val Ser Gln Gln Glu Leu
360 365 370

acc gac cac atc ctg ttc acc gca cag tct tac ggc atg gac cca aac 1267
Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr Gly Met Asp Pro Asn
375 380 385

cag ttc atc ggt cag ctg cag cag tcc ggc cag atc gcg aac ctg ttc 1315
Gln Phe Ile Gly Gln Leu Gln Gln Ser Gly Gln Ile Ala Asn Leu Phe
390 395 400 405

tcc gac gtt cgc cgt ggc aag gct ctt gca cag gct atc tgc cgc gta 1363
Ser Asp Val Arg Arg Gly Lys Ala Leu Ala Gln Ala Ile Cys Arg Val
410 415 420

aac gtg aag gac tcc gag ggt aac gag atc gac cct aag gaa tac ttc 1411
Asn Val Lys Asp Ser Glu Gly Asn Glu Ile Asp Pro Lys Glu Tyr Phe
425 430 435

ggt gaa gaa gaa gta gct gag act gag tct gaa gct taaaaacttt 1457
Gly Glu Glu Glu Val Ala Glu Thr Glu Ser Glu Ala
440 445

aaagaaataa cgc 1470

<210> 582

<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

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20 25 30

Ala Ala Leu Ala Gln Gln Val Gln Ile Pro Gly Phe Arg Lys Gly Lys
35 40 45

Ala Pro Arg Gln Leu Ile Asp Ala Arg Phe Gly Arg Gly Ala Val Leu
 50 55 60
 Glu Gln Val Val Asn Asp Met Leu Pro Asn Arg Tyr Ala Gln Ala Ile
 65 70 75 80
 Glu Ala Glu Gly Ile Lys Ala Ile Gly Gln Pro Asn Val Glu Val Thr
 85 90 95
 Lys Ile Glu Asp Asn Glu Leu Val Glu Phe Val Ala Glu Val Asp Val
 100 105 110
 Arg Pro Glu Phe Glu Leu Pro Lys Phe Glu Asp Ile Thr Val Glu Val
 115 120 125
 Pro Ala Ile Lys Ala Asp Glu Glu Ala Ile Glu Ala Glu Leu Glu Thr
 130 135 140
 Leu Arg Ala Arg Phe Ser Thr Leu Lys Asp His Asn His Lys Leu Lys
 145 150 155 160
 Lys Gly Glu Phe Val Thr Ile Asn Ile Thr Ala Ser Ile Asp Gly Glu
 165 170 175
 Lys Ile Glu Glu Ala Thr Thr Glu Gly Leu Ser Tyr Glu Ile Gly Ser
 180 185 190
 Asp Asp Leu Ile Asp Gly Leu Asp Lys Ala Leu Ile Gly Ala Lys Lys
 195 200 205
 Asp Glu Thr Val Glu Phe Thr Ser Glu Leu Ala Asn Gly Glu His Lys
 210 215 220
 Gly Lys Glu Ala Gln Ile Ser Val Glu Ile Thr Ala Thr Lys Gln Arg
 225 230 235 240
 Glu Leu Pro Glu Leu Asp Asp Glu Phe Ala Gln Leu Ala Ser Glu Phe
 245 250 255
 Asp Thr Ile Glu Glu Leu Arg Glu Ser Thr Val Ser Asp Val Glu Ala
 260 265 270
 Lys Gln Lys Asn Glu Gln Ala Ala Ala Ile Arg Asp Glu Val Leu Ala
 275 280 285
 Ala Ala Leu Gly Glu Ala Asp Phe Ala Leu Pro Gln Ser Ile Val Asp
 290 295 300
 Glu Gln Ala His Ser Gln Leu His Gln Leu Leu Gly Glu Leu Ala His
 305 310 315 320
 Asp Asp Ala Ala Leu Asn Ser Leu Leu Glu Ala Gln Gly Thr Thr Arg
 325 330 335
 Glu Glu Phe Asp Lys Lys Asn Val Glu Asp Ala Glu Lys Ala Val Arg
 340 345 350
 Thr Gln Leu Phe Leu Asp Thr Leu Ser Glu Val Glu Glu Pro Glu Val
 355 360 365
 Ser Gln Gln Glu Leu Thr Asp His Ile Leu Phe Thr Ala Gln Ser Tyr

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<211> 432
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(409)
<223> RXN03040

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Met Ser Xaa Gly Asp																	
1 5																	
aac gca ccg att gat gag gat gcg ttc aaa aac cgc gtc ttg gtt ggg																	163
Asn Ala Pro Ile Asp Glu Asp Ala Phe Lys Asn Arg Val Leu Val Gly																	
10 15 20																	
ttt gaa atc gaa gct atg tcc aac acc tgc acc cat aac ctc aag gct																	211
Phe Glu Ile Glu Ala Met Ser Asn Thr Cys Thr His Asn Leu Lys Ala																	
25 30 35																	
gcg acc gat caa atg ggc atc gac aac atc aac tac gat ttc cga cca																	259
Ala Thr Asp Gln Met Gly Ile Asp Asn Ile Asn Tyr Asp Phe Arg Pro																	
40 45 50																	
acc gga acc cac gcc tgg gat tac tgg aac gaa gcg ctc cac cgc ttc																	307
Thr Gly Thr His Ala Trp Asp Tyr Trp Asn Glu Ala Leu His Arg Phe																	
55 60 65																	
ttc ccg ttg atg atg cag ggc ttc ggc ctc gac ggt ggt ccc atc ccg																	355
Phe Pro Leu Met Met Gln Gly Phe Gly Leu Asp Gly Gly Pro Ile Pro																	
70 75 80 85																	

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ggaactcccg ctgcctaagc gggacatagt tgcaggggac atg cgt tca gat gtt 115
                                         Met Arg Ser Asp Val
                                         1                               5

atc gag tta ccg gag ggg gta agc aag gag aaa gct gac cag cta gaa 163
Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys Ala Asp Gln Leu Glu
                        10                        15                        20

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gtt gcg gaa gcg cga ctt aac gag ggt gca cga ctg atg gca acc acc	211
Val Ala Glu Ala Arg Leu Asn Glu Gly Ala Arg Leu Met Ala Thr Thr	
25 30 35	
ggg tgt gag gtt atg tgg cca acg ggc ttc tca gtt tgt ggc cga att	259
Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser Val Cys Gly Arg Ile	
40 45 50	
ctt gac acc tat cgc cag gtt gga ggt cag ttg tca tgg ctt ggg cca	307
Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu Ser Trp Leu Gly Pro	
55 60 65	
ccg aag tca aac gag ttg acc aat ccc gac ggt gtt ggc aaa aga agt	355
Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly Val Gly Lys Arg Ser	
70 75 80 85	
gaa ttt ttt ggt gga gcc atc tat tgg cac cca gac aca ggc gct tat	403
Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro Asp Thr Gly Ala Tyr	
90 95 100	
gca gtg acc ttg gac ggt ttg cga cag tgg ggg acc ttg aac tgg gaa	451
Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly Thr Leu Asn Trp Glu	
105 110 115	
tca ggg cca ttg ggg tac cca acc tct ggt ccg atg gat aca aac tat	499
Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro Met Asp Thr Asn Tyr	
120 125 130	
ccc ctt act cag cga cag act ttt caa ggt ggt gac aac tac tac aac	547
Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly Asp Asn Tyr Tyr Asn	
135 140 145	
cca ttg act ggc ggt gct gtg tgg ggc gat att aaa cag cgc tac gaa	595
Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile Lys Gln Arg Tyr Glu	
150 155 160 165	
gaa ctt ggc ggc tcg aat cat gcc att ggc atc ccg atc act aat gag	643
Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile Pro Ile Thr Asn Glu	
170 175 180	
cta cct agc ggt act gag tat ttt tac aat aat ttc tcc aat gga aca	691
Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn Phe Ser Asn Gly Thr	
185 190 195	
att tcg tgg cga aat gat cgt cag aca cgg ttt atg tat ttg gct acg	739
Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe Met Tyr Leu Ala Thr	
200 205 210	
cag cgg gtg tgg gat gcg ttg ggt cgg gag acg ggt cgt tta ggt ttt	787
Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr Gly Arg Leu Gly Phe	
215 220 225	
cct gaa gca gat gaa aca cct gag gtt tct ggt cta ttc cat gtg gcg	835
Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly Leu Phe His Val Ala	
230 235 240 245	

<210> 586

<211> 245

<212> PRT

<213> Corynebacterium glutamicum

<400> 586

Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly Val Ser Lys Glu Lys
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 20 25 30

Leu Met Ala Thr Thr Gly Cys Glu Val Met Trp Pro Thr Gly Phe Ser
 35 40 45

Val Cys Gly Arg Ile Leu Asp Thr Tyr Arg Gln Val Gly Gly Gln Leu
 50 55 60

Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu Thr Asn Pro Asp Gly
 65 70 75 80

Val Gly Lys Arg Ser Glu Phe Phe Gly Gly Ala Ile Tyr Trp His Pro
 85 90 95

Asp Thr Gly Ala Tyr Ala Val Thr Leu Asp Gly Leu Arg Gln Trp Gly
 100 105 110

Thr Leu Asn Trp Glu Ser Gly Pro Leu Gly Tyr Pro Thr Ser Gly Pro
 115 120 125

Met Asp Thr Asn Tyr Pro Leu Thr Gln Arg Gln Thr Phe Gln Gly Gly
 130 135 140

Asp Asn Tyr Tyr Asn Pro Leu Thr Gly Gly Ala Val Trp Gly Asp Ile
 145 150 155 160

Lys Gln Arg Tyr Glu Glu Leu Gly Gly Ser Asn His Ala Ile Gly Ile
 165 170 175

Pro Ile Thr Asn Glu Leu Pro Ser Gly Thr Glu Tyr Phe Tyr Asn Asn
 180 185 190

Phe Ser Asn Gly Thr Ile Ser Trp Arg Asn Asp Arg Gln Thr Arg Phe
 195 200 205

Met Tyr Leu Ala Thr Gln Arg Val Trp Asp Ala Leu Gly Arg Glu Thr
 210 215 220

Gly Arg Leu Gly Phe Pro Glu Ala Asp Glu Thr Pro Glu Val Ser Gly
 225 230 235 240

Leu Phe His Val Ala
 245

<210> 587

<211> 456

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(433)

<223> RXN02949

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Val Ser Asp Glu Gln
1 5

aat tct ggc gta ggc gga acg tct cgc cca acg ggt aaa cgc cag ctg 163
Asn Ser Gly Val Gly Gly Thr Ser Arg Pro Thr Gly Lys Arg Gln Leu
10 15 20

tcg ggt gct tcc act acc tct acc tct tct tat gag gct aag cag gta 211
Ser Gly Ala Ser Thr Thr Ser Thr Ser Ser Tyr Glu Ala Lys Gln Val
25 30 35

tct aca cag aag aag tca tcc ggt tcg gat tct aag cct ggc ggc ggt 259
Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser Lys Pro Gly Gly Gly
40 45 50

gtt att tct ttt ctg cct gag gtt gtg gga gaa gtc cgt aag gtt att 307
Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu Val Arg Lys Val Ile
55 60 65

tgg cct act gcg cgc cag atg gtc acg tac acc ctt gtc gtt ttg gga 355
Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr Leu Val Val Leu Gly
70 75 80 85

ttc ttg att gtt ttg acc gct ttg gtg tct ggt gtg gat ttc cta gct 403
Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly Val Asp Phe Leu Ala
90 95 100

ggt ctt gga gtt gag aag att ctg act ccg taggtaggat gtgtaacatc ttt 456
Gly Leu Gly Val Glu Lys Ile Leu Thr Pro
105 110

<210> 588

<211> 111

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

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20 25 30

Glu Ala Lys Gln Val Ser Thr Gln Lys Lys Ser Ser Gly Ser Asp Ser
35 40 45

Lys Pro Gly Gly Gly Val Ile Ser Phe Leu Pro Glu Val Val Gly Glu
50 55 60

Val Arg Lys Val Ile Trp Pro Thr Ala Arg Gln Met Val Thr Tyr Thr
65 70 75 80

Leu Val Val Leu Gly Phe Leu Ile Val Leu Thr Ala Leu Val Ser Gly
85 90 95

Val Asp Phe Leu Ala Gly Leu Gly Val Glu Lys Ile Leu Thr Pro

100

105

110

<210> 589

<211> 618

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(595)

<223> RXN00833

<400> 589

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tttctagcac caaaacaaaa ctctccctag tatgggggtcc atg gct aaa aca cat 115
 Met Ala Lys Thr His
 1 5

ttt caa ggc aac gaa act gct acc tcc ggc gaa ctg cca cag gtc ggc 163
 Phe Gln Gly Asn Glu Thr Ala Thr Ser Gly Glu Leu Pro Gln Val Gly
 10 15 20

gac aac ctc gca gag ttc aac ctc gtc aac acc gaa ctg ggc gag gtc 211
 Asp Asn Leu Ala Glu Phe Asn Leu Val Asn Thr Glu Leu Gly Glu Val
 25 30 35

tcc tca aag gac ttc cag ggc cgc aag ctt gtc ctg aac atc ttc cca 259
 Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val Leu Asn Ile Phe Pro
 40 45 50

tcc gtt gac acc ggc gtt tgt gca aca tca gtc cgc aag ttc aac gag 307
 Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val Arg Lys Phe Asn Glu
 55 60 65

gca gca gca agc ctg gaa aac acc acc gtg ctg tgc atc tcc aag gat 355
 Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu Cys Ile Ser Lys Asp
 70 75 80 85

ctt cca ttc gca ctg ggc cgt ttc tgc tcc gca gaa ggc atc gag aac 403
 Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala Glu Gly Ile Glu Asn
 90 95 100

gtc acc cca gta tcc gca ttc cgt tcc acc ttc ggt gaa gac aac ggc 451
 Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe Gly Glu Asp Asn Gly
 105 110 115

atc gtg ctc gaa ggc tca cca ctt aag ggt ctt ctt gca cgc agc gtc 499
 Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu Leu Ala Arg Ser Val
 120 125 130

atc gtc gtc gat gaa aac ggc aag gtt gct tac acc cag ttg gtt gat 547
 Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr Thr Gln Leu Val Asp
 135 140 145

gag atc ttc act gaa cct gat tac gac gct gca ctt gct ggg ctg aac 595
 Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala Leu Ala Gly Leu Asn
 150 155 160 165

taattttactt cgctcagggg aat 618

<210> 590
 <211> 165
 <212> PRT
 <213> Corynebacterium glutamicum

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 Glu Leu Gly Glu Val Ser Ser Lys Asp Phe Gln Gly Arg Lys Leu Val
 35 40 45
 Leu Asn Ile Phe Pro Ser Val Asp Thr Gly Val Cys Ala Thr Ser Val
 50 55 60
 Arg Lys Phe Asn Glu Ala Ala Ala Ser Leu Glu Asn Thr Thr Val Leu
 65 70 75 80
 Cys Ile Ser Lys Asp Leu Pro Phe Ala Leu Gly Arg Phe Cys Ser Ala
 85 90 95
 Glu Gly Ile Glu Asn Val Thr Pro Val Ser Ala Phe Arg Ser Thr Phe
 100 105 110
 Gly Glu Asp Asn Gly Ile Val Leu Glu Gly Ser Pro Leu Lys Gly Leu
 115 120 125
 Leu Ala Arg Ser Val Ile Val Val Asp Glu Asn Gly Lys Val Ala Tyr
 130 135 140
 Thr Gln Leu Val Asp Glu Ile Phe Thr Glu Pro Asp Tyr Asp Ala Ala
 145 150 155 160
 Leu Ala Gly Leu Asn
 165

<210> 591
 <211> 879
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(856)
 <223> RXN01676

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 Met Ile Leu His Gly
 1 5
 gtt gtg ttc tac gca gga ctt cta gta ctt ctc gtg cca ctt ggc ctt 163
 Val Val Phe Tyr Ala Gly Leu Leu Val Leu Leu Val Pro Leu Gly Leu

				10				15				20							
ggt	gcg	gga	atc	ctc	ggc	gag	ctg	ttt	atc	acc	caa	cgc	cag	acc	atc	211			
Gly	Ala	Gly	Ile	Leu	Gly	Glu	Leu	Phe	Ile	Thr	Gln	Arg	Gln	Thr	Ile				
25								30				35							
atc	gtg	gtt	tca	tcg	atc	gtg	ctg	att	atc	cta	ggt	ttt	gtc	cag	atc	259			
Ile	Val	Val	Ser	Ser	Ile	Val	Leu	Ile	Ile	Leu	Gly	Phe	Val	Gln	Ile				
40								45				50							
ttc	ggc	ggc	gga	ttc	gac	ttc	gga	aaa	gca	ctc	cca	gga	tta	gat	cgt	307			
Phe	Gly	Gly	Gly	Phe	Asp	Phe	Gly	Lys	Ala	Leu	Pro	Gly	Leu	Asp	Arg				
55								60				65							
ctg	caa	tct	aag	gcc	act	gtg	acc	tca	ggt	cta	gga	aag	agc	ttt	tta	355			
Leu	Gln	Ser	Lys	Ala	Thr	Val	Thr	Ser	Gly	Leu	Gly	Lys	Ser	Phe	Leu				
70								75				80				85			
cta	gga	atg	acc	agt	agt	att	gcc	ggt	ttt	tgt	tcc	gga	cca	atc	ctc	403			
Leu	Gly	Met	Thr	Ser	Ser	Ile	Ala	Gly	Phe	Cys	Ser	Gly	Pro	Ile	Leu				
90								95				100							
ggc	gcc	gtt	ctt	act	ttg	gct	gcc	acc	agt	gga	aac	tcc	atc	acc	tca	451			
Gly	Ala	Val	Leu	Thr	Leu	Ala	Ala	Thr	Ser	Gly	Asn	Ser	Ile	Thr	Ser				
105								110				115							
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Ser	Val	Ile	Ser	Gly	Ala	Leu	Ile	Ile	Ala	Val	Gly	Ile	Leu	Phe	Trp				
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Ser	Thr	Asn	Gly	Leu	Val	Ser	Met	Pro	Glu	Leu	Val	Pro	Met	Asp	Thr				
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cag	atc	tgg	cta	cag	gaa	gcc	aca	ttc	tca	ctc	ggg	tca	cca	ctc	ttt	739			
Gln	Ile	Trp	Leu	Gln	Glu	Ala	Thr	Phe	Ser	Leu	Gly	Ser	Pro	Leu	Phe				
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<211> 252

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 592

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Gln Arg Gln Thr Ile Ile Val Val Ser Ser Ile Val Leu Ile Ile Leu
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Gly Phe Val Gln Ile Phe Gly Gly Gly Phe Asp Phe Gly Lys Ala Leu
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Pro Gly Leu Asp Arg Leu Gln Ser Lys Ala Thr Val Thr Ser Gly Leu
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Gly Lys Ser Phe Leu Leu Gly Met Thr Ser Ser Ile Ala Gly Phe Cys
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Ser Gly Pro Ile Leu Gly Ala Val Leu Thr Leu Ala Ala Thr Ser Gly
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Asn Ser Ile Thr Ser Ala Leu Ile Leu Ser Ala Tyr Gly Ala Gly Met
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Val Leu Pro Leu Met Ala Ile Ala Ala Leu Trp Ala Lys Leu Gly Gln
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Arg Gly Gln Gln Met Leu Arg Gly Arg Glu Phe Thr Phe Leu Gly Arg
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Gln Trp His Ile Val Ser Val Ile Ser Gly Ala Leu Ile Ile Ala Val
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Gly Ile Leu Phe Trp Ser Thr Asn Gly Leu Val Ser Met Pro Glu Leu
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Val Pro Met Asp Thr Gln Ile Trp Leu Gln Glu Ala Thr Phe Ser Leu
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Gly Ser Pro Leu Phe Asp Ile Ala Leu Ile Ile Val Ala Ala Gly Leu
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Val Arg Leu Thr Lys
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cta gca gca aca atc ggc tgc gtg aca ctc agc gga ctt gcg cta gta 163
Leu Ala Ala Thr Ile Gly Cys Val Thr Leu Ser Gly Leu Ala Leu Val
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Ala Cys Ser Ser Asp Ser Thr Ala Gly Thr Asp Ala Val Ala Val Gly
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gga acc ttc caa ttc cac tcc ccg gat gga aag atg gaa att ttc tac 259
Gly Thr Phe Gln Phe His Ser Pro Asp Gly Lys Met Glu Ile Phe Tyr
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90 95 100

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Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu Gln Ala Ala Gly Asn
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Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile Asn Val Arg Asp Tyr
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tcc cgc gac atc gcc caa gac ttt gtc acc gac aac ggc ctt gat tac 547
Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp Asn Gly Leu Asp Tyr
135 140 145

cca agc att tac gat cca cca ttt atg aca gca gca tcc ctc ggt ggt 595
Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala Ala Ser Leu Gly Gly
150 155 160 165

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Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val Leu Asp Lys Gln His
170 175 180

cgc ccc gca gca gtg ttc ttg cgc gaa gtc acc tcc aaa gat gtg ttg 691
Arg Pro Ala Ala Val Phe Leu Arg Glu Val Thr Ser Lys Asp Val Leu
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 <213> Corynebacterium glutamicum

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 35 40 45
 Met Glu Ile Phe Tyr Asp Glu Ala Asp Arg Gln Gln Leu Pro Asp Ile
 50 55 60
 Gly Gly Asp Ser Leu Met Glu Glu Gly Thr Gln Ile Asn Leu Ser Asp
 65 70 75 80
 Phe Glu Asn Gln Val Val Ile Leu Asn Ala Trp Gly Gln Trp Cys Ala
 85 90 95
 Pro Cys Arg Ser Glu Ser Asp Asp Leu Gln Ile Ile His Glu Glu Leu
 100 105 110
 Gln Ala Ala Gly Asn Gly Asp Thr Pro Gly Gly Thr Val Leu Gly Ile
 115 120 125
 Asn Val Arg Asp Tyr Ser Arg Asp Ile Ala Gln Asp Phe Val Thr Asp
 130 135 140
 Asn Gly Leu Asp Tyr Pro Ser Ile Tyr Asp Pro Pro Phe Met Thr Ala
 145 150 155 160
 Ala Ser Leu Gly Gly Val Pro Ala Ser Val Ile Pro Thr Thr Ile Val
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Glu Asp Pro Ile Glu Lys Ser Arg Arg Asp Pro Asp Asp Val Asn Lys

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Ala Leu Ala Ala Ala Asp Met Tyr Val Leu Met Asn Gln Pro Asp Thr			
230	235	240	245
gcg ctc gcg cac ctt gca gca cta ttg cca aaa ccg gag gct gcc cgg			883
Ala Leu Ala His Leu Ala Ala Leu Leu Pro Lys Pro Glu Ala Ala Arg			
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Arg Ile Val Glu Leu Leu Asn Leu Phe Asp Pro Leu Asp Leu Val Ala			
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<400> 596

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Pro His Glu Gly Lys Val Ala Asn Ile Thr Lys Val Thr Ser Ser Asn			
	35	40	45
Met Glu His Thr Ile Thr Gln Ala Ser Lys Ala Lys Glu Val Val Val			
	50	55	60
Leu Ile Gly His Ser Leu Leu Pro Thr Phe Gln Asp Leu Glu Lys Asp			
	65	70	80
Ile Leu His Phe Gln Ala Gly Asn Lys Gly Arg Phe Ser Val Ala Ile			
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Val Asp Pro Asp Arg Ser Ala Asp Val Val Ala Arg Phe Arg Pro Lys			
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Gln Ile Pro Val Ala Tyr Val Val Lys Asp Gly Ala Ser Ile Ala Glu			
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Phe Asn Ser Leu Asn Lys Glu Pro Val Ala Gln Trp Leu Asp His Phe			
	130	135	140
Val Ser Arg Glu Thr Ile Pro Asn Glu Lys Glu Gly Asp Val Asp Lys			
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Gln Ile Asp Pro Arg Leu Trp Arg Ala Ala Glu Leu Val Asn Ala Gly			
	165	170	175
Asp Phe Arg Ala Ala Leu Ala Leu Tyr Glu Gln Leu Pro Gln Asp Ala			

180					185					190						
Thr	Val	Lys	Arg	Ala	His	Ala	Ala	Val	Ser	Val	Leu	Ala	Arg	Met	Ser	
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Asn	Gln	Pro	Asp	Thr	Ala	Leu	Ala	His	Leu	Ala	Ala	Leu	Leu	Pro	Lys	
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Pro	Glu	Ala	Ala	Arg	Arg	Ile	Val	Glu	Leu	Leu	Asn	Leu	Phe	Asp	Pro	
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Ser																

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 Met Ala Lys Leu Ile 5
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 gct ttt gac cag gac gcc cgc gaa ggc att ctc cgg ggc gtt gac gct 163
 Ala Phe Asp Gln Asp Ala Arg Glu Gly Ile Leu Arg Gly Val Asp Ala 20
 10 15
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 Leu Ala Asn Ala Val Lys Val Thr Leu Gly Pro Arg Gly Arg Asn Val 35
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 Val Leu Asp Lys Ala Phe Gly Gly Pro Leu Val Thr Asn Asp Gly Val 50
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 Thr Ile Ala Arg Asp Ile Asp Leu Glu Asp Pro Phe Glu Asn Leu Gly 65
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 Ala Gln Leu Val Lys Ser Val Ala Val Lys Thr Asn Asp Ile Ala Gly 85
 70 75 80

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Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro Met Glu Leu Asn Lys	
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Ala Thr Glu Val Ser Asp Thr Lys Glu Ile Ala Asn Val Ala Thr Val	
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Lys Val Gly Lys Asp Gly Val Val Thr Val Glu Glu Ser Gln Ser Ile	
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Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser Phe Asp Lys Gly Tyr	
185 190 195	
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Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro Leu Gln Thr Leu Val	
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Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val Ala Val Lys Ser Pro	
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Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp Asp Leu Ala Ile Val	
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Thr Lys Ala Thr Val Val Asp Pro Glu Val Gly Ile Asn Leu Asn Glu	
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Ala Gly Glu Glu Val Phe Gly Thr Ala Arg Arg Ile Thr Val Ser Lys	
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 Ala Leu Ile Ala Glu Gly Leu Arg Asn Val Ala Ala Gly Ala Asn Pro
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 Glu Ser Gln Ser Ile Glu Thr Ala Leu Glu Val Thr Glu Gly Ile Ser
 180 185 190
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 195 200 205
 Gln Gln Ala Val Leu Asp Asn Pro Ala Val Leu Leu Val Arg Asn Lys
 210 215 220
 Ile Ser Ser Leu Pro Asp Phe Leu Pro Leu Leu Glu Lys Val Val Glu
 225 230 235 240
 Ser Asn Arg Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly Glu Pro
 245 250 255
 Leu Gln Thr Leu Val Val Asn Ser Ile Arg Lys Thr Ile Lys Val Val
 260 265 270
 Ala Val Lys Ser Pro Tyr Phe Gly Asp Arg Arg Lys Ala Phe Met Asp
 275 280 285
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 305 310 315 320

Ile Thr Val Ser Lys Asp Glu Thr Ile Ile Val Asp Gly Ala Gly Ser
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 Ala Glu Asp Val Glu Ala Arg Arg Gly Gln Ile Arg Arg Glu Ile Ala
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 Lys Leu Ser Gly Gly Ile Ala Val Ile Arg Val Gly Ala Ala Thr Glu
 370 375 380
 Thr Glu Val Asn Asp Arg Lys Leu Arg Val Glu Asp Ala Ile Asn Ala
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 Pro Ala Tyr Trp Ile Ala Ser Asn Ala Gly Leu Asp Gly Ser Val Val
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 Val Ala Arg Thr Ala Ala Leu Pro Asn Gly Glu Gly Phe Asn Ala Ala
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 Thr Leu Glu Tyr Gly Asn Leu Ile Asn Asp Gly Val Ile Asp Pro Val
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 Met Gly Arg Ala Val
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Gly	Glu	Pro	Val	Val	Ile	Ala	Asn	Ala	Glu	Gly	Ser	Arg	Thr	Thr	Pro	
			25					30					35			
tcc	gtc	gtt	gca	ttc	gca	aag	aac	ggg	gaa	gtt	cta	gtc	ggc	cag	tcc	259
Ser	Val	Val	Ala	Phe	Ala	Lys	Asn	Gly	Glu	Val	Leu	Val	Gly	Gln	Ser	
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gct	aag	aac	cag	gcg	gtc	acc	aac	gtt	gac	cgc	acc	att	cgc	tcc	gtc	307
Ala	Lys	Asn	Gln	Ala	Val	Thr	Asn	Val	Asp	Arg	Thr	Ile	Arg	Ser	Val	
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aag	cgc	cac	atc	ggc	acc	gac	tgg	tcc	gtt	gct	atc	gat	gac	aag	aac	355
Lys	Arg	His	Ile	Gly	Thr	Asp	Trp	Ser	Val	Ala	Ile	Asp	Asp	Lys	Asn	
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Tyr	Thr	Ser	Gln	Glu	Ile	Ser	Ala	Arg	Thr	Leu	Met	Lys	Leu	Lys	Arg	
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gac	gct	gaa	gca	tac	ctg	ggc	gag	gac	gtc	act	gat	gct	gtt	att	acc	451
Asp	Ala	Glu	Ala	Tyr	Leu	Gly	Glu	Asp	Val	Thr	Asp	Ala	Val	Ile	Thr	
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Val	Pro	Ala	Tyr	Phe	Glu	Asp	Ser	Gln	Arg	Gln	Ala	Thr	Lys	Glu	Ala	
		120					125					130				
ggg	cag	atc	gca	ggc	ctt	aac	gtt	ctg	cgt	att	gtt	aac	gag	cca	acc	547
Gly	Gln	Ile	Ala	Gly	Leu	Asn	Val	Leu	Arg	Ile	Val	Asn	Glu	Pro	Thr	
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gcg	gct	gca	ctt	gca	tac	ggc	ctt	gag	aag	ggc	gag	cag	gag	cag	acc	595
Ala	Ala	Ala	Leu	Ala	Tyr	Gly	Leu	Glu	Lys	Gly	Glu	Gln	Glu	Gln	Thr	
	150				155					160					165	
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Ile	Leu	Val	Phe	Asp	Leu	Gly	Gly	Gly	Thr	Phe	Asp	Val	Ser	Leu	Leu	
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gag	atc	ggc	gac	ggg	gtt	gtt	gag	gtt	cgc	gca	acc	tcc	ggc	gat	aac	691
Glu	Ile	Gly	Asp	Gly	Val	Val	Glu	Val	Arg	Ala	Thr	Ser	Gly	Asp	Asn	
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gag	ctc	ggg	ggc	gac	gac	tgg	gat	cag	cgt	atc	gtt	gac	tgg	ctg	gta	739
Glu	Leu	Gly	Gly	Asp	Asp	Trp	Asp	Gln	Arg	Ile	Val	Asp	Trp	Leu	Val	
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Glu	Lys	Phe	Gln	Ser	Ser	Asn	Gly	Ile	Asp	Leu	Thr	Lys	Asp	Lys	Met	
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gcc	ctg	cag	cgt	ctg	cgt	gag	gca	gct	gag	aag	gca	aag	atc	gag	ctg	835
Ala	Leu	Gln	Arg	Leu	Arg	Glu	Ala	Ala	Glu	Lys	Ala	Lys	Ile	Glu	Leu	
	230				235					240					245	
tcc	tct	tcc	cag	agt	gca	aac	atc	aac	ctt	cct	tac	atc	acc	gtt	gat	883
Ser	Ser	Ser	Gln	Ser	Ala	Asn	Ile	Asn	Leu	Pro	Tyr	Ile	Thr	Val	Asp	

250										255					260					
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ttc	cag	cgc	atc	acc	cag	gac	ctc	ctg	gcc	cgc	acc	aag	act	cct	ttc	979				
Phe	Gln	Arg	Ile	Thr	Gln	Asp	Leu	Leu	Ala	Arg	Thr	Lys	Thr	Pro	Phe					
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aac	cag	gtt	gtt	aag	gac	gct	ggc	gtg	tcc	gtc	tcg	gag	atc	gac	cac	1027				
Asn	Gln	Val	Val	Lys	Asp	Ala	Gly	Val	Ser	Val	Ser	Glu	Ile	Asp	His					
		295				300					305									
gtt	gtt	ctc	gtc	ggc	ggc	tcc	acc	cgt	atg	cct	gct	gtt	acc	gaa	ctg	1075				
Val	Val	Leu	Val	Gly	Gly	Ser	Thr	Arg	Met	Pro	Ala	Val	Thr	Glu	Leu					
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gat	gag	gtt	gtt	gca	gtt	ggc	gca	gca	ctt	cag	gcc	ggc	gtt	ctc	cgc	1171				
Asp	Glu	Val	Val	Ala	Val	Gly	Ala	Ala	Leu	Gln	Ala	Gly	Val	Leu	Arg					
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Asn	Gln	Pro	Ser	Val	Gln	Ile	Gln	Val	Phe	Gln	Gly	Glu	Arg	Glu	Ile					
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Pro	Ala	Pro	Arg	Gly	Val	Pro	Gln	Ile	Glu	Val	Thr	Phe	Asp	Ile	Asp					
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gcc	aac	ggc	atc	gtc	cac	gtc	acc	gca	aag	gac	aag	ggc	act	ggc	aag	1507				
Ala	Asn	Gly	Ile	Val	His	Val	Thr	Ala	Lys	Asp	Lys	Gly	Thr	Gly	Lys					
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gaa	aac	acc	atc	acc	att	cag	gac	ggc	tcc	ggc	ctc	tcc	cag	gat	gaa	1555				
Glu	Asn	Thr	Ile	Thr	Ile	Gln	Asp	Gly	Ser	Gly	Leu	Ser	Gln	Asp	Glu					
470					475				480						485					
att	gat	cgc	atg	atc	aag	gat	gct	gaa	gct	cac	gct	gat	gag	gac	aag	1603				
Ile	Asp	Arg	Met	Ile	Lys	Asp	Ala	Glu	Ala	His	Ala	Asp	Glu	Asp	Lys					
				490				495						500						

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Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn Ala Glu Ser Leu Val
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tac cag acc cgc aag ttc gtt gaa gag aac tcc gag aag gtc tcc gaa 1699
Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser Glu Lys Val Ser Glu
520 525 530

gac ctc aag gca aag gtc gaa gag gca gcc aag ggc gtt gaa gaa gca 1747
Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys Gly Val Glu Glu Ala
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ctc aag ggc gag gac ctc gag gca atc aag gct gca gtt gag aag ctg 1795
Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala Ala Val Glu Lys Leu
550 555 560 565

aac acc gag tcc cag gaa atg ggt aag gct atc tac gag gct gac gct 1843
Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile Tyr Glu Ala Asp Ala
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gct gct ggt gca acc cag gct gac gca ggt gca gaa ggc gct gca gat 1891
Ala Ala Gly Ala Thr Gln Ala Asp Ala Gly Ala Glu Gly Ala Ala Asp
585 590 595

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Gly Glu Asp Lys Lys
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<212> PRT

<213> Corynebacterium glutamicum

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35 40 45

Leu Val Gly Gln Ser Ala Lys Asn Gln Ala Val Thr Asn Val Asp Arg
50 55 60

Thr Ile Arg Ser Val Lys Arg His Ile Gly Thr Asp Trp Ser Val Ala
65 70 75 80

Ile Asp Asp Lys Asn Tyr Thr Ser Gln Glu Ile Ser Ala Arg Thr Leu
85 90 95

Met Lys Leu Lys Arg Asp Ala Glu Ala Tyr Leu Gly Glu Asp Val Thr
100 105 110

Asp Ala Val Ile Thr Val Pro Ala Tyr Phe Glu Asp Ser Gln Arg Gln
 115 120 125
 Ala Thr Lys Glu Ala Gly Gln Ile Ala Gly Leu Asn Val Leu Arg Ile
 130 135 140
 Val Asn Glu Pro Thr Ala Ala Ala Leu Ala Tyr Gly Leu Glu Lys Gly
 145 150 155 160
 Glu Gln Glu Gln Thr Ile Leu Val Phe Asp Leu Gly Gly Gly Thr Phe
 165 170 175
 Asp Val Ser Leu Leu Glu Ile Gly Asp Gly Val Val Glu Val Arg Ala
 180 185 190
 Thr Ser Gly Asp Asn Glu Leu Gly Gly Asp Asp Trp Asp Gln Arg Ile
 195 200 205
 Val Asp Trp Leu Val Glu Lys Phe Gln Ser Ser Asn Gly Ile Asp Leu
 210 215 220
 Thr Lys Asp Lys Met Ala Leu Gln Arg Leu Arg Glu Ala Ala Glu Lys
 225 230 235 240
 Ala Lys Ile Glu Leu Ser Ser Ser Gln Ser Ala Asn Ile Asn Leu Pro
 245 250 255
 Tyr Ile Thr Val Asp Ala Asp Lys Asn Pro Leu Phe Leu Asp Glu Thr
 260 265 270
 Leu Ser Arg Ala Glu Phe Gln Arg Ile Thr Gln Asp Leu Leu Ala Arg
 275 280 285
 Thr Lys Thr Pro Phe Asn Gln Val Val Lys Asp Ala Gly Val Ser Val
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 Ser Glu Ile Asp His Val Val Leu Val Gly Gly Ser Thr Arg Met Pro
 305 310 315 320
 Ala Val Thr Glu Leu Val Lys Glu Leu Thr Gly Gly Arg Glu Pro Asn
 325 330 335
 Lys Gly Val Asn Pro Asp Glu Val Val Ala Val Gly Ala Ala Leu Gln
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 Ala Gly Val Leu Arg Gly Glu Val Lys Asp Val Leu Leu Leu Asp Val
 355 360 365
 Thr Pro Leu Ser Leu Gly Ile Glu Thr Lys Gly Gly Val Met Thr Lys
 370 375 380
 Leu Ile Glu Arg Asn Thr Thr Ile Pro Thr Lys Arg Ser Glu Thr Phe
 385 390 395 400
 Thr Thr Ala Glu Asp Asn Gln Pro Ser Val Gln Ile Gln Val Phe Gln
 405 410 415
 Gly Glu Arg Glu Ile Ala Thr Ala Asn Lys Leu Leu Gly Ser Phe Glu
 420 425 430
 Leu Gly Gly Ile Ala Pro Ala Pro Arg Gly Val Pro Gln Ile Glu Val

435	440	445
Thr Phe Asp Ile Asp Ala Asn Gly Ile Val His Val Thr Ala Lys Asp 450 455 460		
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Leu Ser Gln Asp Glu Ile Asp Arg Met Ile Lys Asp Ala Glu Ala His 485 490 495		
Ala Asp Glu Asp Lys Lys Arg Arg Glu Glu Gln Glu Val Arg Asn Asn 500 505 510		
Ala Glu Ser Leu Val Tyr Gln Thr Arg Lys Phe Val Glu Glu Asn Ser 515 520 525		
Glu Lys Val Ser Glu Asp Leu Lys Ala Lys Val Glu Glu Ala Ala Lys 530 535 540		
Gly Val Glu Glu Ala Leu Lys Gly Glu Asp Leu Glu Ala Ile Lys Ala 545 550 555 560		
Ala Val Glu Lys Leu Asn Thr Glu Ser Gln Glu Met Gly Lys Ala Ile 565 570 575		
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<223> RXN01345

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	Met Arg Phe Gly Leu	
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Asp Leu Gly Thr Thr Arg Thr Ile Ala Ala Ala Val Asp Arg Gly Asn	
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tat ccc atc gtc act gtg gaa gat tct tta ggc gac acc cac gat ttc	211
Tyr Pro Ile Val Thr Val Glu Asp Ser Leu Gly Asp Thr His Asp Phe	
25 30 35	

att cca tct gtg gtg gcc ctc aag gca gat agg att gtc gcg ggt tgg	259
Ile Pro Ser Val Val Ala Leu Lys Ala Asp Arg Ile Val Ala Gly Trp	
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Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser Phe Val Arg Ser Phe	
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aaa cgc cta ctc tct gaa ccc aat gtc acg gaa gcc acc ccg gtc tac	355
Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu Ala Thr Pro Val Tyr	
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Leu Gly Asp His Val His Pro Leu Gly Ala Val Leu Glu Ala Phe Ala	
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Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln Thr Gln Leu Gly Asp	
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acc tcc ccg atc gaa gta gtc att ggt gtg ccc gcc aac tcc cac agc	499
Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro Ala Asn Ser His Ser	
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gcc cag cga ctg ctc acc atg tcc gcc ttc agc gcc aca ggc atc acc	547
Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser Ala Thr Gly Ile Thr	
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Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala Ala Phe Glu Tyr Thr	
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His Arg His Ala Arg Thr Leu Asn Ser Lys Arg Gln Ala Ile Val Val	
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Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser Leu Ile Arg Ile Asp	
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Gly Thr His His Glu Val Val Ser Ser Ile Gly Ile Ser Arg Leu Gly	
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Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys Ala Leu Lys Ala Ala	
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Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala Lys Asn Thr Leu Leu	
230 235 240 245	
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Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val Pro Gln Ser Arg Arg	
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Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr Val Pro Val Asn Lys	
265 270 275	
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Phe	Tyr	Glu	Ala	Ala	Thr	Pro	Leu	Val	Glu	Lys	Ser	Leu	Ser	Ile	Met	
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Glu	Pro	Leu	Ile	Gly	Val	Asp	Asp	Leu	Lys	Asp	Ser	Asp	Ile	Ala	Gly	
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Ile	Tyr	Leu	Val	Gly	Gly	Gly	Ser	Ser	Leu	Pro	Leu	Val	Ser	Arg	Leu	
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Leu	Arg	Glu	Arg	Phe	Gly	Arg	Arg	Val	His	Arg	Ser	Pro	Phe	Pro	Ser	
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ggg	tcc	act	gcg	gtg	ggg	ctg	gcc	atc	gcg	gct	gac	cct	tcc	tct	ggg	1171
Gly	Ser	Thr	Ala	Val	Gly	Leu	Ala	Ile	Ala	Ala	Asp	Pro	Ser	Ser	Gly	
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Phe	His	Leu	Arg	Asp	Arg	Val	Ala	Arg	Gly	Ile	Gly	Val	Phe	Arg	Glu	
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His	Asp	Ser	Gly	Arg	Ala	Val	Ser	Phe	Asp	Pro	Leu	Ile	Ala	Pro	Asp	
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Thr	Asp	Ser	Ala	Thr	Val	Ala	Lys	Arg	Cys	Tyr	Lys	Ala	Val	His	Asn	
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Ile	Gly	Trp	Phe	Arg	Phe	Val	Glu	Tyr	Ser	Thr	Val	Ser	Glu	Asp	Gly	
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agc	ccc	gga	gat	att	tcc	ctg	ctc	agt	gaa	atc	aag	att	cct	ttt	gat	1411
Ser	Pro	Gly	Asp	Ile	Ser	Leu	Leu	Ser	Glu	Ile	Lys	Ile	Pro	Phe	Asp	
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Ser	Ser	Ile	Thr	Asp	Val	Asp	Ala	Thr	Glu	Ile	Ser	Arg	Phe	Asp	Gly	
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Pro	Glu	Val	Glu	Glu	Thr	Ile	Thr	Val	Asn	Asp	Asn	Gly	Val	Ala	Ser	
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Ile	Ser	Ile	Lys	Ile	Leu	Gly	Gly	Val	Thr	Val	Glu	His	Thr	Ile		
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Ile Val Ala Gly Trp Asp Ala Ile Glu Val Gly Gln Asp His Pro Ser	50	55	60
Phe Val Arg Ser Phe Lys Arg Leu Leu Ser Glu Pro Asn Val Thr Glu	65	70	75
Ala Thr Pro Val Tyr Leu Gly Asp His Val His Pro Leu Gly Ala Val	85	90	95
Leu Glu Ala Phe Ala Glu Asn Val Val Thr Ala Leu Arg Ala Phe Gln	100	105	110
Thr Gln Leu Gly Asp Thr Ser Pro Ile Glu Val Val Ile Gly Val Pro	115	120	125
Ala Asn Ser His Ser Ala Gln Arg Leu Leu Thr Met Ser Ala Phe Ser	130	135	140
Ala Thr Gly Ile Thr Val Val Gly Leu Val Asn Glu Pro Ser Ala Ala	145	150	155
Ala Phe Glu Tyr Thr His Arg His Ala Arg Thr Leu Asn Ser Lys Arg	165	170	175
Gln Ala Ile Val Val Tyr Asp Leu Gly Gly Gly Thr Phe Asp Ser Ser	180	185	190
Leu Ile Arg Ile Asp Gly Thr His His Glu Val Val Ser Ser Ile Gly	195	200	205
Ile Ser Arg Leu Gly Gly Asp Asp Phe Asp Glu Ile Leu Leu Gln Cys	210	215	220
Ala Leu Lys Ala Ala Gly Arg Gln His Asp Ala Phe Gly Lys Arg Ala	225	230	235
Lys Asn Thr Leu Leu Asp Glu Ser Arg Asn Ala Lys Glu Ala Leu Val	245	250	255
Pro Gln Ser Arg Arg Leu Val Leu Glu Ile Gly Asp Asp Asp Ile Thr	260	265	270
Val Pro Val Asn Lys Phe Tyr Glu Ala Ala Thr Pro Leu Val Glu Lys	275	280	285
Ser Leu Ser Ile Met Glu Pro Leu Ile Gly Val Asp Asp Leu Lys Asp	290	295	300
Ser Asp Ile Ala Gly Ile Tyr Leu Val Gly Gly Gly Ser Ser Leu Pro	305	310	315
Leu Val Ser Arg Leu Leu Arg Glu Arg Phe Gly Arg Arg Val His Arg	325	330	335

Ser Pro Phe Pro Ser Gly Ser Thr Ala Val Gly Leu Ala Ile Ala Ala
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 Asp Pro Ser Ser Gly Phe His Leu Arg Asp Arg Val Ala Arg Gly Ile
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 Gly Val Phe Arg Glu His Asp Ser Gly Arg Ala Val Ser Phe Asp Pro
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 Lys Ala Val His Asn Ile Gly Trp Phe Arg Phe Val Glu Tyr Ser Thr
 405 410 415
 Val Ser Glu Asp Gly Ser Pro Gly Asp Ile Ser Leu Leu Ser Glu Ile
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 Lys Ile Pro Phe Asp Ser Ser Ile Thr Asp Val Asp Ala Thr Glu Ile
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 Met Ile Phe Glu Leu
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 ccg gat acc acc acc cag caa att tcc aag acc cta act cga ctg cgt 163
 Pro Asp Thr Thr Thr Gln Gln Ile Ser Lys Thr Leu Thr Arg Leu Arg
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 Glu Ser Gly Thr Gln Val Thr Thr Gly Arg Val Leu Thr Leu Ile Val
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 Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val Thr Glu Ser Thr Asn
 40 45 50

gaa gcc tcg cgc gag cac cca tct cgc gtg atc att ttg gtg gtt ggc	307
Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile Ile Leu Val Val Gly	
55 60 65	
gat aaa act gca gaa aac aaa gtt gac gca gaa gtc cgt atc ggt ggc	355
Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu Val Arg Ile Gly Gly	
70 75 80 85	
gac gct ggt gct tcc gag atg atc atc atg cat ctc aac gga cct gtc	403
Asp Ala Gly Ala Ser Glu Met Ile Ile Met His Leu Asn Gly Pro Val	
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gct gac aag ctc cag tat gtc gtc aca cca ctg ttg ctt cct gac acc	451
Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu Leu Leu Pro Asp Thr	
105 110 115	
ccc atc gtt gct tgg tgg cca ggt gaa tca cca aag aat cct tcc cag	499
Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro Lys Asn Pro Ser Gln	
120 125 130	
gac cca att gga cgc atc gca caa cga cgc atc act gat gct ttg tac	547
Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile Thr Asp Ala Leu Tyr	
135 140 145	
gac cgt gat gac gca cta gaa gat cgt gtt gag aac tat cac cca ggt	595
Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu Asn Tyr His Pro Gly	
150 155 160 165	
gat acc gac atg acg tgg gcg cgc ctt acc cag tgg cgg gga ctt gtt	643
Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln Trp Arg Gly Leu Val	
170 175 180	
gcc tcc tca ttg gat cac cca cca cac agc gaa atc act tcc gtg agg	691
Ala Ser Ser Leu Asp His Pro Pro His Ser Glu Ile Thr Ser Val Arg	
185 190 195	
ctg acc ggt gca agc ggc agt acc tcg gtg gat ttg gct gca ggc tgg	739
Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp Leu Ala Ala Gly Trp	
200 205 210	
ttg gcg cgg agg ctg aaa gtg cct gtg atc cgc gag gtg aca gat gct	787
Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg Glu Val Thr Asp Ala	
215 220 225	
ccc acc gtg cca acc gat gag ttt ggt act cca ctg ctg gct atc cag	835
Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro Leu Leu Ala Ile Gln	
230 235 240 245	
cgc ctg gag atc gtt cgc acc acc ggc tcg atc atc atc acc atc tat	883
Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile Ile Ile Thr Ile Tyr	
250 255 260	
gac gct cat acc ctt cag gta gag atg ccg gaa tcc ggc aat gcc cca	931
Asp Ala His Thr Leu Gln Val Glu Met Pro Glu Ser Gly Asn Ala Pro	
265 270 275	
tcg ctg gtg gct att ggt cgt cga agt gag tcc gac tgc ttg tct gag	979
Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser Asp Cys Leu Ser Glu	
280 285 290	
gag ctt cgc cac atg gat cca gat ttg ggc tac cag cac gca cta tcc	1027

Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr Gln His Ala Leu Ser
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 Gly Leu Ser Ser Val Lys Leu Glu Thr Val
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<213> Corynebacterium glutamicum

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Leu Thr Leu Ile Val Val Thr Asp Ser Glu Ser Asp Val Ala Ala Val
 35 40 45

Thr Glu Ser Thr Asn Glu Ala Ser Arg Glu His Pro Ser Arg Val Ile
 50 55 60

Ile Leu Val Val Gly Asp Lys Thr Ala Glu Asn Lys Val Asp Ala Glu
 65 70 75 80

Val Arg Ile Gly Gly Asp Ala Gly Ala Ser Glu Met Ile Ile Met His
 85 90 95

Leu Asn Gly Pro Val Ala Asp Lys Leu Gln Tyr Val Val Thr Pro Leu
 100 105 110

Leu Leu Pro Asp Thr Pro Ile Val Ala Trp Trp Pro Gly Glu Ser Pro
 115 120 125

Lys Asn Pro Ser Gln Asp Pro Ile Gly Arg Ile Ala Gln Arg Arg Ile
 130 135 140

Thr Asp Ala Leu Tyr Asp Arg Asp Asp Ala Leu Glu Asp Arg Val Glu
 145 150 155 160

Asn Tyr His Pro Gly Asp Thr Asp Met Thr Trp Ala Arg Leu Thr Gln
 165 170 175

Trp Arg Gly Leu Val Ala Ser Ser Leu Asp His Pro Pro His Ser Glu
 180 185 190

Ile Thr Ser Val Arg Leu Thr Gly Ala Ser Gly Ser Thr Ser Val Asp
 195 200 205

Leu Ala Ala Gly Trp Leu Ala Arg Arg Leu Lys Val Pro Val Ile Arg
 210 215 220

Glu Val Thr Asp Ala Pro Thr Val Pro Thr Asp Glu Phe Gly Thr Pro
 225 230 235 240

Leu Leu Ala Ile Gln Arg Leu Glu Ile Val Arg Thr Thr Gly Ser Ile
 245 250 255

Ile Ile Thr Ile Tyr Asp Ala His Thr Leu Gln Val Glu Met Pro Glu
 260 265 270

Ser Gly Asn Ala Pro Ser Leu Val Ala Ile Gly Arg Arg Ser Glu Ser
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Asp Cys Leu Ser Glu Glu Leu Arg His Met Asp Pro Asp Leu Gly Tyr
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Gln His Ala Leu Ser Gly Leu Ser Ser Val Lys Leu Glu Thr Val
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 Met Gln Glu Ser Ser
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cgt gat aat ttc caa gtt gac ctc ggc ggc gtt gtt gat ctt ttg agt 163
 Arg Asp Asn Phe Gln Val Asp Leu Gly Gly Val Val Asp Leu Leu Ser
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cgc cac att tat tcc ggt ccg agg gtg tat gtg cgt gag ttg ctg cag 211
 Arg His Ile Tyr Ser Gly Pro Arg Val Tyr Val Arg Glu Leu Leu Gln
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aat gcg gtt gat gct tgt act gca cgt tct gaa cag ggt gag gag ggc 259
 Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu Gln Gly Glu Glu Gly
 40 45 50

tac gag ccg agt att cgt att ccg ccg gtg acc aag gat cgt gcc acg 307
 Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr Lys Asp Arg Ala Thr
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 Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr Ala Gln Glu Ala Arg
 70 75 80 85

gaa ttg ctg gcg acg gtg ggg ccg acg tcg aaa cgc gat gaa ttc ggt 403
 Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys Arg Asp Glu Phe Gly
 90 95 100

ctg cag ccg gaa ggt cgc ctg ggg caa ttt ggc atc ggg ctg ctt agt 451
 Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly Ile Gly Leu Leu Ser
 105 110 115

tgt ttc atg gtg gcg gat gag atc acc atg gtg tcg cat gcg gag ggt 499
 Cys Phe Met Val Ala Asp Glu Ile Thr Met Val Ser His Ala Glu Gly

120	125	130	
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gag att ctt ggg gat gac gca acg gat gtc att ccg gtg ggc acg act Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile Pro Val Gly Thr Thr 150 155 160 165			595
gtg cac ctg act ccg cgc cct gat gag cgc acg ttg ctg acg gaa aat Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr Leu Leu Thr Glu Asn 170 175 180			643
tcc gtg gtc acc att gct agt aat tat ggc cgc tac ctg ccg att cct Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg Tyr Leu Pro Ile Pro 185 190 195			691
att gtg gtg cag ggt gag aaa aac acc acc atc act aca tcg ccg gtg Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile Thr Thr Ser Pro Val 200 205 210			739
ttt gca aag gat act gat cag cag cac agg ctg tat gcc ggc cgg gag Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu Tyr Ala Gly Arg Glu 215 220 225			787
cgc ctt ggt aaa act cct ttt gat gtc atc gat ctc acc ggt cct ggc Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp Leu Thr Gly Pro Gly 230 235 240 245			835
atc gag ggt gtg gct tat gta ttg ccg gag gcc cag gct ccg cat atg Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala Gln Ala Pro His Met 250 255 260			883
tcc agg cgt cac agt att tat gtc aac cgc atg ttg gtc tct gat ggg Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met Leu Val Ser Asp Gly 265 270 275			931
cct tcc acg gtg ctg ccc aac tgg gcg ttc ttt gtg gaa tgt gaa atc Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe Val Glu Cys Glu Ile 280 285 290			979
aat tca acc gat ttg gaa ccc acc gca tcg cgt gaa gcg ctc atg gat Asn Ser Thr Asp Leu Glu Pro Thr Ala Ser Arg Glu Ala Leu Met Asp 295 300 305			1027
gac acc gcg ttc gcg gca acc agg gaa cat atc ggt gag tgc att aaa Asp Thr Ala Phe Ala Ala Thr Arg Glu His Ile Gly Glu Cys Ile Lys 310 315 320 325			1075
tcg tgg ctg att aat ctc gcc atg acc aag cct cac cgc gtg cgg gaa Ser Trp Leu Ile Asn Leu Ala Met Thr Lys Pro His Arg Val Arg Glu 330 335 340			1123
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cgt ggt cgc atc tcg atc ggt gag atc acc acg ttg tcc atc acc gag	1267
Arg Gly Arg Ile Ser Ile Gly Glu Ile Thr Thr Leu Ser Ile Thr Glu	
375 380 385	
gat gtg tcg ctg cag ctg gct acc acg ttg gat gat ttc agg cag ctc	1315
Asp Val Ser Leu Gln Leu Ala Thr Thr Leu Asp Asp Phe Arg Gln Leu	
390 395 400 405	
aac acc att gcg cgc ccg gac acc ttg att att aat ggc ggc tac att	1363
Asn Thr Ile Ala Arg Pro Asp Thr Leu Ile Ile Asn Gly Gly Tyr Ile	
410 415 420	
cac gac agc gat ctg gct cgg ctc att ccc gtt cac tac cca ccg ctt	1411
His Asp Ser Asp Leu Ala Arg Leu Ile Pro Val His Tyr Pro Pro Leu	
425 430 435	
acg gta tct act gct gac ctg cgc gaa tcc atg gat ctg atg gag ctt	1459
Thr Val Ser Thr Ala Asp Leu Arg Glu Ser Met Asp Leu Met Glu Leu	
440 445 450	
ccg ccg ctg cag gac att gag aaa gcc aag gca ctg gat gcg cag gtc	1507
Pro Pro Leu Gln Asp Ile Glu Lys Ala Lys Ala Leu Asp Ala Gln Val	
455 460 465	
acg gaa tca ttg aag gat ttt cag atc aag ggc gca acg agg gtt ttt	1555
Thr Glu Ser Leu Lys Asp Phe Gln Ile Lys Gly Ala Thr Arg Val Phe	
470 475 480 485	
gaa ccc gca gat gtt cct gcc gtg gtg atc att gat tcc aag gcg cag	1603
Glu Pro Ala Asp Val Pro Ala Val Val Ile Ile Asp Ser Lys Ala Gln	
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gcc tca cgg gat cgc aat gaa aca caa agc gca acc act gat cgt tgg	1651
Ala Ser Arg Asp Arg Asn Glu Thr Gln Ser Ala Thr Thr Asp Arg Trp	
505 510 515	
gct gac att ttg gca acg gtg gat aac acg ttg agc cgt caa aca gcc	1699
Ala Asp Ile Leu Ala Thr Val Asp Asn Thr Leu Ser Arg Gln Thr Ala	
520 525 530	
aac att cca cag gat cag gga ctg tcg gcg ttg tgc ttg aat tgg aac	1747
Asn Ile Pro Gln Asp Gln Gly Leu Ser Ala Leu Cys Leu Asn Trp Asn	
535 540 545	
aat tcg ctg gtc agg aaa ttg gcg tcc act gat gac acc gcc gtg gtg	1795
Asn Ser Leu Val Arg Lys Leu Ala Ser Thr Asp Asp Thr Ala Val Val	
550 555 560 565	
tcg cgc acg gtg cgt ttg ctc tac gtt cag gca ttg ttg tcc agc aag	1843
Ser Arg Thr Val Arg Leu Leu Tyr Val Gln Ala Leu Leu Ser Ser Lys	
570 575 580	
agg cca ctg cgg gtg aag gaa cgc gcg ctg ctt aat gat tcg ctg gca	1891
Arg Pro Leu Arg Val Lys Glu Arg Ala Leu Leu Asn Asp Ser Leu Ala	
585 590 595	
gat ctg gtt tct ttg tct ttg tca tcc gat atc taagacaatc ctccgcta	1944
Asp Leu Val Ser Leu Ser Leu Ser Ser Asp Ile	
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ctt

1947

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<213> Corynebacterium glutamicum

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Arg Glu Leu Leu Gln Asn Ala Val Asp Ala Cys Thr Ala Arg Ser Glu
 35 40 45

Gln Gly Glu Glu Gly Tyr Glu Pro Ser Ile Arg Ile Arg Pro Val Thr
 50 55 60

Lys Asp Arg Ala Thr Phe Ser Leu Val Asp Asn Gly Thr Gly Leu Thr
 65 70 75 80

Ala Gln Glu Ala Arg Glu Leu Leu Ala Thr Val Gly Arg Thr Ser Lys
 85 90 95

Arg Asp Glu Phe Gly Leu Gln Arg Glu Gly Arg Leu Gly Gln Phe Gly
 100 105 110

Ile Gly Leu Leu Ser Cys Phe Met Val Ala Asp Glu Ile Thr Met Val
 115 120 125

Ser His Ala Glu Gly Ala Ser Ala Ile Arg Trp Thr Gly His Ala Asp
 130 135 140

Gly Thr Phe Asn Leu Glu Ile Leu Gly Asp Asp Ala Thr Asp Val Ile
 145 150 155 160

Pro Val Gly Thr Thr Val His Leu Thr Pro Arg Pro Asp Glu Arg Thr
 165 170 175

Leu Leu Thr Glu Asn Ser Val Val Thr Ile Ala Ser Asn Tyr Gly Arg
 180 185 190

Tyr Leu Pro Ile Pro Ile Val Val Gln Gly Glu Lys Asn Thr Thr Ile
 195 200 205

Thr Thr Ser Pro Val Phe Ala Lys Asp Thr Asp Gln Gln His Arg Leu
 210 215 220

Tyr Ala Gly Arg Glu Arg Leu Gly Lys Thr Pro Phe Asp Val Ile Asp
 225 230 235 240

Leu Thr Gly Pro Gly Ile Glu Gly Val Ala Tyr Val Leu Pro Glu Ala
 245 250 255

Gln Ala Pro His Met Ser Arg Arg His Ser Ile Tyr Val Asn Arg Met
 260 265 270

Leu Val Ser Asp Gly Pro Ser Thr Val Leu Pro Asn Trp Ala Phe Phe

275					280					285					
Val	Glu	Cys	Glu	Ile	Asn	Ser	Thr	Asp	Leu	Glu	Pro	Thr	Ala	Ser	Arg
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Glu	Ala	Leu	Met	Asp	Asp	Thr	Ala	Phe	Ala	Ala	Thr	Arg	Glu	His	Ile
305					310					315					320
Gly	Glu	Cys	Ile	Lys	Ser	Trp	Leu	Ile	Asn	Leu	Ala	Met	Thr	Lys	Pro
				325					330					335	
His	Arg	Val	Arg	Glu	Phe	Thr	Ala	Ile	His	Asp	Leu	Ala	Leu	Arg	Glu
			340					345					350		
Leu	Cys	Gln	Ser	Asp	Ala	Asp	Leu	Ala	Glu	Thr	Met	Leu	Gly	Leu	Leu
		355					360					365			
Thr	Leu	Glu	Thr	Ser	Arg	Gly	Arg	Ile	Ser	Ile	Gly	Glu	Ile	Thr	Thr
		370				375					380				
Leu	Ser	Ile	Thr	Glu	Asp	Val	Ser	Leu	Gln	Leu	Ala	Thr	Thr	Leu	Asp
385					390					395					400
Asp	Phe	Arg	Gln	Leu	Asn	Thr	Ile	Ala	Arg	Pro	Asp	Thr	Leu	Ile	Ile
				405					410					415	
Asn	Gly	Gly	Tyr	Ile	His	Asp	Ser	Asp	Leu	Ala	Arg	Leu	Ile	Pro	Val
			420					425					430		
His	Tyr	Pro	Pro	Leu	Thr	Val	Ser	Thr	Ala	Asp	Leu	Arg	Glu	Ser	Met
		435					440					445			
Asp	Leu	Met	Glu	Leu	Pro	Pro	Leu	Gln	Asp	Ile	Glu	Lys	Ala	Lys	Ala
		450				455					460				
Leu	Asp	Ala	Gln	Val	Thr	Glu	Ser	Leu	Lys	Asp	Phe	Gln	Ile	Lys	Gly
465					470					475					480
Ala	Thr	Arg	Val	Phe	Glu	Pro	Ala	Asp	Val	Pro	Ala	Val	Val	Ile	Ile
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Asp	Ser	Lys	Ala	Gln	Ala	Ser	Arg	Asp	Arg	Asn	Glu	Thr	Gln	Ser	Ala
			500					505					510		
Thr	Thr	Asp	Arg	Trp	Ala	Asp	Ile	Leu	Ala	Thr	Val	Asp	Asn	Thr	Leu
		515					520					525			
Ser	Arg	Gln	Thr	Ala	Asn	Ile	Pro	Gln	Asp	Gln	Gly	Leu	Ser	Ala	Leu
		530				535					540				
Cys	Leu	Asn	Trp	Asn	Asn	Ser	Leu	Val	Arg	Lys	Leu	Ala	Ser	Thr	Asp
545					550					555					560
Asp	Thr	Ala	Val	Val	Ser	Arg	Thr	Val	Arg	Leu	Leu	Tyr	Val	Gln	Ala
				565					570					575	
Leu	Leu	Ser	Ser	Lys	Arg	Pro	Leu	Arg	Val	Lys	Glu	Arg	Ala	Leu	Leu
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ggg gtt gca tct ccg gta gct caa gca caa gtg gaa gat caa ttt gag 163															
Gly Val Ala Ser Pro Val Ala Gln Ala Gln Val Glu Asp Gln Phe Glu 20															
ctt gta aaa gaa atc agt gat gag cag ttt gct gat gat ggt gtt gac 211															
Leu Val Lys Glu Ile Ser Asp Glu Gln Phe Ala Asp Asp Gly Val Asp 35															
tat gtt ccc aat agg aat gct ccg act gtt aag gaa caa ctt gag gat 259															
Tyr Val Pro Asn Arg Asn Ala Pro Thr Val Lys Glu Gln Leu Glu Asp 50															
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Phe Glu Ser Ala His Pro Glu Val Val Ile Glu Tyr His Glu His Val 65															
aac gat agt aaa gac aat gtt gag gaa ctt ccg cta cct aag cgg gac 355															
Asn Asp Ser Lys Asp Asn Val Glu Glu Leu Pro Leu Pro Lys Arg Asp 85															
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Ile Val Ala Gly Glu Met Arg Ser Asp Val Ile Glu Leu Pro Glu Gly 100															
gtg agc aag gac gaa gct gat cag gtg gag gtt gcg gaa gcg cga ctt 451															
Val Ser Lys Asp Glu Ala Asp Gln Val Glu Val Ala Glu Ala Arg Leu 115															
aat gag ggc gca cga ttg atg gct gca act ggg tgt gag gct atg tgg 499															
Asn Glu Gly Ala Arg Leu Met Ala Ala Thr Gly Cys Glu Ala Met Trp 130															
cca aca ggt ttc tca gtt tgt ggc cgg att ctt gac gct tat cgg cag 547															
Pro Thr Gly Phe Ser Val Cys Gly Arg Ile Leu Asp Ala Tyr Arg Gln 145															
gtt gga ggt cag ttg tca tgg ctt ggg cca cca aag tca aac gag ttg 595															
Val Gly Gly Gln Leu Ser Trp Leu Gly Pro Pro Lys Ser Asn Glu Leu 165															
acc aat ccc gac ggt gtt ggc aaa aga agt gaa ttt gtt ggg ggt gcc 643															
Thr Asn Pro Asp Gly Val Gly Lys Arg Ser Glu Phe Val Gly Gly Ala															

170										175					180					
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Ile	Tyr	Trp	His	Pro	Asp	Thr	Gly	Ala	Tyr	Ala	Val	Thr	Leu	Asp	Gly					
			185					190					195							
ttg	agg	cag	tgg	ggg	acc	ttg	aac	tgg	gaa	tca	ggg	cca	ttg	ggg	tac	739				
Leu	Arg	Gln	Trp	Gly	Thr	Leu	Asn	Trp	Glu	Ser	Gly	Pro	Leu	Gly	Tyr					
		200					205					210								
cca	acc	tct	ggc	ccg	atg	gat	aca	aac	tat	ccc	ctt	act	cag	cga	cag	787				
Pro	Thr	Ser	Gly	Pro	Met	Asp	Thr	Asn	Tyr	Pro	Leu	Thr	Gln	Arg	Gln					
		215				220					225									
act	ttt	caa	ggc	ggc	gac	aac	tat	tac	aac	cca	ttg	act	ggc	ggc	gct	835				
Thr	Phe	Gln	Gly	Gly	Asp	Asn	Tyr	Tyr	Asn	Pro	Leu	Thr	Gly	Gly	Ala					
230					235					240					245					
gtg	tgg	ggc	gat	att	aaa	cag	cgc	tac	gaa	gaa	ctt	ggc	ggc	tcg	aat	883				
Val	Trp	Gly	Asp	Ile	Lys	Gln	Arg	Tyr	Glu	Glu	Leu	Gly	Gly	Ser	Asn					
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cat	gcc	att	ggc	atc	ccg	atc	act	aac	gag	cta	cct	agc	ggc	act	gag	931				
His	Ala	Ile	Gly	Ile	Pro	Ile	Thr	Asn	Glu	Leu	Pro	Ser	Gly	Thr	Glu					
			265					270					275							
tat	ttt	tac	aat	aat	ttc	ttc	aat	gga	aca	att	tcg	tgg	cga	aat	gat	979				
Tyr	Phe	Tyr	Asn	Asn	Phe	Phe	Asn	Gly	Thr	Ile	Ser	Trp	Arg	Asn	Asp					
		280					285					290								
cgt	cag	aca	cgg	ttt	atg	tat	ttg	gct	acg	cag	cgg	gtg	tgg	gat	gcg	1027				
Arg	Gln	Thr	Arg	Phe	Met	Tyr	Leu	Ala	Thr	Gln	Arg	Val	Trp	Asp	Ala					
		295				300					305									
ttg	ggc	cgg	gag	acg	ggc	cgt	tta	ggc	ttt	cct	gaa	gca	gat	gaa	aca	1075				
Leu	Gly	Arg	Glu	Thr	Gly	Arg	Leu	Gly	Phe	Pro	Glu	Ala	Asp	Glu	Thr					
310					315					320					325					
cct	gag	gtt	tct	ggc	cta	ttc	cat	gtg	gtg	aat	ttt	gcg	gag	cgc	ggc	1123				
Pro	Glu	Val	Ser	Gly	Leu	Phe	His	Val	Val	Asn	Phe	Ala	Glu	Arg	Gly					
				330					335					340						
gtg	att	gcg	tgg	aat	gga	atc	cta	ggc	gcc	aga	gag	ctg	tat	ggc	gat	1171				
Val	Ile	Ala	Trp	Asn	Gly	Ile	Leu	Gly	Ala	Arg	Glu	Leu	Tyr	Gly	Asp					
			345					350					355							
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Val	Tyr	Ser	Leu	Trp	Leu	Gln	Tyr	Gln	Asn	Thr	Asp	Thr	Pro	Leu	Gly					
		360					365					370								
tgg	ccg	ata	cca	tca	ttg	aca	tca	tta	aat	gag	tca	ctc	gaa	caa	gaa	1267				
Trp	Pro	Ile	Pro	Ser	Leu	Thr	Ser	Leu	Asn	Glu	Ser	Leu	Glu	Gln	Glu					
		375				380					385									
ttc	acc	aga	ggc	gtt	gtt	tta	ggc	tca	ggc	gat	gca	ctg	aca	tgg	att	1315				
Phe	Thr	Arg	Gly	Val	Val	Leu	Gly	Ser	Gly	Asp	Ala	Leu	Thr	Trp	Ile					
390					395					400					405					
cct	gac	gat	gaa	gaa	aga	agt	ttg	gag	gat	ttc	ctc	cca	att	gga	agt	1363				
Pro	Asp	Asp	Glu	Glu	Arg	Ser	Leu	Glu	Asp	Phe	Leu	Pro	Ile	Gly	Ser					
				410					415					420						

agc ggc tca tcc tca tcg agc caa gag atg acc ctg ttt tcc cag cgt 1411
 Ser Gly Ser Ser Ser Ser Ser Ser Gln Glu Met Thr Leu Phe Ser Gln Arg
 425 430 435

gca caa tac gtg gat tgc aag aat ctt ccc gat tta gat gag cag aga 1459
 Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp Leu Asp Glu Gln Arg
 440 445 450

aaa act gaa aac aac att gaa aag aat ggt ggc ccg atc aaa aaa gag 1507
 Lys Thr Glu Asn Asn Ile Glu Lys Asn Gly Gly Pro Ile Lys Lys Glu
 455 460 465

tat agt tcg cga ggt ttc ccc acc gag ttc aga ttt gtc gtg aga aaa 1555
 Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg Phe Val Val Arg Lys
 470 475 480 485

ggg cat tat gac cgt tac agg aat gaa ggc tgg gga tat tta aaa aac 1603
 Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp Gly Tyr Leu Lys Asn
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tat tgc aaa cac aac ttc gcc aac cac gct atg gct gag gcc gta gta 1651
 Tyr Cys Lys His Asn Phe Ala Asn His Ala Met Ala Glu Ala Val Val
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gat aaa gcg gtg att gat tat ggc tca tcg cca gga acc agc tat tac 1699
 Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro Gly Thr Ser Tyr Tyr
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aag ttc gag aaa acg gtg tac ttt cta gat tgc aga act tat aca ttc 1747
 Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys Arg Thr Tyr Thr Phe
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 Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala Pro Gln Trp Val Thr
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att att tac aat cct cat act ttc act gga gca aat tcg aac aga ccc 1843
 Ile Ile Tyr Asn Pro His Thr Phe Thr Gly Ala Asn Ser Asn Arg Pro
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aag ggg gta att tca gca tgg tgt aat tca acc cca cct ggt gga atc 1891
 Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr Pro Pro Gly Gly Ile
 585 590 595

gaa cac gag ccg gaa att tcc caa tgt cct gat cat gtg aat ctt tat 1939
 Glu His Glu Pro Glu Ile Ser Gln Cys Pro Asp His Val Asn Leu Tyr
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Asp Asp Gly Val	Asp Tyr Val Pro	Asn Arg Asn Ala	Pro Thr Val Lys
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Glu Gln Leu Glu	Asp Phe Glu Ser	Ala His Pro Glu	Val Val Ile Glu
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Tyr His Glu His	Val Asn Asp Ser	Lys Asp Asn Val	Glu Glu Leu Pro
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Leu Pro Lys Arg	Asp Ile Val Ala	Gly Glu Met Arg	Ser Asp Val Ile
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Glu Leu Pro Glu	Gly Val Ser Lys	Asp Glu Ala Asp	Gln Val Glu Val
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Ala Glu Ala Arg	Leu Asn Glu Gly	Ala Arg Leu Met	Ala Ala Thr Gly
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Cys Glu Ala Met	Trp Pro Thr Gly	Phe Ser Val Cys	Gly Arg Ile Leu
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Asp Ala Tyr Arg	Gln Val Gly Gly	Gln Leu Ser Trp	Leu Gly Pro Pro
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Lys Ser Asn Glu	Leu Thr Asn Pro	Asp Gly Val Gly	Lys Arg Ser Glu
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Phe Val Gly Gly	Ala Ile Tyr Trp	His Pro Asp Thr	Gly Ala Tyr Ala
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Val Thr Leu Asp	Gly Leu Arg Gln	Trp Gly Thr Leu	Asn Trp Glu Ser
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Gly Pro Leu Gly	Tyr Pro Thr Ser	Gly Pro Met Asp	Thr Asn Tyr Pro
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Leu Gly Gly Ser	Asn His Ala Ile	Gly Ile Pro Ile	Thr Asn Glu Leu
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Pro Ser Gly Thr	Glu Tyr Phe Tyr	Asn Asn Phe Phe	Asn Gly Thr Ile
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Ser Trp Arg Asn	Asp Arg Gln Thr	Arg Phe Met Tyr	Leu Ala Thr Gln
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Arg Val Trp Asp	Ala Leu Gly Arg	Glu Thr Gly Arg	Leu Gly Phe Pro
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Glu Ala Asp Glu	Thr Pro Glu Val	Ser Gly Leu Phe	His Val Val Asn
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Phe Ala Glu Arg Gly Val Ile Ala Trp Asn Gly Ile Leu Gly Ala Arg
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 Leu Phe Ser Gln Arg Ala Gln Tyr Val Asp Cys Lys Asn Leu Pro Asp
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 Pro Ile Lys Lys Glu Tyr Ser Ser Arg Gly Phe Pro Thr Glu Phe Arg
 465 470 475 480
 Phe Val Val Arg Lys Gly His Tyr Asp Arg Tyr Arg Asn Glu Gly Trp
 485 490 495
 Gly Tyr Leu Lys Asn Tyr Cys Lys His Asn Phe Ala Asn His Ala Met
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 Ala Glu Ala Val Val Asp Lys Ala Val Ile Asp Tyr Gly Ser Ser Pro
 515 520 525
 Gly Thr Ser Tyr Tyr Lys Phe Glu Lys Thr Val Tyr Phe Leu Asp Cys
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 Arg Thr Tyr Thr Phe Asn Lys Asn Ser Gly Cys Lys Glu Met His Ala
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 565 570 575
 Asn Ser Asn Arg Pro Lys Gly Val Ile Ser Ala Trp Cys Asn Ser Thr
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 His Val Asn Leu Tyr Asn Lys Leu Arg Ile
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(2176)

<223> RXS02641

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                                   1 5

ttg acc gcc gta ttg ggc gca tct ggc ctt gca gcc gct ggc act cag 163
Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala Ala Ala Gly Thr Gln
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tac ctc aat act cag ggc gaa ggc atc ggt ccg gtc gcc gtc caa aac 211
Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro Val Ala Val Gln Asn
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gac agt gaa tcg ttt aat tcc ggc acc aac gtg gtt gtt gaa gac gca 259
Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val Val Val Glu Asp Ala
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gca gtc acc gcc cag ggt gaa ggc gga ggc gct cgc acc gtc aag gaa 307
Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala Arg Thr Val Lys Glu
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Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala Leu Thr Trp Thr Gly
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aaa aaa gac atc act gct ttt gtt cgc gca gaa cag gaa gac ggc acc 403
Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu Gln Glu Asp Gly Thr
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Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val Asn Glu Asp Gln Gly
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acc aac gga act gag ctg atc tgg cac ggc cct acc aac aag atc cag 499
Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro Thr Asn Lys Ile Gln
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gtt tcc acc ctc aac gtg gat ctc ttt gga gca gat gct gca gcc gct 547
Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala Asp Ala Ala Ala Ala
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cca gca gca gaa cct gca cca gct gaa gca cca gtc gag gaa gct cct 643
Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro Val Glu Glu Ala Pro
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gca cct gtc gca gaa cca gca cca gct gct gaa cct atc gct gag cca 691
Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu Pro Ile Ala Glu Pro
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gtc gct gat tac tca gca aat gac ggc ctc gct ccc ctg cca tcc aac 739

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Ile	Gly	Asp	Tyr	Ser	Tyr	Asn	Ala	Pro	Pro	Gln	Glu	Thr	Ile	Asn	Ala		
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2199

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Val Val Glu Asp Ala Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala
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Arg Thr Val Lys Glu Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala
 65 70 75 80

Leu Thr Trp Thr Gly Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu
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Gln Glu Asp Gly Thr Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val
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Asn Glu Asp Gln Gly Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro
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Thr Asn Lys Ile Gln Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala
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Asp Ala Ala Ala Ala Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp
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Ala Ala Glu Ala Ala Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro
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Val Glu Glu Ala Pro Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu
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Pro Ile Ala Glu Pro Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala
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Pro Leu Pro Ser Asn Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp
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Asp Gly Leu Asn Ala Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val
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Gly Ile Ala Asn Val Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser
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Arg Ala Gly Trp Gly Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr
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Ile Asp Asp Gly Val Ser Ala Ile Thr Ile His His Thr Ala Gly Ser
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 Asn Asn Tyr Thr Glu Ala Gln Ala Ala Ala Gln Val Arg Ser Ala Tyr
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 Ser Tyr His Ala Lys Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser
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 Leu Val Asp Lys Tyr Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met
 325 330 335
 Thr Asn Ala Val Gln Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr
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 Trp Ala Ile Ser Met Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln
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 Glu Thr Ile Asn Ala Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val
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 Ala Gly Phe Asp Pro Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr
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 Ser Tyr Ala Lys Tyr Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile
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 Tyr Ala Gln Met Glu Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr
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 Ser Leu Gln Asn Gly Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr
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 Gln Leu Val Thr Pro Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala
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 Lys Ile Thr Asp Val Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr
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 gcc ctt gtt gcc ggt gga gcc ttg gga aac gtg ttg gac cgg ttg ttc 499
 Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val Leu Asp Arg Leu Phe
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 Arg Asp Pro Ser Phe Phe Phe Gly His Val Val Asp Tyr Ile Ser Val
 135 140 145

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 Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala Ser Ile Ser Cys Gly
 150 155 160 165

 gtc gtg gtg ttc ctg atc gga atg ttc ctt gag gac cgt gaa aac gcc 643
 Val Val Val Phe Leu Ile Gly Met Phe Leu Glu Asp Arg Glu Asn Ala
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 35 40 45

 Ile Met Leu Ser Trp Leu Glu Pro Gly Val Pro Val Pro Ile Ile Gly
 50 55 60

 Asp Trp Phe Arg Phe Tyr Leu Leu Phe Asn Pro Gly Ala Ala Phe Ser
 65 70 75 80

 Met Gly Gly Glu Asn Ser Thr Trp Ile Phe Thr Thr Ile Gln Leu Ser
 85 90 95

 Phe Val Ile Gly Ile Ala Ile Tyr Ala Pro Arg Ile Lys His Lys Trp
 100 105 110

 Ile Ala Ala Gly Leu Ala Leu Val Ala Gly Gly Ala Leu Gly Asn Val
 115 120 125

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 130 135 140

Asp Tyr Ile Ser Val Gly Asn Phe Ala Val Phe Asn Ile Ala Asp Ala
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Ser Ile Ser Cys Gly Val Val Val Phe Leu Ile Gly Met Phe Leu Glu
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Met Thr Thr Pro Leu
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25 30 35

caa atg cct gca ccg ttc gga ctc atc cgt tac ggc gtt gct cca gac 259
Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp
40 45 50

cac cca cgc atc aag ggc atc gtt aag tcc ctg cac aac gtg ttg gac 307
His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Leu Asp
55 60 65

aag cca cgc ctg cgc ctg ctc ggt aac att gaa atc ggc aaa gac atc 355
Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu Ile Gly Lys Asp Ile
70 75 80 85

acc gtc gaa gaa ctc cgc gac tac tac gat gca gtc gtg ttc tcc acc 403
Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala Val Val Phe Ser Thr
90 95 100

ggc gca gtt gca gac cgc gac ctc aac atc ccc gga att gaa gca gaa 451
Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro Gly Ile Glu Ala Glu
105 110 115

ggc tcc ttc ggt gcc ggc gag ttc gtt ggc ttc tac gac ggc aac cca 499
Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro
120 125 130

cgc ttc gag cgc tcc tgg gat ctg tct gca cag tcc gtc gct gtt atc	547
Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln Ser Val Ala Val Ile	
135 140 145	
ggc gtt ggt aac gtc ggc ctc gac gta gcc cgc atc ctg gct aag aca	595
Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg Ile Leu Ala Lys Thr	
150 155 160 165	
ggc gac gag ctc aaa gtc acc gaa att tcc gac aac gtc tac gac tcc	643
Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp Asn Val Tyr Asp Ser	
170 175 180	
ctc aaa gaa aac aag gcc act gaa gtg cac gtt ttc gga cgt cgt ggc	691
Leu Lys Glu Asn Lys Ala Thr Glu Val His Val Phe Gly Arg Arg Gly	
185 190 195	
cca gca cag gtc aag ttc acc cca cag gaa ctc aaa gaa ctc gac cac	739
Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu Lys Glu Leu Asp His	
200 205 210	
tcc ccc acc atc aac gtg gtt gtt gat cca gaa gac atc gac tac gac	787
Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu Asp Ile Asp Tyr Asp	
215 220 225	
ggc gcc tct gaa gaa gcc cgc cgc gca tcc aag tcc cag gac ctg gtc	835
Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys Ser Gln Asp Leu Val	
230 235 240 245	
tgc cag atc ctg gaa cag tac gca atc cgc gag cca aag gac gct ccg	883
Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu Pro Lys Asp Ala Pro	
250 255 260	
cac acc ctg cag atc cac ctc ttt gaa aac cca gtt gag gtt ctt caa	931
His Thr Leu Gln Ile His Leu Phe Glu Asn Pro Val Glu Val Leu Gln	
265 270 275	
aag gac ggc aag gtt gtt ggc ctg cgc acc gaa cgc acc tca ctt gat	979
Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu Arg Thr Ser Leu Asp	
280 285 290	
ggc aac ggc ggc gta aac gga acc ggc gaa ttc aag gac tgg cca gtc	1027
Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe Lys Asp Trp Pro Val	
295 300 305	
cag gct gtc tac cgc gca gtc ggc tac aag tcc gac ccc atc gac ggc	1075
Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser Asp Pro Ile Asp Gly	
310 315 320 325	
gtc cca ttc gat gag aac aag cac gtc atc cct aat gac ggc gga cat	1123
Val Pro Phe Asp Glu Asn Lys His Val Ile Pro Asn Asp Gly Gly His	
330 335 340	
gtc ctc acc gct cca ggc gca gaa cca gta cca ggc ctc tat gca acc	1171
Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro Gly Leu Tyr Ala Thr	
345 350 355	
ggc tgg atc aag cgt gga cca atc ggt cta atc ggc aac acc aag tcc	1219
Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser	
360 365 370	

gac gcc aag gaa acc acc gac atc ctc atc aag gat gcc gtc gcc ggt 1267
 Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys Asp Ala Val Ala Gly
 375 380 385

gta ctt gaa gct cca aag cac cag ggc gaa gaa gcc atc atc gag ctt 1315
 Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu Ala Ile Ile Glu Leu
 390 395 400 405

ctc gat tcc cgc aac atc cca ttc acc acc tgg gaa ggc tgg tac aaa 1363
 Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp Glu Gly Trp Tyr Lys
 410 415 420

ctc gac gca gca gag cgc gca ctc ggt gaa gcc gaa ggc cgc gag cgc 1411
 Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala Glu Gly Arg Glu Arg
 425 430 435

aag aag att gtt gat tgg gaa gaa atg gtc cgc cag gcc cgc gaa gct 1459
 Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg Gln Ala Arg Glu Ala
 440 445 450

cca gca att gtc taaattgttt taacgcgtga agc 1494
 Pro Ala Ile Val
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<210> 614

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

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Val Asp Leu Phe Glu Gln Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr
 35 40 45

Gly Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu
 50 55 60

His Asn Val Leu Asp Lys Pro Arg Leu Arg Leu Leu Gly Asn Ile Glu
 65 70 75 80

Ile Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Asp Tyr Tyr Asp Ala
 85 90 95

Val Val Phe Ser Thr Gly Ala Val Ala Asp Arg Asp Leu Asn Ile Pro
 100 105 110

Gly Ile Glu Ala Glu Gly Ser Phe Gly Ala Gly Glu Phe Val Gly Phe
 115 120 125

Tyr Asp Gly Asn Pro Arg Phe Glu Arg Ser Trp Asp Leu Ser Ala Gln
 130 135 140

Ser Val Ala Val Ile Gly Val Gly Asn Val Gly Leu Asp Val Ala Arg
 145 150 155 160

Ile Leu Ala Lys Thr Gly Asp Glu Leu Lys Val Thr Glu Ile Ser Asp
 165 170 175
 Asn Val Tyr Asp Ser Leu Lys Glu Asn Lys Ala Thr Glu Val His Val
 180 185 190
 Phe Gly Arg Arg Gly Pro Ala Gln Val Lys Phe Thr Pro Gln Glu Leu
 195 200 205
 Lys Glu Leu Asp His Ser Pro Thr Ile Asn Val Val Val Asp Pro Glu
 210 215 220
 Asp Ile Asp Tyr Asp Gly Ala Ser Glu Glu Ala Arg Arg Ala Ser Lys
 225 230 235 240
 Ser Gln Asp Leu Val Cys Gln Ile Leu Glu Gln Tyr Ala Ile Arg Glu
 245 250 255
 Pro Lys Asp Ala Pro His Thr Leu Gln Ile His Leu Phe Glu Asn Pro
 260 265 270
 Val Glu Val Leu Gln Lys Asp Gly Lys Val Val Gly Leu Arg Thr Glu
 275 280 285
 Arg Thr Ser Leu Asp Gly Asn Gly Gly Val Asn Gly Thr Gly Glu Phe
 290 295 300
 Lys Asp Trp Pro Val Gln Ala Val Tyr Arg Ala Val Gly Tyr Lys Ser
 305 310 315 320
 Asp Pro Ile Asp Gly Val Pro Phe Asp Glu Asn Lys His Val Ile Pro
 325 330 335
 Asn Asp Gly Gly His Val Leu Thr Ala Pro Gly Ala Glu Pro Val Pro
 340 345 350
 Gly Leu Tyr Ala Thr Gly Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile
 355 360 365
 Gly Asn Thr Lys Ser Asp Ala Lys Glu Thr Thr Asp Ile Leu Ile Lys
 370 375 380
 Asp Ala Val Ala Gly Val Leu Glu Ala Pro Lys His Gln Gly Glu Glu
 385 390 395 400
 Ala Ile Ile Glu Leu Leu Asp Ser Arg Asn Ile Pro Phe Thr Thr Trp
 405 410 415
 Glu Gly Trp Tyr Lys Leu Asp Ala Ala Glu Arg Ala Leu Gly Glu Ala
 420 425 430
 Glu Gly Arg Glu Arg Lys Lys Ile Val Asp Trp Glu Glu Met Val Arg
 435 440 445
 Gln Ala Arg Glu Ala Pro Ala Ile Val
 450 455

<210> 615

<211> 1488

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1465)

<223> RXS01438

<400> 615

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tccacatttt ttagaacccc ttttaaggaat cgaactttat atg tct cgc cct ttg 115
Met Ser Arg Pro Leu
1 5

cgt gtt gcc gtt gtc ggt gca ggt cca gca gga atc tac gcg tct gat 163
Arg Val Ala Val Val Gly Ala Gly Pro Ala Gly Ile Tyr Ala Ser Asp
10 15 20

ttg ttg atg aaa tcc gac acg gac gtg cag att gat ctt ttt gaa cgt 211
Leu Leu Met Lys Ser Asp Thr Asp Val Gln Ile Asp Leu Phe Glu Arg
25 30 35

atg cca gcg cct ttc ggt ttg atc cgt tat ggt gtt gcg cct gat cac 259
Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly Val Ala Pro Asp His
40 45 50

cct cgc atc aag ggc atc gtg aag tcc ctg cac aat gtg atg gac aag 307
Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His Asn Val Met Asp Lys
55 60 65

gag cag ctg cgt ttc ttg ggc aac att gag gtc ggc aag gac atc act 355
Glu Gln Leu Arg Phe Leu Gly Asn Ile Glu Val Gly Lys Asp Ile Thr
70 75 80 85

gtt gag gag ttg cgt gag ttt tat gac gcg atc gtg ttc tcc act ggc 403
Val Glu Glu Leu Arg Glu Phe Tyr Asp Ala Ile Val Phe Ser Thr Gly
90 95 100

gct act ggc gac cag gat ctt cgg gtt cca ggt tct gat ctg gaa ggt 451
Ala Thr Gly Asp Gln Asp Leu Arg Val Pro Gly Ser Asp Leu Glu Gly
105 110 115

tcg tgg ggc gct ggc gag ttc gtt ggt ttc tat gat ggc aac ccg aac 499
Ser Trp Gly Ala Gly Glu Phe Val Gly Phe Tyr Asp Gly Asn Pro Asn
120 125 130

ttt gaa cgc aac tgg gat ctt tct gct gag aag gta gcg gtt gtt ggt 547
Phe Glu Arg Asn Trp Asp Leu Ser Ala Glu Lys Val Ala Val Val Gly
135 140 145

gtc ggt aac gtg gcg ttg gac gtt gct cgt att ttg gcg aag act ggc 595
Val Gly Asn Val Ala Leu Asp Val Ala Arg Ile Leu Ala Lys Thr Gly
150 155 160 165

gat gag ctg cta gtt act gaa atc cct gac aat gtc tat gag agc ttg 643
Asp Glu Leu Leu Val Thr Glu Ile Pro Asp Asn Val Tyr Glu Ser Leu
170 175 180

gct aag aat cag gct aag gaa gtg cac gtt ttt ggt cgt cgt gga cct 691
Ala Lys Asn Gln Ala Lys Glu Val His Val Phe Gly Arg Arg Gly Pro
185 190 195
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gct cag gcg aag ttc act ccg ttg gag ctg aag gaa ctt gac cat tcc	739
Ala Gln Ala Lys Phe Thr Pro Leu Glu Leu Lys Glu Leu Asp His Ser	
200 205 210	
gac acc atc gag gtg atc gtg aac cct gag gac att gat tac gat gca	787
Asp Thr Ile Glu Val Ile Val Asn Pro Glu Asp Ile Asp Tyr Asp Ala	
215 220 225	
gct tcg gag cag gct cgt cgt gat tcc aag tct cag gac ctc gtg tgc	835
Ala Ser Glu Gln Ala Arg Arg Asp Ser Lys Ser Gln Asp Leu Val Cys	
230 235 240 245	
cag act ttg gaa agc tac gcg atg cgc gat cct aag ggc gct cct cac	883
Gln Thr Leu Glu Ser Tyr Ala Met Arg Asp Pro Lys Gly Ala Pro His	
250 255 260	
aag ctg ttc att cac ttc ttt gag tcc cca gtg gag atc ctc ggt gag	931
Lys Leu Phe Ile His Phe Phe Glu Ser Pro Val Glu Ile Leu Gly Glu	
265 270 275	
gac ggc aag gtt gtt ggc ctc aag act gag cgt act cag ctg gac ggc	979
Asp Gly Lys Val Val Gly Leu Lys Thr Glu Arg Thr Gln Leu Asp Gly	
280 285 290	
aac ggt ggc gtg act ggc acc ggc gag ttc aag acc tgg gat atg cag	1027
Asn Gly Gly Val Thr Gly Thr Gly Glu Phe Lys Thr Trp Asp Met Gln	
295 300 305	
tca gtt tac cgc gcg gta ggt tac cgt tct gat gcg atc gag ggt gtt	1075
Ser Val Tyr Arg Ala Val Gly Tyr Arg Ser Asp Ala Ile Glu Gly Val	
310 315 320 325	
cct ttt gac gat gag cgc gcg gtt gtc ccc aac gac ggc ggc cac atc	1123
Pro Phe Asp Asp Glu Arg Ala Val Val Pro Asn Asp Gly Gly His Ile	
330 335 340	
atc gat cct gag gtc ggc tcc ccc atc act ggc ctg tac gcc act ggc	1171
Ile Asp Pro Glu Val Gly Ser Pro Ile Thr Gly Leu Tyr Ala Thr Gly	
345 350 355	
tgg atc aag cgt ggc cca att gga ctg atc ggc aac acc aag tcc gac	1219
Trp Ile Lys Arg Gly Pro Ile Gly Leu Ile Gly Asn Thr Lys Ser Asp	
360 365 370	
gcc aag gaa acc act gag atg ctg ctt gct gat cac gct gct ggt tct	1267
Ala Lys Glu Thr Thr Glu Met Leu Leu Ala Asp His Ala Ala Gly Ser	
375 380 385	
ttg cct gcg cct gca aag cct gag ttg gag tcc atc att gag ttc ctc	1315
Leu Pro Ala Pro Ala Lys Pro Glu Leu Glu Ser Ile Ile Glu Phe Leu	
390 395 400 405	
gat gag cgc aag gtt gcg ttc acc aca tgg gat ggc tgg cac ctg ctg	1363
Asp Glu Arg Lys Val Ala Phe Thr Thr Trp Asp Gly Trp His Leu Leu	
410 415 420	
gat gct gcg gag cgc gcg ctg ggt gag cct gag ggc cgc gag cgc aag	1411
Asp Ala Ala Glu Arg Ala Leu Gly Glu Pro Glu Gly Arg Glu Arg Lys	
425 430 435	

aag atc gtt gag tgg aat gac atg gtg cgc cat gct cgt cca gaa tac 1459
 Lys Ile Val Glu Trp Asn Asp Met Val Arg His Ala Arg Pro Glu Tyr
 440 445 450

gac atc taaagtcgct taaagcctca aaa 1488
 Asp Ile
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<210> 616

<211> 455

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Ser Arg Pro Leu Arg Val Ala Val Val Gly Ala Gly Pro Ala Gly
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Ile Tyr Ala Ser Asp Leu Leu Met Lys Ser Asp Thr Asp Val Gln Ile
 20 25 30

Asp Leu Phe Glu Arg Met Pro Ala Pro Phe Gly Leu Ile Arg Tyr Gly
 35 40 45

Val Ala Pro Asp His Pro Arg Ile Lys Gly Ile Val Lys Ser Leu His
 50 55 60

Asn Val Met Asp Lys Glu Gln Leu Arg Phe Leu Gly Asn Ile Glu Val
 65 70 75 80

Gly Lys Asp Ile Thr Val Glu Glu Leu Arg Glu Phe Tyr Asp Ala Ile
 85 90 95

Val Phe Ser Thr Gly Ala Thr Gly Asp Gln Asp Leu Arg Val Pro Gly
 100 105 110

Ser Asp Leu Glu Gly Ser Trp Gly Ala Gly Glu Phe Val Gly Phe Tyr
 115 120 125

Asp Gly Asn Pro Asn Phe Glu Arg Asn Trp Asp Leu Ser Ala Glu Lys
 130 135 140

Val Ala Val Val Gly Val Gly Asn Val Ala Leu Asp Val Ala Arg Ile
 145 150 155 160

Leu Ala Lys Thr Gly Asp Glu Leu Leu Val Thr Glu Ile Pro Asp Asn
 165 170 175

Val Tyr Glu Ser Leu Ala Lys Asn Gln Ala Lys Glu Val His Val Phe
 180 185 190

Gly Arg Arg Gly Pro Ala Gln Ala Lys Phe Thr Pro Leu Glu Leu Lys
 195 200 205

Glu Leu Asp His Ser Asp Thr Ile Glu Val Ile Val Asn Pro Glu Asp
 210 215 220

Ile Asp Tyr Asp Ala Ala Ser Glu Gln Ala Arg Arg Asp Ser Lys Ser
 225 230 235 240

Gln Asp Leu Val Cys Gln Thr Leu Glu Ser Tyr Ala Met Arg Asp Pro

245										250					255				
Lys	Gly	Ala	Pro	His	Lys	Leu	Phe	Ile	His	Phe	Phe	Glu	Ser	Pro	Val				
			260					265					270						
Glu	Ile	Leu	Gly	Glu	Asp	Gly	Lys	Val	Val	Gly	Leu	Lys	Thr	Glu	Arg				
		275					280					285							
Thr	Gln	Leu	Asp	Gly	Asn	Gly	Gly	Val	Thr	Gly	Thr	Gly	Glu	Phe	Lys				
	290					295					300								
Thr	Trp	Asp	Met	Gln	Ser	Val	Tyr	Arg	Ala	Val	Gly	Tyr	Arg	Ser	Asp				
305					310					315					320				
Ala	Ile	Glu	Gly	Val	Pro	Phe	Asp	Asp	Glu	Arg	Ala	Val	Val	Pro	Asn				
				325					330					335					
Asp	Gly	Gly	His	Ile	Ile	Asp	Pro	Glu	Val	Gly	Ser	Pro	Ile	Thr	Gly				
			340					345					350						
Leu	Tyr	Ala	Thr	Gly	Trp	Ile	Lys	Arg	Gly	Pro	Ile	Gly	Leu	Ile	Gly				
		355				360						365							
Asn	Thr	Lys	Ser	Asp	Ala	Lys	Glu	Thr	Thr	Glu	Met	Leu	Leu	Ala	Asp				
	370					375					380								
His	Ala	Ala	Gly	Ser	Leu	Pro	Ala	Pro	Ala	Lys	Pro	Glu	Leu	Glu	Ser				
385					390					395					400				
Ile	Ile	Glu	Phe	Leu	Asp	Glu	Arg	Lys	Val	Ala	Phe	Thr	Thr	Trp	Asp				
			405					410						415					
Gly	Trp	His	Leu	Leu	Asp	Ala	Ala	Glu	Arg	Ala	Leu	Gly	Glu	Pro	Glu				
		420						425					430						
Gly	Arg	Glu	Arg	Lys	Lys	Ile	Val	Glu	Trp	Asn	Asp	Met	Val	Arg	His				
	435					440					445								
Ala	Arg	Pro	Glu	Tyr	Asp	Ile													
	450				455														

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 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 617
 ggaaacagta tgaccatg

18

<210> 618
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer